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MOLECULE TYPE: protein
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US-09-920-923B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-08-579-667-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDTLRYCYHVAGVVGLMMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 DDVLEYSYHVAGVVGWMARVMGVQDDAVLDRACDLGLAPQLTNIARDVIDDAAIGRCYL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PESWLEEEGLTKANYAAPENRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---ATVEGPVPSDALYSVIIRLLDAARPYASARQGIPHLPPRCAWSIAAA 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAVGSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 KQVYRKIGVKVEQAGKQAWDHRQSTSTAEKLTLLLTASGQAVTSRMKTYPPRPAHLWQRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
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44.7%; Score e86.5; LL 1.6e-67;

Best Local Similarity 48.7%; Pred. No. 1.6e-67;

Matches 146; Conservative 35; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION.
APPLICANT: Pasamontes, Luis
APPLICANT: Pasamontes, Luis
APPLICANT: Tsygamcov, Yuli
APPLICANT: Tsygamcov, Yuli
TILE OF INVENTION: Fermentaive Carotenoid Production
FILE REFERENCE: 15464 US (C38435/125944)
CURRENT APPLICATION NUMBER: US/09/920, 923B
CURRENT APPLICATION NUMBER: 08/980, 832
PRIOR FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 303
LENGTH: 303
LENGTH: 303
LYPE: PRT
ORGANISM: Plavobacterium sp. R1534
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
RILING DATE:
                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGBAT INDERMATION:
NAME: POKRAS, Bruce A.
REGISTRATION NUMBER: 32,746
REFERENCE/POCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
TELEPHONE: (201) 235-5801
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.09-920-923B-3
Sequence 3, Application US/09920923B
Patent No. 6677134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 303 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
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61 LEMKTRQAYAGSQMHE-----PAFAAFQEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTL 115
                                                                                                                                                                                                                      70 LRADTLAA-----IHEDGFMSPPFAALRQVARRHDFPDLWPWDLIBGFAMDVADRBYRSL 124
                                                                                                                                                                                                                                                                                            116 DDTLRYCYHVAGVVGLMMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYL 175
                                                                                                                                                                                                                                                                                                                      176 PESWIEEEGLIKANYAAPENROALSRIAGRLVREAEPYYVSSMAGLAOLPLRSAWAIATA 235
                                                                                                                                                                                                                                                                                                                                                                                                                          185 PADWLAEAG---ATVEGPVPSDALYSVIIRLLDAAEPYYASARQGLPHLPPRCAWSIAAA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 KQVYRKIGVKVEQAGKQAWDHRQSISIAEKLILLIASGQAVISRWKTYPPRPAHLWORP 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAVGSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQ 60
                                                                                                                                        12 IAQGSQSFAQAAKIMPPGIREDTVMLYAWCRHADDVIDGOVMGSAPEAGGD--PQARLGA 69
                                                   Gaps
                                                   15;
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APPLICANT: Hellmann, Gary M.
APPLICANT: Grill, Laurence K.
APPLICANT: Grill, Laurence K.
APPLICANT: Kunagai, Monto H.
APPLICANT: Della-Cioppa, Guy R.
TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN
ILITLE OF INVENTION: PHYTOENE BIOSYNTHESIS
NUMBER OF SEQUENCES: 19
  Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 410;
  ; Score 686.5; DB 4; Length 3; Pred. No. 1.6e-67; 35; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Virginia C. Bennett
STREET: 1211 East Morehead Street, PO Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/579,667
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 318.5; DB 1
Pred. No. 1.3e-26;
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STRET: 1211 L.
CITY: Charlotte
STATE: No. 5705624th Carolina
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ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFRENCE/POCKET NUMBER: 627-:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08579667
Patent No. 5705624
44.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.7%;
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amino acid
     Query Match
Best Local Similarity 48.78
Matches 146; Conservative
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INFORMATION FOR SEQ ID NO:
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                                                                          65 TRQAYAGSQMHEPAFAAFQEVAMAH--DIAPAYAFDHLBGFAMDVRETRYLTLDDTLRYC 122
                                                                                                                                                               182 LEDVFSG-RPFDWLDAALSDTVSQFPVDIQPFR--DMIEGMRMDLRKSRYRNFDELYLYC 238
                                                                                                                                                                                                                           YHVAGVVGLMMAQIMGVRDN-----ATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLP 176
                                                                                                                                                                                                                                                                      239 YYVAGTVGLMSVPIMGIAPDSKATTESVYNAALALGIANQLTNILRDVGEDARRGRVYLP 298
                                                                                                                                                                                                                                                                                                                    177 ESWLEEEGLTKANYAAPENROALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATAK 236
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                                             5 SKSPATASTLEDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQLEMK
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Gaps
19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fitzmaurice, Wayne P.
APPLICANT: Fitzmaurice, Wayne P.
APPLICANT: Fitzmaurice, Gary M.
APPLICANT: Grill, Laurence K.
APPLICANT: Kumagai, Monto H.
APPLICANT: Kumagai, Monto H.
APPLICANT: Kumagai, Monto H.
APPLICANT: Kumagai, Monto H.
APPLICANT: North Polita C. Bernett
TITLE OF INVENTION: PHYTOENE BIOSYNTHESIS
NUMBER OF SAUTHON: PHYTOENE BIOSYNTHESIS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Virginia C. Bennett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.6%; Score 315.5; DB 1; Length 410; 28.6%; Pred, No. 2.9e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                               359 LLYRQILDEIBANDYNNFTRRAYVSKPKKLISLPIAYAKSLVPPTRT 405
                                                                                                                                                                                                                                                                                                                                                                                                           237 QVYRKIGVKVEQAGKQAMDHRQSTSTAEKLTLLLTASGQAVTSRMKT 283
57; Mismatches 129; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRATION APPLICATION DATA:
APPLICATION NUMBER: US/08/579,667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57; Mismatches
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1211 East Morehead Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08579667
Patent No. 5705624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Charlotte
STATE: No. 5705624th Carolina
CGUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Bennett, Virginia C. REGISTRATION NUMBER: 37,092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 62
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 28.6
Matches 82; Conservative
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IS-08-579-667-2
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  Matches
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182 LEDVFSG-RPFDMLDAALSDTVSKFPVDIQPFR--DMIEGMRMDLRXSRYRNFDELYLYC 238
                                                                                                                                                                                                                                                                      299 ODELAHAGISDDDIFAGKVTDKWRSFMKKOIORARKFFDBAEEGVTOLSSASRWPVWASL 358
                                                                            65 TROAYAGSOMHEPARAAFQEVAMAH--DIAPAYAFDHLEGFAMDVRETRYLTLDDTLRYC 122
                                                                                                                                                                                                                              123 YHVAGVVGLAMAQIMGVRDNA-----TLDRACDIGLAFQLTNIARDIVDDAQVGRCYLP 176
                                                                                                                                                                                                                                                                                                                                                                               177 BSWLEEEGLTKANYAAPENRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATAK 236
130 AKTFYLGTWLMTPERRRAIWAIYVWCRRTDELVDGPN-----ASHITPQGLDRWSDL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 QVYRKIGVKVEQAGKQAMDHRQSTSTAEKLTLLLTASGQAVTSRMKŢ 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359 LLYRQILDEIBANDYNNFTKRAYVSKSKKLISLPIANAKSLVPPTRT 405
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completed: February 29, 2004, 14:55:04 as : 10.9949 secs

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                                           February 29, 2004, 14:26:38; Search time 34.9969 Seconds (without alignments) 2389.754 Million cell updates/sec
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                                                                                   1535
1. MAVGSKSFATASTLFDAKTR......VISRMKTYPPRPAHLWQRPI 296
                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                              Aaw99097 E Aaw93845 E Aaw70465 C Aaw16492 E Aaw10492 E Aaw10121 E Aaw00172 E Aaw50343 E Aaw30471 E Aaw3046516 I Aaw66516 I
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Aay44217
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                                                                                                                                               1586107
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                              stal number of hits satisfying chosen parameters:
                                                                                                                               1586107 segs, 282547505 residues
                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                   Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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genescq2003s: *
genescq2003bs: *
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Gapop 10.0 , Gapext
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length: 2000000000
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Match Length DB
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ALIGNMENTS

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Carotenoid, isopentenyl pyrophosphate; antheraxanthin, astaxanthin, diet; anti-oxidant; steroid; flavour; fragrance; electro-optic application; aquaculture; enzyme; phytoene synthase; CrtB.
                                                                                                                                                                                                      Pantoea stewartii phytoene synthase (CrtB) enzyme
AAE22315 standard; protein; 296 AA
                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 Pantoea stewartii
                                                                                                                                     25-JUL-2002
                                                                 AAE22315;
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WO200218617-A2.

04-SEP-2001; 2001WO-US027420

01-SEP-2000; 2000US-0229858P 01-SEP-2000; 2000US-0229907P

Koffas M, Miller ES, Dicosimo DJ, Rouviere PE; õ Brzostowicz PC, Cheng Q, Odom JM, Picataggio SK,

WPI; 2002-351711/38. N-PSDB; AAD35513.

Producing carotenoid compounds e.g. antheraxanthin and astaxanthin, by using microorganisms having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolize single carbon substrates

Claim 17; Page 144-145; 156pp; English

The invention relates to a method for producing carotenoid compounds. The method comprises a transformed metabolising host cell, comprising suitable levels of isopertenyl pyrophosphate and a nucleic acid molecule encoding an enzyme in the carotenoid biosynthetic pathway, under the control of regulatory sequences, and contacting the host cell with carbon substrate to produce a carotenoid compound. The method is useful for producing carotenoid compounds such as antheraxanthin and asteaxanthin, by using microorganism having a nucleic acid molecule encoding enzymes in

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the carotenoid biosynthetic pathway and which metabolise single carbon substrates. The carotenoids have potent anti-oxidant properties useful in diet, and aquaculture elements. The carotenoids are also useful as intermediates in the synthesis of steroids flavours and fragrances and compounds for potential electro-optic applications. The present sequence is Pantoea stewartii phytoene synthase (CTLB) enzyme used in the
                                                                                                                                                                                                                                                                    LEMKTRQAYAGSQMHEPAFAAFQEVAMAHDIAPAYAFDHLEGFAMDVRETRYETLDDFLR 120
                                                                                                                                                                                                                                                                                                          YCYHVAGVVGLMMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLPBSWL 180
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                                                                                                                                                                                                              1 MAVGSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQ 60
                                                                                                                                                                                               1 MAVGSKSFATASTLFDAKTRRSVIALYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQ
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                                                                                                                                       Score 1535; DB 5;
Pred. No. 1.7e-167;
Mismatches 0;
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larity 100.0%;
Conservative 0.
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N-PSDB; ABT14194.
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                                                                                                                                                    Similarity
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                                                                                                              Sequence 296 AA;
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hes 296;
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The invention comprises the amino acid and coding sequence of a number of carotenoid (crt)-related proteins. The crt-related DNA and protein

74pp; English

Claim 32; Page 64-65;

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sequences of the invention are useful for engineering cells which are able to produce carotenoids. The present amino acid sequence represents crt-related protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acid molecule isolated from Pantoea stewartii encom
carotenoid biosynthetic enzyme, useful for regulating carotenoid
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                                                                                             100.0%; Score 1535; DB 6;
100.0%; Pred. No. 1.7e-167;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 296; Conservative
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                                                                   Sequence 296 AA;
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carotenoid biosynthesis in an organism, by over-expressing (I) in an organism, such that the carotenoid biosynthesis is altered in the organism. (I) and the genes encoding (I) are useful for converting phytoene to the carotenoids, for creating recombinant organisms that have the ability to produce various carotenoid compounds, and also for enhancing or manipulating carotenoid compounds. (I) can also be used for producing gene products having enhanced or altered activity
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(KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO
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                                                                                                                                                                        Sequence 296 AA;
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10-MAR-1999
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adonixanthin-3'-glucosides. The specification also describes a method for the preparation of a carotenoid glycoside, in which all, or part of, carotenoid biosynthesis genes crf8, crt8, crt1, crt2, crt2, crtx, ortx, crtx, crtx, ortx, ortx, ortx, ortworted are introduced to a microbe or plant and expressed. The transformed organism is cultured and astaxanthin diglucosides, adonixanthin-3'-glucosides, and/or astaxanthin monoglucosides, adonixanthin-3'-carotenoid glucosides are used as food additives. (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   180
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                                                                                                                                                                                                                                                                                                                                                         61 LEMKTRQAYAGSQMHEPAFAAFQEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLR 120
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                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                          Length 296;
                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                          89.1%; Score 1368; DB 2;
88.9%; Pred. No. 2.8e-148;
iive 11; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erwinia uredovora crtB protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 11-12; 17pp; Japanese.
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                                                                                                                                                                                                        Query Match
Best Local Similarity 88.9°
Matches 263; Conservative
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N-PSDB; AAX19117.
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                                                                                                                                                                        Sequence 296 AA;
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(KIRI ) KIRIN BEER KK
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                                                                                          Similarity
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                                                        Sequence 309 AA;
                                                                                       Local Simi.
hes 263;
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                                                                                                                                                                                                                                                                                                                                                                                                                     AAR07467;
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Matches
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                                                                                                                                                                                                                                                         EHEGINKENYAAPENRQALSKIARRIVQEAEPYYLSATAGLAGLERSAMAIATAKQVYR 240
                                                                                                                                                                                               YCYHVAGVVGLMMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLPESWL 180
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                                                                                                                 1 MAVGSKSFATASKLFDAKTRRSVLMLYAWGRHCDDVIDDQTLGFQARQPALQTPEQRLMQ
                                                                                                                                                                   IEMKTRQAYAGSQMHEPAFAAFQEVAMAHDIAPAYAFDHLEGFAMDVREAQYSQLDDTIR
                                                                                                                                                                                                                                            EEEGLTKANYAAPENRQALSRIAGRIVREAEPYYVSSMAGLAQLPERSAWAIATAKQVYR
                                                                                                                                                   LEMKTRQAYAGSQMHEPAFAAFQEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLR
                                                                                                                                                                                                              YCYFVAGVVGLMMAQIMGVRDNATLDRACDLGLAFQLTNIARDI VDDAFAGRCYLPASWL
                                                                                                      MAVGSKSPATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQ
 S
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                                                                                                                                                                                                                                                                                                     Gaps
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invention. (Updated on 17-OCT-2003 to standardise
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                                                        Length 296;
                                                                             Indels
                                                      ;; Score 1368; DB 2;
;; Pred. No. 2.8e-148;
11; Mismatches 22;
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                                                       Similarity 88.9%; Similarity 88.9%; Si Conservative 1
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Best Local Simil
Matches 263; C
                                 Sequence 296
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25-JUN-1999
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    for prodn.
    etc.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an animal and expressed in said animal, an anti-carcinogenic promoter agent or a caneer cell growth inhibitor containing phytone, a cancer-preventive cosmetic material or a cosmetic consisting of phytone. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                               Length 309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carotenoid biosynthesis; vitamin A; cancer; food coloring
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                               89.1%; Score 1368; DB 2;
88.9%; Pred. No. 2.9e-148;
iive 11; Mismatches 22;
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Brwinia herbicola phytoene synthase (AAW16492) catalyses the biosynthesis of phytoene, a precursor of the red carotenoid lycopene, from geranylgeranyl pyrophosphate. Its expression in transgenic plant material can be utilised as a means of visually distinguishing such material from non-transgenic cells and tissues. Novel binary vector pEr0203 (ATCC 97282) includes an expression cassette comprising the tomato EB promoter (see also AAT66533), a plastid targetting signal (AAT66535) fused to the phytoene synthase gene (AAT6634), and a 3' non-translated region (AAT66536). Transgenic plant cells and tissues are identified by the appearance of orange colour. (Updated on 17-0CT-2003 to standardise OS
                                                                                                                                                                                             14 LEMKTRQAYAĞSQMHEPAFAAFQƏVAMAHDIAPAYAFDHLEGFPNDVREAQYSQLDDTLR 133
                      MAVGSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQ
                                             14 MAVGSKSFATASKLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFQARQPALQTPEQRLMQ
                                                                                              LEMKTRQAYAGSQMHBPAFAAFQEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLR
                                                                                                                                                                        YCYHVAGVVGLMMAQIMGVRDNATLDRACDIGLAFQLTNIARDIVDDAQVGRCYLPESWL
                                                                                                                                                                                                                                                      EEEGLIKANYAAPENRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWAIATAKQVYR
                                                                                                                                                                                                                                                                           EHEGINKENYAAPENRQALSKIARRIVQEAEPYYLSATAGLAGLPLRSAWALATAKQVYR
                                                                                                                                                                                                                                                                                                                              241 KIGVKVEQAGKQAWDHRQSTSTAEKLILLITASGQAVTSRMKTYPPRPAHLWQRPI 296
                                                                                                                                                                                                                                                                                                                                                 Visual identification of transgenic plant material - from production carotenoid pigment encoded by cassette containing Erwinia phytoene synthase gene, useful for selecting material for regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic plant; selectable marker; carotenoid; pigment;
phytoene synthase; lycopene; plasmid pBT0203.
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                                                                                                                                                                                                                                                                       YCYHVAGVVGLMMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLPESWL 180
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                                                                                                                                               1 MAVGSKSFATASKLFDAKTRRSVIMLYAWCRHCDDVIDDQTLGFQARQPALQTPEQRLMQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene useful for increase in carotenoid production - and preparation of carotenoid.
                                                                                                                 1 MAVGSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQO
                                                                                                                                                                                                                                                                                                                                                 EEEGLTKANYAAPENRQALSRIAGRLVREAEPYYVSSMAGLAQLPLRSAWALATAKQVYR
                                                                                                                                                                                                                                                                                                                                                                                                                               KIGVKVEQAGKQAWDHRQSTSTAEKLTLLLTASGQAVTSRMKTYPPRPAHLWQRPI 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 KIGVKVEQASQQAMDQRQSTTTPEKLTLLLAASGQALTSRWRAHPPRPAHLMQRPL 296
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HMG-CoA; 3-hydroxy-3-methylglutaryl coenzyme A reductase; crtB; carotenoid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.8%; Score 1363; DB 2; Length 309;
88.5%; Pred. No. 1.1e-147;
ive 11; Mismatches 23; Indels
                                       Length 296;
                                                                         23; Indels
                                    88.8%; Score 1363; DB 2;
88.5%; Pred. No. 1e-147;
ive 11; Mismatches 23;
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                                                                         Matches 262; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C. utilis crtB protein.
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N-PSDB; AAV73180.
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                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 309 AA;
Sequence 296 AA;
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16-JUL-1999
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Matches 262;
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                                  Query Match
Best Local (
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16-OCT-2003
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18-MAY-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coli cells to produce GSPP and the carotenoids phytoene through zeaxanthin diglucoside, which is the final prod. identified in the carotenoid pathway contd. in plasmid pARC376 (contg. a ca. 13 kb chromosomal DNA fragment isolated by Perry et al., J. Bacteriol., 168:607 (1986). The genes for geranylgeranyl pyrophosphate (GGPP) synthase, phytoene synthase, phytoene dehydrogenase-4H, lycopene cyclase, beta-carotene hydroxylase, and zeaxanthin glycosylase are represented in
                                                                                                                                                         EEEGLIKANYAAPENRQALSRIAGRLVREAEPYYVSSMAGLAQIPLRSAWALAIAKQVYR 240
                                                                             LEMKTRQAYAGSQMHEPAFAAFQEVAMAHDIAPAYAFDHIEGFAMDVRETRYLTLDDTLR 120
                                                                                      74 LRILILAAFEGAEMQDPAFAAPQEVALTHGITPRMALDHIDGFAMDVAQTRYVTFEDTIR 133
                                                                                                                    YCYHVAGVVGLMMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLPBSWL 180
                                                                                                                                 YCYHVAGVVGLMMARVMGVRDERVLDRACDLGLAFQLTNIARDIIDDAAIDRCYLPAEWL 193
                                                                                                                                                                     DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are a total of six relevant genes in a 7900 bp region that cause
                                       1 MAVGSKSFATASTLFDAKTRRSVEMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              using
                                                                                                                                                                                                           KIGVKVEQAGKQAMDHRQSTSTAEKLTLLLTASGQAVTSRMKTYPPRPAHLWQRPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biosynthesis of carotenoid(s) in genetically engineered hosts encoding enzymes from Erwinia herbicola.
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 DB 2; Length 309;
                   Indels
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  4e-109;
68;
                                                                                                                                                                                                                                                                                                                                                                 GGPP; carotenoid; phytoene; zeaxanthin; lycopene
                    36; Mismatches
 67.0%; Score 1028;
64.9%; Pred. No. 4e
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                                                                                                                                                                                                                                                                  AAR13983 standard; protein; 308
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90US-0052551.
90US-00562674.
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                    Conservative
                                                                                                                                                                                                                                                                                                        (revised)
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N-PSDB; AAQ13718.
         Best Local Similarity
Matches 192; Conserv
                                                                                                                                                                                                                                                                                                                                                Phytoene synthase.
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25-MAR-2003
26-NOV-1991
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28-FEB-1991;
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Yen HC;
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18-MAY-1990;
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  Query Match
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AAQ13716, AAQ13718, AAQ13719, AAQ13722, AAQ13724 and AAQ13726 respectively. Recombinant expression plasmids can be used to produce large ames. of the carotemoids which they synthesise. Carotemoids are pigments with a variety of applications. (Updated on 25-WAR-2003 to correct PP field.) (Updated on 25-WAR-2003 to correct PP Corp. (Updated on 25-WAR-2003 to correct PP Corp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LEMKTRQAYAGSQMHEPAFAAFQEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAVGSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPBQRLQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 EEEGLTKAMYAAPENRQALSRIAGRIVREAEPYYVSSMAGLAQUPLRSAWAIATAKQVYR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 308;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 65.0%; Score 997.5; DB 2; Best Local Similarity 63.9%; Pred. No. 1.3e-105; Matches 189; Conservative 36; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
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90US-00525551.
90US-00562674.
91US-0062921.
91US-00785566.
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(first entry)
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N-PSDB; AAT40791.
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 308 AA;
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28-FBB-1991;
30-OCT-1991;
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Increasing prodn. of total carotenoid(s) in a higher plant - by transforming with vector encoding chloroplast transit peptide operably linked to the Erwinia herbicola lycopene cyclase structural gene.
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Example 4; Fig 4; 99pp; English.

The present sequence is that of the Erwinia herbicola phytoene synthase which acts on geranylgeranyl pyrophosphate (GGPP) (produced by the action of GGPP) approphosphate and dependently layly pyrophosphate). GGPP is a 20-carbon atom precursor of phytoene, the first carotenoid in the carotenoid biosynthesis pathway. Production of total carotenoids in a plant can be increased by transforming the plant with DNA encoding enzymes involved in the biosynthesis pathway, in particular the lycopene syclass gene (AAT40795). Lycopene is prepared biosynthetically from phytoene through four sequential dehydrogenation reactions which can be carried out by a single dehydrogenase (AAT40793) in Erwinia sp. Beta-carotene is produced by the tobacco libulose bis-phosphate carboxylase-oxygenase gene (see AAT40794) is operatively linked in frame to the 5' end of the lycopene cyclase structural gene. This leads to increased production of total carotenoids in the chloroplast of transformed plants as compared to native, non-transformed plants of the same type. Beta-carotene is an effective and apparently harmless food colourant and is also in the pathway for biological synthesis of further C40 carotenoids such as zeaxanthin and zeaxanthin diglucoside. (Updated on 16-OCT-2003 to standardise OS field)

Sequence 308 AA;

120 180 240 133 YCYHVAGVVGIMMARVMGVRDERVLDRACDLGLAFQLTNMARDIIDDAAIDRCYLPABWL 193 9 73 1 MAVGSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQ 14 MANGSKSFATAAKLFDPATRRSVIMLYTWCRHCDDVIDDQTHGFASEAAAEEEATQRLAR LEMKTRQAYAGSQMHEPAFAAFQEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLR YCYHVAGVVGLMMAQIMGVRDNATLDRACDLGLAPQLTNIARDIVDDAQVGRCYLPBSWL 181 EEEGLTKANYAAPENRQALSRIAGRIVREAEPYYVSSMAGLAQIPLRSAWAIATAKOVYR 241 KIGVKVEQAGKQAWDHRQSTSTAEKLTLLLTASGQAVTSRMKTYPPRPAHLWQRPI 296 65.0%; Score 997.5; DB 2; Length 308; 63.9%; Pred. No. 1.3e-105; live 36; Mismatches 70; Indels 1 Matches 189; Conservative Best Local Similarity 63 74 Query Match

AAW00172 standard; protein; 308 AA SULT 12

120

73

133

240

(revised) (revised) 16-OCT-2003 25-MAR-2003 17-OCT-1996 AAW00172;

E. herbicola phytoene synthase encoded by pARC285.

(first entry)

E. herbicola, geranylgeranyl pyrophosphate synthase, pARC376, GGPP synthase, blosynthesis, carotenoid; lycopene; farnesyl pyrophosphate, phytoene; FPP, isopentyl pyrophosphate, IPP, tail to tail dimerisation; phytoene synthase; phytoene dehydrogenase-4H; food colourant; herbicide, norflurazon.

RESULT 13

This sequence represents Erwinia herbicola phytoene synthase encoded by plassing places. The plantage is an enzyme which is involved in the plosynthesis of carotenoids, esp. lycopene, from the ubiquitous of carotenoids, esp. lycopene, from the ubiquitous precursor, farnesyl pyrophosphate. In E. herbicola, phytoene has been found to be formed blosynthetically in a two-step process. The initial step is the condensation of farnesyl pyrophosphate (PPP) and isopentyl pyrophosphate. Lycopene is immediately followed by a tail to tail thy towns. Lycopene is produced from phytoene by the catalytic action of phytoene dehydrogenase. He lycopene commercial production of lycopene which is used as a food colourant. Commercial production of lycopene which is used as a food colourant. Planta transformed with the phytoene dehydrogenase. He coding sequence are protected from the herbicide norflunazon. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 16-OCT-2003 to standardise OS field) 14 MANGSKSFATAAKLFDPATRRSVLMLYTWCRHCDDVIDDOTHGFASEAAAEEEATQRLAR 61 LEMXTRQAYAGSQMHEPAFAAFQEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLR YCYHVAGVVGLMMAQIMGVRDNATLDRACDLGLAFQLFNIARDIVDDAQVGRCYLPESWL 181 BEEGLTKANYAAPENROALSRIAGRIVREAEPYYVSSMAGLAQLPLRSAWAFATAKQVYR 194 ODAGLAPENYAARENRPALARWR-RLIDAABPYYISSQAGLHDLRRRSAWAIATARSVYR 1 MAVGSKSFATASTLFDAKTRRSVL/MLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQ KIGVKVEÇAĞKQAWDHRQSTSTARKLTLLLTASGQAVTSRMKTYPPRPAHLWQRPI 296 DNA encoding Brwinia herbicola phytoene dehydrogenase-4H - used fo prodh. of lycopene, and to produce transgenic plants resistant to norflurazon. Length 308; Indels Proffitt J, Mukharji I, Yarger 65.0%; Score 997.5; DB 2; 63.9%; Pred. No. 1.3e-105; ive 36; Mismatches 70; Example 4; Fig 4; 87pp; English. 90US-00487613. 90US-0052551. 90US-00562674. 91US-00662921. 91US-00785568. 93US-00096043. Local Similarity 63.99 nes 189; Conservative Brinkhaus FL, Pantoea agglomerans. 1996-308824/31. N-PSDB; AAT37093 Sequence 308 AA; (STAD) AMOCO 22-JUL-1993; 30-OCT-1991; US5530189-A. 03-AUG-1990; 25-JUN-1996 121 74 241 Query Match Yen HB, Ausich F ઠે 임 à 쉱 δ 셤 ò 셤 ò

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us-09-941-947a-34.rag

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(revised)
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Best Local Similarity
Matches 189; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT91543.
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Brinkhaus Fi;
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21-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence encodes wild type phytoene synthase. Phytoene synthase is an enzyme which, along with geranylgeranyl pyrophosphate (GGPP) synthase (see also AAT4174.42), catalyse the formation of carotenoids, particularly phytoene. An N-terminal by truncated form of GGPP synthase which has the first thirteen amino acids replaced by four heterologous amino acids derived from the plasmid pARC306A was found to be about twice as the wild type enzyme. A C-terminal truncated protein was cound to have even higher activity and was cloned into plasmid pARC489D. The phytoene synthase coding sequences may be attached to the transit peptide coding sequence given in AFM4.744, for transport into tobacco chloroplasts. This allows the tobacco plants to produce high levels of phytoene for use in the treatment of skin disorders. (Updated on 25-MAR-2013) to correct PP field.) (Updated on 16-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transformed plants containing DNA encoding Erwinia herbicola enzymes - esp. geranyl:geranyl pyrophosphate synthase and phytoene synthase, allows large scale production of phytoene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                       Wild type; N-terminally truncated, geranylgeranyl pyrophosphate; GGPP; GGPP synthase; phytoene synthase; carotenoid; phytoene; pARC306A; pARC489D; transit peptide; tobacco; chloroplast; skin disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LEMKTRQAYAGSQMHEPAFAAFQEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAVGSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDGFLGFHADQPSSQMPEQRLQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 MANGSKSFATAAKLFDFATRRSVLALYTWCRHCDDVIDDQTHGFASBAAABEBATQRLAR
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63.9%; Pred. No. 1.3e-105;
ive 36; Mismatches 70;
                                             AAW00343 standard; protein; 308 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 4; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90US-00487613.
90US-00525551.
90US-00562674.
91US-00662921.
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                                                                                                                                                      (revised)
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es 189; Conserv
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                                                                                                                                                                                                                                                               Phytoene synthase.
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28-FEB-1991;
30-OCT-1991;
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25-MAR-2003
10-DEC-1996
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18-MAY-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding Erwinia herbicola lycopene cyclase - for producing recombinant enzyme, and transgenic organisms with increased beta-carotene
EEEGLIKANYAAPENROALSRIAGRIVREASPYYVSSMAGLAQIPLRSAWAIATAKQVYR 240
                                 DNA molecule has been isolated which encodes an Brwinia herbicola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pyrophosphate synthase; Erwinia herbicola; GGPP;
se; recombinant enzyme; transgenic organism; beta-carotene;
                                                                                                                                                      241 KIGVKVEQAGKQAWDHRQSTSTAEKLTLLLTASGQAVTSRMKTYPPRPAHLWQRPI 296
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63.9%; Pred. No. 1.3e-105;
ive 36; Mismatches 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Erwinia herbicola phytoene synthase.
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yeast; plant; vitamin A; cancer.
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90US-00562674.
91US-00662921.
93US-00095726.
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                                                                                                                                                                       MAVGSKSFATASTLFDAKTRRSVLMLYAWCRHCDDVIDDQTLGFHADQPSSQMPEQRLQQ 60
                                  73
                    OBAGLAPENYAARENRPALARWR-RIDDAAEPYISSQAGLHDLRRRSAWAIATARSVYR
                                                                      LEMKTROAYAGSOMHEPAFAAFQEVAMAHDIAPAYAFDHLEGFAMDVRETRYLTLDDTLR
                                                                                                                                                YCYHVAGVVGLMMAQIMGVRDNATLDRACDLGLAFQLTNIARDIVDDAQVGRCYLPESWL
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M70124

ABM70124 standard; protein; 309 AA. ABM70124; Photorhabdus luminescens protein seguence #3221

(first entry)

20-NOV-2003

detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague; Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; whooping cough.

Photorhabdus luminescens

WO200294867-A2

28-NOV-2002

07-FEB-2002; 2002WO-IB003040

07-FEB-2001; 2001FR-00001659

(INSP) INST PASTEUR. (CNRS) CNRS CENT NAT RECH SCI

Danchin A; Kunst F, Frangeul L, Glaser P, Duchaud E, Taourit S, Buchrieser C; Genomic sequence of Photorhabdus luminescens and encoded polypeptides useful e.g. as therapeutic antimicrobials and agricultural pesticides

WPI; 2003-148459/14.

Claim 2; SEQ ID NO 3221; 1205pp; French.

The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. luminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and

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               genes, proteins, vectors containing the genes and Ab are also useful therapeutically (to treat microbial infection by bacteria or fungi that are sensitive to P. luminescens-encoded toxins or antibiotics) and as biopesticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of funan diseases for which P. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
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antibacterials useful as insecticides, bactericides and fungicides.
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Q93164 paracoccus
G91764 flavobacte
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AC	08GCS1;						
늄	01-MAR-2003	(TrEMBLrel.	rel.	23,	Created)		
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3	CRII.						
SO	Pantoea stewartii.	rartii.					
8	Bacteria; Pi	roteobac	teria	ن ت	Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,	a; Enteropac	teriales;
8	Enterobacteriaceae;	riaceae;	Pantoea	oea.			
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	a	stewartii.		
	Bacteria; Pr	oteobacteria, Ga	mmaproteo	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
	Enterobacteriaceae; NCBI TaxID=66269;	laceae; Pantoea. 6269;		
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	SEQUENCE FROM N.A.	M.A.		
	desoura M L	Kollmann S.R.	Schroede	33 1-
	"Carotenoid	"Carotenoid Biosynthesis (WO 02/079395 A2).";	02/07939	5 A2).";
	Submitted (C	Submitted (OCT-2002) to the EMBL/GenBank/DDBJ	EMBL/GenB	ank/DDBJ databases.
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	GO, GO: 00061	18; P:electron t	ransport;	IEA.
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	InterPro, IF	R008150; Bac_phy	toene_dh.	
	Pfam; PF0159	3; Amino oxidase	-i '	
	PROSITE; FS0 SEQUENCE 4	2500982; PHITOENE DH; 1 492 AA; 54836 MW; F	н; т. , РЭDCD2	L. P3DCD224547ASFBA CRC64;
á	Query Match	100.08;		Score 2606; DB 2; Length 492;
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Σ	tches 492;	Conservative	0; Mismatches	tches u; indeis u; caps
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SAIEBLFALAGKQLKDYVELLPVTPFYRLCWESGKVFNYDNDQAQLEAQIQQFNPRDVAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Protecobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
NCBI_TaxID=549;
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TO K.Y., Lai E.M., Lee L.Y., Lin T.P., Hung C.H., Chen C.L.,
Chang Y.S., Liu S.T.;
Analysis of the gene cluster encoding carotenoid biosynthesis
Erwinia herbicola Bhol3.";
Microbiology 140:331-339(1994).
EMBL, M90689; AAAX1263.1;
PIR, S52586; S52586.
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GO; GO:0009058; P:biosynthesis; IEA.
GO; GO:0009058; P:biosynthesis; IEA.
InterPro; IPR002937; Amino oxidase.
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Fram; PF01593; Amino oxidase; I.
Prodom; PD139017; Phytn dehydro;
PROSTIE; PS00982; PHYTOENE DH; 1.
ERQUENCE 492 AA; 55010 WH; 2D65E1A2A32D0635 CRC64;
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01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2003 (TrEMBLrel. 24,
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                                                                                                                      9
                                                                                                                                                               Famiunten H., Hirata R.;

*Isolation and characterization of carotenoid biosynthesis genes from Pantoa agglomerans pv. milletiae Wist 801.";

*Submitted (DEC-2001) to the EWBL/GenBank/DDBJ databases.

*EWBL; AB076662; BAB79603.1; -.

*GO; GO:0009056; P:Diosynthesis; IEA.

*GO; GO:0009056; P:Diosynthesis; IEA.

*GO; GO:00018; P:electron transport; IEA.

*InterPro; IPR008151; Amino oxidase.

InterPro; IPR008151; Phytocene_dh.

*InterPro; IPR008151; Phyt
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                                                                                                                  1 MKPTTVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITDP
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
MCBI TaxID=182454;
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Pred. No. 3.2e-178;
                                        Indels
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Pred. No. 7.9e-191;
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                                            14; Mismatches
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ProDom; PD13017; Phytn dehydro; 1.
PROSITE; PS00982; PHYTORNE DH; 1.
SEQUENCE 492 AA; 54802 MW; C9EE
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88.0%;
            93.78;
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                                                Matches 461; Conservative
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SEQUENCE FROM N.A.
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241 NARVSHMETVGDKIQAVQLEDGRRPETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQSK 300
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                                                                                                                                                        62 AIBELFALAGKQLKDYVELLPVTPFYRLCWESGKVFNYDNDQAQLEAQIQQFNPRDVAGY
                                                                                                                                                                                                                                                                                                                                 RAPLDYSRAVENEGYLKI, GTVPFILSFKDMI, RAAPQLAKI, QAWRSVYSKVAGYI EDEHLIRO
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                                                                                                                       KPTTVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITDPS
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                      Length 506;
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Hyphomicrobiaceae; Xanthobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        National R.A., Metcalf W.W., Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF40848; AAL02000.1, ...

GO; GO:0016491; P:oxidoreductase activity; IEA.

GO; GO:0009058; P:biosynthesis; IEA.

GO; GO:0009058; P:biosynthesis; IEA.

InterPro; IPR002917; Amino oxidase.

InterPro; IPR008150; Amino oxidase.

InterPro; IPR008151; Phytn dehydro.

ProDom; PD139017; Phytn dehydro.

ProDom; PD139017; Phytn dehydro.

PROSITE; PS00982; PHYTOENE DH; 1.
                                                                     Indels
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01-DBC-2001 (TrEMBLrel. 19, Created)
01-DBC-2001 (TrEMBLrel. 19, Last sequence update)
01-UDN-2003 (TrEMBLrel. 24, Last annotation update)
Phytoene dehydrogenase.
                      DB 2;
                Score 1749.5; DB 2; Pred. No. 1.4e-133; 55; Mismatches 102;
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                   67.1%;
67.8%;
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                Query Match
Best Local Similarity 67.8%
Matches 332; Conservative
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KATARVILED 498
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                                                                                1 MARTTVIGAGEGGLALAIRLQASGVPTRLLEQRDKPGGRAYVYQDQGFTFDAGPTVITDP
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J. Bacteriol. 182:3850-3853(2000).
EMBL; AP218415; AAF78201.1; -.
GO; GO:0005491; F. RAF78201.1; -.
GO; GO:000558; P. Diosynthesis; IEA.
GO; GO:000558; P. Diosynthesis; IEA.
GO; GO:000518; P. Diosynthesis; IEA.
InterPro; IPR002037; Amino oxidase.
InterPro; IPR008151; Phytn dehydro.
Pfam; PF01593; Amino_oxidase: 1.
PROSITE; PS00592; PHYTOENE DH; 1.
PROSITE; PS00592; PHYTOENE DH; 1.
                                                 1 MKPTTVIGAGEGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITDP
Gaps
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Bradyrhizobiaceae, Bradyrhizobium,
Indels
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Last annotation update)
33;
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Mismatches
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01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2003 (TrEMBLrel. 24,
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CRTI.
Bradyrhizobium sp. ORS278.
Conservative
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63.5%; Pred. No. 1.2e-123;
tive 58; Mismatches 121;
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   Best Local Similarity 63.59
Matches 311; Conservative
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489 ATAQVMLSDL 498
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CRII.
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249 TSPVDEIVVEGQRATAVYCLKSGETLPFDLVASNADVVHTYRHLLRGAARGRSEGARLAKT 308
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IRRAAVIGSGFGGLSLAIRLQAAGIRTTVFEQRDKPGGRAYVYEQDGFTFDGGPTVITDP 68
                                                                                                         1 MKPTTVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITDP 60
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                                           Gaps
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Rhodobacteraceae; Paracoccus.
NCBI_TaxID=59779;
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EMBL; Y15112; CAB56062.1; -
G G) GO:0016491; P:oxidoreductase activity; IEA.
GO; GO:0016491; P:oxidoreductase activity; IEA.
GO; GO:000518; P:biosynthesis; IEA.
GO; GO:000518; P:electron transport; IEA.
InterPro; IPR002150; Amino_oxidase.
InterPro; IPR003150; Bac_phytoene_dh.
InterPro; IPR003150; Bac_phytoene_dh.
InterPro; IPR003151; Phytn_dehydro.
Pfam; PF01593; Amino_oxidase; 1.
ProDom; PP0139017; Phytn_dehydro; 1.
PROSITE; PS00982; PHYTOENE DH; 1.
SEQUENCE 501 AA; 55109 WW; FOFAAED92A0E8D16 CRC64;
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       66.0%; Pred. No. 1.3e-130;
tive 56; Mismatches 111; Indels
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                                           Matches 324; Conservative
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                                               2 KPTTVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITDPS
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Pasamontes L., Hug D., Tessier M., Hohmann H.P., Schierle J.,
van Loon A.P.;
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Flavobacteriaceae; Flavobacterium.
NCBI_TaxID=50286;
Indels
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                                                                                                                            6 VIGAGEGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITDPSAIEE
                                                                                                                                                  278 QVHTQGTKATEVETKSGWKERPDAVCSNADIMHSYKELLGESDRGRKYAKSLARKSYSPS
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                                                              54.3%; Score 1415; DB 2; Length 5 55.1%; Pred. No. 2.4e-106; ive 77; Mismatches 141; Indels
ProDom; PD139017; Phytn dehydro; 1.
PROSITE; PS00982; PHYTOENE DH; 1.
SEQUENCE 526 AA; 58469 WW; 668B6F366F652232 CRC64;
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MEDLINE=94132007; PubMed=8300574;
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                                                                                               268; Conservative
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                                                                                 Similarity
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NCBI_TaxID=28068;
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                                                                                                                                                                                                          YRAFLDYSRAVFNEGYLKLGTVPPLSFKDMLRAAPQLAKLQAWRSVYSKVAGYIEDEHLR 180
                                                                                                                                                                                                                                                                                                                                      NARVSHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQSK 300
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                                                Gaps
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MBDLINE=7711406; PubMed=9168123;
MATSUMMARA H., Flusakabe E., Burgess J.G., Matsumaga T.;
"Cloning, sequencing and expression the carotenoid biosynthesis gene, lycopene cyclase and phytocene desaturase, from the aerobic photosynthetic bacterium Erythrobacter longus sp.strain Och 101 in Escherichia Coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0TL-1997 (TrEMBirel. 04, Created)
01-0TL-1997 (TrEMBirel. 04, Last sequence update)
01-0TL-1997 (TrEMBirel. 24, Last sequence update)
01-0TL-2003 (TrEMBirel. 24, Last annotation update)
Phytome desaturase.
CRTI
Exrthrobacter longus.
Barteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
                                              Ö
                 Length 494;
                                              122; Indels
          tch 61.2%; Score 1595; DB 2; al Similarity 61.9%; Pred. No. 4.9e-121; 304; Conservative 65; Mismatches 122;
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EMBL; D83514; BAA20276.1; -. Gene 189:166-174(1997).

GO; GO:0016491; Foroxidoreductase activity; IEA. GO; GO:0009058; P:biosynthesis; IEA. GO; GO:000918; P:biosynthesis; IEA. GO; GO:0006118; P:electron transport; IEA. InterPro; IPR002137; Amino oxidase.

InterPro; IPR008150; Bac_phytoene_dh.
InterPro; IPR008151; Phytn_dehydro.
Pfam; PF01593; Amino_oxidase; 1.
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          Query Match
Best Local S:
Matches 304
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Nagashima K.V., Matsuura K., Ohyama S., Shimada K., matsuuture and transcription of genes encoding B870 and photosynthetic reaction center apoproteins from Rubrivivax
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Nagasabhaa K.V., Shimada K., Matsuura K.;
Phylogenetic analysis of photosynthetic genes of Rhodocyclus gelatinosus: Possibility of horizontal gene transfer in purple
                                                                                                                                                                                                                  Rhodocyclus gelatinosus (Rhodopseudomonas gelatinosa).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Comamonadaceae; Rubrivivax.
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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STRAIN=S1;
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323 LFVWYEGIDRRYEDVPHHMWVLGPRYRELLDDIFRKKKLASDFSIYLHRPTATDPSMAPA 382
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mechanisms and effects (Proceedings of the 11th international congress
on photosynthesis), pp.4:2889-2892, Kluwer Academic Publishers,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Dark aerobic growth conditions induce the synthesis of a high midpoint potential cytochrome c8 in the photosynthetic bacterium Rubrivivax gelatinosus.";
Biochemistry 38:15218-15244(1999),
EMBL; ABO34704; BAA344063.1;
PIR; T50916; TS0910.
                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=11144;
MEDLINE=20031519; PubMed=10563807;
Menin L., Yoshida M., Jaquinod M., Nagashima K.V., Matsuura K.
Parot P., Vermeglio A.;
Parot P., Vermeglio A.;
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                                                                                                                                       Igarashi N., Shimada K., Matsuura K., Nagashima K.V.;
"Photosynthetic gene cluster in purple bacterium, Rubrivivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO: GO: 0016491; F: extidoreductase activity; IBA. GO: GO: 00049018; P: Diosynthesis; IBA. GO: GO: 0004118; P: Diosynthesis; IBA. GO: GO: 0004118; P: Diosynthesis; IBA. GO: GO: 0004118; P: Diectron transport; IEA. InterPro: IPR008129; Amino oxidase. InterPro: IPR00815; Bac_phytoene_dh. InterPro: IPR00815; Phytn dehydro. Fam: PP0159; Amino oxidase; 1. ProDom; PP0159; Amino oxidase; 1. ProDom; PP019017; Phytn dehydro. PROSITE; PS09082; PHYTGENE DH; 1. SEQUENCE 511 AA; 56818 MW; 9E64897196033903 CRC64;
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42.2%; Score 1099.5; DB 2; Length
Best Local Similarity 42.3%; Pred. No. 1e-80;
Matches 204; Conservative 100; Mismatches 177; Indels
gelatinosus.";
J. Biol. Chem. 269:2477-2484(1994).
                                                                                                                                                                                            gelatinosus.";
(In) Garab G. (eds.);
                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 DYSRAVFNEGYLKIGTVPFLSFKDMLRAAPOLAKIOAWRSVYSKVAGYIEDEHLROAFSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 QSLLIGGNPFSVTSMYALVNALERQWGVHWAMGGTGELIRGLVDVFBGMGGTMRLKAEVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPVLYFGLNHHHDQLAHHTVCFGPRYRELIHBIFNHDGLAEDFSLYLHAPCVTDPSLAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGSYYVLAPVPHLGTANLDWAVEGPRIRDRIFDYLEQHYMPGLRSQLVTHRMFTPFDFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;;
T
                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhodocyclus gelatinosus (Rhodopseudomonas gelatinosa).
Bacteria, Proteobacteria, Betaproteobacteria; Burkholderiales,
Comamonadaceae; Rubrivivax.
NCBI_TaxID=28068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouchane S., Steunou A.-S., Astier C., Photosynthesis Gene Regulation in Rubrivivax gelatinosus:
Transcription Factor PpsR is Involved in both Negative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AY23438, AA093135.1; --
GO, GO:0006491; F:oxidoreductase activity; IEA.
GO; GO:0006491; F:oxidoreductase activity; IEA.
GO; GO:000618; P:electron transport; IEA.
InterPro; IPR002937; Amino oxidase.
InterPro; IPR008150; Bac phytoene_dh.
InterPro; IPR008151; Phytn_dehydro.
IPfam; PP01593; Amino oxidase; 1.
ProDom; P201593; Amino oxidase; 1.
ProDom; P201593; Phytnadehydro.
IPfam; PP01593; Phytnadehydro.
IPfam; PP01593; Phytnadehydro.
IPfam; PP01593; Phytnadehydro.
IPfam; PF01593; Phytnadehydro.
IPfam; PF01593; Phytnadehydro; 1.
IPROSITE; PS00982; PHYTOENE DH; 1.
SEQUENCE 513 AA; 57074 WW; 9C46447BB02F682D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
42.0%; Score 1093.5; DB 2; Length
Best Local Similarity 42.1%; Pred. No. 3.2e-80;
Matches 203; Conservative 101; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases EMBL; AY234385; AAO93135.1; -.
                                                                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                      513 AA
                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                            Phytoene dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
486 EW 487
                                                             503
                              502 VL
                                                                                                                                                                                                                                                                                                           01-JUN-2003
01-OCT-2003
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326 CFGPRYRELIHEIFNHDGLAEDFSLYLHAPCVTDPSLAPEGCGSYYVLAPVPHLGTANLD 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77; Mismatches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        environmental samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 22, (TrEMBLrel. 22, 1 (TrEMBLrel. 25, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uncultured proteobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
NCBI_TaxID=153809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 415:630-633(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phytoene dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2002 (01-0CT-2002 (01-0CT-2003 (01-0C
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                                                                                                                                                                                                                               386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8KZ28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
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HRILSYKGAGFGLEPLLLQSAYFRPHNRSEDVKNLFMVGASTHPGAGVPGVIMSAKALES 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 GKVFNYDNDQAQLBAQIQQFNPRDVAGYRAFLDYSRAVFNEGYLKLGTVPFLSFKDMLRA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 APQLAKLOAWRSVYSKVAGYIEDEHLRQAFSFHSLLVGGNPFATSSIYTLIHALEREWGV 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 LVASNGDWANTY--LKRVRPSARLVNSDLRVKAASESMSLLVVYFGFRGGDDLPLKHHNI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPTTVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQ-EQGFTFDAGPTVITDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SAIBELFA--------LAGKQLKD-----YVELLPVTPFYRLCWES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 WFPRGGTGALVNGMIKLFQDLGGEVVLNARVSHMETVGD-----KIQAVQLEDGRRFETC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAINER! ARCC 13939 / DSM 20539 / NCIB 9279;
STRAINER! ARCC 13939 / DSM 20539 / NCIB 9279;
Milto O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W. Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makazrova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Feraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.3%; Score 1051; DB 16; Length 548; Larity 43.5%; Pred. No. 1e-76; Conservative 72; Mismatches 185; Indels 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome Sequence of the radioresistant bacterium Deinococcus radiodurans R1.", Science 286:1571-1577(1999).
EMBL: AR01940; AR2410439.1; -. PIR; C75466; C75466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OSRNOB;

OJ-MAY-2000 (TrEMBLrel. 13, Created)

OJ-MAY-2000 (TrEMBLrel. 13, Last sequence update)

OJ-MAY-2000 (TrEMBLrel. 13, Last sequence update)

OJ-JUN-2003 (TrEMBLrel. 24, Last annotation update)

Phytocene dehydrogenase.

DROB61.

DROB61.

Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcacee, binococcacee; Dinococcacee; Dinoc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR002937; Amino oxidase.
Interpro; IPR008191; Phyrin dehydro.
Pfam: PP01593; Amino oxidase; I
ProDom; PD139017; Phytn dehydro; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al Similarity
229; Conserv
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VL 505
                                                                                                    486 IM 487
     444
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Matches
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375 LLGPRYEALLSEIFGTKRLGEDFSOYLHVPTLTDPALAPAGHHAAYTLVPVPHNG-SGID 433
                                                            WAVEGPRIRDRIFDYLEQH-YMPGLRSQLVTHRMFTPFDFRDELNAWQGSAFSVEPILTQ 444
                                                                                                                         434 WDVEGPKLARAALADIERRGLIPGLRERLTHFEFTTPDYFAGTLDSYLGNAFGPEPRLVQ 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MBDLINE-21822632; PubMed-11832943; Beja O, Suzuki MT., Heldelberg J.F., Nelson W.C., Preston C.M., Hamada T., Eisen J.A., Fraear C.M., DeLong E.F.; "Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 LWAACGRDFHADVDIRPLBPFYEIRWPDGSYFRASGDDEKMOSEVORLNPADLPGYKRFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 LFALAGKOLKDYVELLPVTPFYRLCWESGKVPNYDNDQAQLEAQIQQFNPRDVAGYRAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 DYSRAVPNEGYLKLGTVPPLSPKOMIRAAPQLAKLQAWRSVYSKVAGYIEDEHLRQAFSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 HSLLVGGNPPATSSIYTLIHALEREWGVWFPRGGTGALVNGMIKLFQDLGGEVVINARVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 HMETVGDKI-----QAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 HONAVADELLIKNGAAQAVALTDGQRFDAPLIVSNADAGHTYDHLLRNHSRRRWTTGKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 VIGAGFGGLALAIRLQAAGIPVALLLEORDKPGGRAYVYQEQGFTFDAGPTVITDPSAIBE
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                                                                                                                                                                                            445 SAWFRPHNRDKHIDNLYLVGAGTHPGAGIPGVIGSAKATAGLMLED 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMB1, AR008921, AAM48646.1; ...

EMB1, AR008921, AAM48646.1; ...

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:0009088; P:bliosynthesis; IEA.

GO; GO:0006189; P:electron transport; IEA.

InterPro; IPR002937; Amino oxidase.

InterPro; IPR008151; Phytn dehydro.

FEAN; PODIS93; Amino oxidase; 1.

ProDom; PD199017; Phytn dehydro.

PROSURE: PROSURE DH; 1.
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304 POKLNSMBYTCGAFMLYLGVNRRYDNLHLHNIYFTFDYKXSMDELFTRQQLPQDPAMYVY 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16; Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Firmicutes; Bacillales; Bacillaceae; Oceanobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
27.1%; Score 706.5; DB 16; Length
Best Local Similarity 33.2%; Pred. No. 9.6e-49;
Matches 170; Conservative 91; Mismatches 212; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phytoene dehydrogenase (phytone desaturase) (EC 1.3.-).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    511 AA
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STRAIN=FIRES1 / JCM 11309;
STRAIN=2222075, PubMed=1223536;
Takami H., Fakaki Y., Uchiyama I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 30:3927-3935(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                            PGVIGSAKATAGLALED 490
                                                                                                                                                                                                                                                                                                                           PVVLVCGKLVSEQVLAD 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 YFKDLGRNIEDYLDLVRVNPCYHLHFTDGTCMKPSIDLKELLDBIRSFNPDDVDGYLRYL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LFALAGKOLKDYVELLPVTPFYRLCWESGKVFNYDNDQAQLEAQIQQFNPRDVAGYRAFL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----DYSRAVPNEGYLKLGTVPFLSFK-DMLRAAPQLAKLQAWRSVYSKVAGYIEDE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 HLRQAFSFHSLLVGGNPPATSSIYTLI----HALEREWGVWFPRGGTGALVNGMIKLFQD 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGGEVVILNARVSHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQ 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 AKKLQSKRMSNSLFVLYFGLNHHHDQLAHHTVCFGPRYRELIHBIFNHDGLAEDFSLYLH 353
6 VIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITDPSAIEE
                                                                                                    THRMFTPPDFRDELNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVGAGTHPGAGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heliobacillus mobilis.
Bacteria; Firmicutes; Clostridia; Clostridiales; Heliobacteriaceae;
Heliobacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 28.9%; Score 752; DB 2; Length 51 Best Local Similarity 34.2%; Pred. No. 2e-52; Matches 170; Conservative 91; Mismatches 214; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                           517 AA
                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diapophytoene dehydrogenase
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GVISSAEVLSKLV 499
                                                                                                                                                                                                  GVIGSAKATAGLM 487
                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 LYRZVFELTGRNPDDYIPMERIDPMYNVFRGNTPEDRYQISSDLIQLIDEIEAISDKDAA
354 APCVTDPSLAPEGCGSYYVLAPVPHLGTANLDWAVEGPRLRDRIFDYLEQHYMPGLRSQL
                                                   364 RPTKYDDSVAPPGKDIIYVLVPVPNNL-SSGIDWKKETHRYRELVIKKLERQGVTDLSKHI
                                                                                                                                                              VIHRMFTPPDFRDELNAWQGSAFSVRPILTQSAWFRPHNRDKHIDNLYLVGAGTHPGAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 AIEELFALAGKOLKDYVELLPVTPFYRLCWESGKVFNY--DNDQAOLEAQIQQFNPRDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 GYRAFLD--YSRAVFNEGYLKLGTVPFLSFKDMLRAAPQLAKLQ-----AWRSVYSKVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 GEITYLINKIYOR-------FOLAKDHFIORPFRHPWOFFTPKTLWNGLKLRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 G-----YIEDEHLRQAFSFHSLLVGGNPFATSSIYTLIHALEREWGVWFPRGGTGAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 KPTTVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITDPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 VNGMIKLFQDLGGEVVINARVSHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takami H., Takaki Y., Uchiyama I.; "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme
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289 IQDIKAKGKYTDEKIDKWKYSCSCFIMYLGANKKYDEVSNVHNFPFSENLKETMDDIFTG 348
                                                                                                                                                                                342 DGLAEDFSLYTHAPCVYDPSLAPEGCGSYYVLAPVPHLGYANLDWAVEG-PRLRDRIFDY 400
                                                                                                                                                                                                                                                   | || :::|:
349 KRL-EDPAFYTYIGSKXDPSLAPEGKDGIYVLVPVSDLSTAQYSWGDETIAYYREKVFEK 407
                                                                                                                                                                                                                                                                                                                                                                                                           LEQ-HYMPGLRSQLVTHRMFTPFDFRDELNAWQGSAFSVEPILTQSAMFRPHNRDKHIDN 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 RAFLDYSRAVFNEGYLKLGTVPFLSFKDMLRAAPQL---AK-LQAWRSVYSKVAGYIEDE 177
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EMBL, BX294151; CAD78796.1; -.
Oxidoreductase; Complete proteome.
SEQUENCE 537 AA; 60136 MW; Al6C389C746949B6 CRC64;
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Oy 414 VTHRMFTPPDFRDELNAWQGSAFSVEPILITQSAWFRPHNRDKHIDNLYLVGAGTHPGAGI 473

Db 436 RVEHQITPDDWQSDYSIYKGATFNLAKNLGQMLHKRPRNRFBELDGVYLVGGGTHPGSGL 495

OY 474 PGVIGSAKATAGIMLEDL 491

Db 496 PVIYESSRISSRILLQDL 513

Search completed: February 29, 2004, 14:51:01

Job time : 43.4556 secs
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377 NAGVIDPILAPACHSSLYVLVPVTH-DIENVDWSKEAAGFRELTIDKLGELGLIDVRDRI 435

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1 MKPTTVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEGGFTFDAGPTVITDP
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 MKPTTVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYEDQGFTFDAGPTVITDP
                                                                                                  121 YROFLDYSRAVFKEGYLKLGTVPPLSFRDMLRAAPOLAKLOAMRSVYSKVASYIBDEHLR
                                                                                                                                                                                                   NARVSHMETVGDKI QAVQLBDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKGLQSK
                                                                                                                                                                                                                                                                                                                                  SLAPEGCGSYYVLAPVPHLGTANLDWTVEGPKLRDRIFAYLEQHYMPGLRSQLVTHRMFT
                                                                                                                                                                                                                                                                                                                                                                        PFDFRDELNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVGAGTHPGAGIPGVIGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=10088634; PubMed=2263648; Arstrong G.A., Alberti M., Hearst J.E.; Arstrong G.A., Alberti M., Hearst J.E.; Arstrong G.A., Alberti M., Hearst J.E.; and processives mediate the early reactions of carotenoid biosynchesis in nonphorosynthetic and photosynthetic proxaryotes."; Proc. Natl. Acad. Sci. U.S.A. 87:9975-9978 (1990)
-!- FINCTION: This enzyme converts phytocene into lycopene via the intermediaries of phytofluene, zeta-carotene and neurosporene by the introduction of four double bonds.
-!- COFACTOR: FAD (Probable)
-!- PATHWAY: Carotenoid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1991 (Rel. 19, Created)
1-AUG-1991 (Rel. 19, Last sequence update)
28-FBB-2003 (Rel. 4), Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase)
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EMBL; M87280; AAA64981.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SAIEELFALAGKOLKDYVELLPVTPFYRLCWESGKYFNYDNDQAQLEAQIQQFNPRDVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NARVSHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 SLAPPGCASFYVLAPVPHIGNAPLDWAQBGPKLRDRIFDYLSERYWPGLRSQLVTQRIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 PFDFRDELNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVGAGTHPGAGIPGVIGSA
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                                                                                                                                                                          NAD
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Misawa N., Satomi Y., Kondo K., Yokoyama A., Kajiwara S., Saito
Ohtani T., Miki W.;
                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                492;
                                                                                                                                                                          FAD; Flavoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
1-OCT-19996 (Rel. 34, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99..) (Phytoene desaturase)
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Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium.
WCBI_TaxID=44155;
                                                                                                                                                                                                                                                                                77.6%; Score 2023; DB 1; Length 4 76.8%; Pred. No. 1.8e-156; tive 42; Mismatches 72; Indels
                                                                                                                                                                                                AD (ADP PART) (POTENTIAL) REDCSDB1562083F2 CRC64;
interPro; IPR002937; Amino oxidase.
InterPro; IPR008150; Bac_phytoene_dh.
InterPro; IPR008151; Phytn dehydro.
Prom; PP01593; Amino oxidase; 1.
ProDom; PD139017; Phytn dehydro; 1.
PROSITE; PS00982; PHYTOENE_DH; I.
Carotemoid biosynthesis; Oxidoreductase; PA.
NP_BIND
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                                                                                                                                                                                                                          492 AA; 54503 MW;
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Best Local Similarity 76.8
Matches 377; Conservative
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Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
01-AUG-1990 (Rel. 15, Created)
1-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99..) (Phytoene desaturase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERRATUM
   STACER REPRESENTATION OF THE PROPERTY SERVING 
                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                   FUNCTION: This enzyme converts phytoene into lycopene via the intermediaries of phytofluene, zeta-carctene and neurosporene the introduction of four double bonds (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD139017; Phytn dehydro; 1.
PROSITE; PS00982; PHYTOENE DH; 1.
Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD.
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0
                                                                                                                                               PATHWAY: Carotenoid biosynthesis. Involved in astaxanthin
                                                                                                                                                                           biosynthetic pathway. SIMILARITY: Belongs to the phytoene dehydrogenase family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 62.9%; Score 1638; DB 1; Length 50 Best Local Similarity 63.9%; Pred. No. 3.3e-125; Matches 313; Conservative 61; Mismatches 116; Indels
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InterPro; IPR002937; Amino oxidase.
InterPro; IPR008150; Bac phytoene di
InterPro; IPR008151; Phytn_dehydro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01593; Amino_oxidase; 1
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ATACVMLSDL 498
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524 A.A.

PRT;

STANDARD;

SULT 4 TI_RHOCA CRTI_RHOCA P17054;

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R PIR; A32617; A32617.

R InterPro; IPR000759; Adrndx_reductase.

R InterPro; IPR000237; Amino oxidase.

R InterPro; IPR000315; Bac_phytoene_dh.

R InterPro; IPR000315; Phyto dehydro.

DR InterPro; IPR000315; Phyto dehydro.

DR Prodon; PF01593; Amino oxidase; 1.

DR Prodon; PF01593; Amino oxidase; 1.

DR Prodon; PF01593; Amino oxidase; 1.

R Prodon; PF01593; Amino oxidase; 1.

R Prodon; PF01593; Amino oxidase; 1.

R PROSITE; PS00982; PHYTOENE DH; 1.

KW PROSYTHESIS; Chlorophyll biosynthesis; Carotenoid biosynthesis; KW Oxidoreductase; FAD; Flavoprotein; NAD:

"No annum 12 45 Flavoprotein; NAD:

"No annum 12 45 Flavoprotein; Contennes of                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                               SEQUENCE FROM N.A.
STRAIN-SB1003 / St Louis, and BEC404;
STRAIN-SB103563; PubMed=2747617;
Alberti M., Alberti M., Leach F., Hearst J.E.;
*Nucleotide sequence, organization, and nature of the protein products of the carotenoid biosynthesis gene cluster of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90168827; PubMed=2144293;
Bartley G. E., Schnidhauser T.J., Yanofsky C., Scolnik P.A.;
Bartley G. E., Schnidhauser T.J., Yanofsky C., Scolnik P.A.;
Carotenoid desaturases from Rhodobacter capsulatus and Neurospora crassa are structurally and functionally conserved and contain domains homologous to flavoprotein disulfide oxidoreductases.";
J. Biol. Chem. 265:16020-16024(1990).
J. FUNCTION: This enzyme converts phytoene into zeta-carotene via intermediary of phytofluene by the symmetrical introduction of double bonds at the C-11 and C-11 positions of phytoene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bartley G.B., Scolnik P.A.; Carotenoid biosynthesis in photosynthetic bacteria. Genetic characterization of the Rhodobacter capsulatus Crtl protein."; J. Biol. Chem. 264:13109-13113(1989).
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-!- PATHWAY: Carotenoid and chlorophyll biosynthesis.
-!- SIMILARITY: Belongs to the phytoene dehydrogenase family.
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J. Biol. Chem. 264:18260-18260(1989).
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MEDLINE=89327279; PubMed=2546948;
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EMBL; X52291; CAA36533.1; -.
EMBL; Z11165; CAA77540.1; -.
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Matches 204; Conservative
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Best Local Similarity
NCBI_TaxID=1061;
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MEDLINE=20115911; PubMed=10648776;
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                                                                                                                                  181 QAFSFHSLLVGGNPPATSSIYTLIHALEREWGVWFPRGGTGALVNGMIKLFQDLGGEVVL 240
                                                                                                                                                                                      188 FALSFHPLFIGGDPFHVTSMYILVSQLEKKFGVHYAAIGGVQAIADAMAKVITDQGGGEMRL 247
                                                                                                                                                                                                                         NARVSHMETVGD-KIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQS 299
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              9
                                     8 MGRAVVIGAGLGGLAAAMKLGAKGYKVTVVDRLDRPGGRGSSITKGGHRFDLGPTIVTVP 67
              MKPTTVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
MEDLINE=94292403; PubMed=8021167;
Lang H.P., Coddell R.J., Gardiner A.T., Hunter C.N.;
Lang reps in carctenoid biosynthesis: sequences and transcriptional analysis of the crtI and crtB genes of Rhodobacter spheroides and overexpression and reactivation of crtI in Escherichia coli and R. sphaeroides.";
J. Bacteriol. 176:3859-3869(1994).
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MEDLINE=95238278; PubMed=7721699;
Lang H.P., Cogdell R.J., Takaichi S., Hunter C.N.;
"Complete DNA sequence, specific TnS insertion map, and gene assignment of the carotenoid biosynthesis pathway of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides),
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
NCB:_TaxID=1063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P54980; Q3RFD0; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase)
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STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                     Choudhary M., Kaplan S.; "DNA sequence analysis of the photosynthesis region of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002937; Amino oxidase.
InterPro; IPR0015937; Amino oxidase.
InterPro; IPR00150; NAD-BS.
InterPro; IPR00151; Phyru dahydro.
ProDom; PF01593; Amino oxidase; 1.
ProDom; P510991; PHYTOĞNE DH; 1.
PROCSITE; PS00991; PHYTOĞNE DH; 1.
PROCSITE; PS00992; PHYTOĞNE DH; 1.
Photosynthesis; Chlorophyl Diosynthesis; Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD.
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R -> C (IN REF. 3).

T -> S (IN REF. 3).

L -> F (IN REF. 3).

Q -> P (IN REF. 3).

Q -> P (IN REF. 3).

Hy, 423B3515639EFBFI CRC64;
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174 174 T
292 L
395 395 Q
518 AA, 57244 MW;
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PIR; T50745; T50745.
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InterPro; IPR000759; Adrack reductase.
InterPro; IPR002937; Amino oxidase.
InterPro; IPR008150; Bac phroene_dh.
InterPro; IPR000205; NAD_BS.
InterPro; IPR008151; Phytn dehydro.
Pfam; PF01593; Amino_oxidase; 1.
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FDFRDE-LNAWQGSAFSVEPILTQSAWFRPENRDKHIDNLYLVGAGTHPGAGIPGVIGSA
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MIDININE=96061955; PubMed=7588751;
MIDININE=96061955; PubMed=7588751;
MOLININE=96061955; PubMed=7588751;
MA Cluster of structural and regulatory genes for light-induced carotenogenesis in Myxococcus xanthus.";
FUNCTION: This enzyme converts phytoene into zeta-carotene via tintermediary of phytofluene by the symmetrical introduction of the double bonds at the C-11 and C-11' positions of phytoene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: FAD (Probable).
-!- PATHWAY: Carotenoid biosynthesis.
-!- SIMILARITY: Belongs to the phytoene dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Myxococcus.
NCBL_TaxID=34;
                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase)
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CECDD74AB9F9F8CB CRC64;
                                                                                                                                                                                                   517 AA
                                                                                                                                                                                                                                                         Last sequence update)
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TheerPro; PRR000759; Adridx reductase.
InterPro; PRR000237, Amino oxidase.
InterPro; PRR000150; Bac_phytoene_dh.
InterPro; PRR000150; MAD Bs.
InterPro; PRR00151; Phytn dehydro.
Pfam; PP01593; Amino_oxidase, 1.
ProDom; PD199017; Phytn dehydro;
PROSITE; PS00982; PHYTOENE_DH; 1.
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                                                                                                                                                                                                                                        Created)
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Matches 173; Conservative
                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34,
01-OCT-1996 (Rel. 34,
28-FEB-2003 (Rel. 41,
                                                                      481 KATAGL 486
                                                                                                         EVMAKL 498
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422
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                               367
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SFHSLLVGGNPFATSSIYTLIHALEREWGVWFPRGGTGALVNGMIKLFQDLGGEVVLNAR 243
                                                                                                                                     244 VSHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQSKRMS 303
                                                                                                                                                                                                                                                                 304 NSLFVLYFGLNHEHHDQLAHHTVCFGPRYRBLIHBIFNHDGLAEDFSLYLHAPCVTDPSLA 363
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Mol. Gen. Genet. 252:658-666[1996].
-!- FUNCTION: This enzyme converts phytoene into zeta-carotene via intermediary of phytofluene by the symmetrical introduction of double bonds at the C-11 and C-11' positions of phytoene.
-!- COPACTOR: PAD (Probable).
-!- COPACTOR: PAD (Probable).
-!- PATHWAY: Carotenoid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase).
CRTI OR CRTE.
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-PBB-2003 (Rel. 41, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                        66 LFALAGKQLKDYVELLPVTPFYRLCWESGKVFNYDNDQAQLEAQIQQFNPRDVAGYRAFL 125
                                                                                                                                                                                                                                                                                                                                                                                                    DYSR-AVENEGYLKLGTVPFL--SFKDMLRAA-PQLAKLQA---WRSVYSKVAGYIEDEH 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRQAPSFHSLLVGGNPFATSSIYTLIHALEREWGVWFPRGGTGALVNGMIKLFQDLGGEV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 VLNARVSHMETVGDKIQAVQLEDGRRPETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQ 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 SKRMSNSLFVLYFGLANHHDQLAHHTVCFGPRYRELIHEIFNHDGLAEDFSLYLHAPCVT 358
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                                                                                                                                                                                                                                                                                              417 RMFTPFDFRDELNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVGAGTHPGAGIPGV
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-!- COFACTOR: RAD [Probable].
-!- PAITHWAY: Carotenoid biosynthesis.
-!- SIMILARITY: Belongs to the phytoene dehydrogenase family.
ProDom, PD139017; Phytn_dehydro; 1.
PROSLTE; PS00382; PHYTOENE DH; 1.
Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD.
NP BLND 12 45
FAD (ADP PART) (POTENTIAL).
SEQUENCE 507 AA; 54509 MW; PBB97F7?E696B2AC CRC64;
                                                                                                                                                                                                          23;
                                                                                                                                                     h Similarity 35.0%; Pred. No. 7.6e-47; Similarity 35.0%; Pred. No. 7.6e-47; Conservative 80; Mismatches 214; Indels 23
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28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase).
Streptcomyces seconii.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptcomycineae; Streptcomycetaceae; Streptomyces.
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                                                                                                                                                          Query Match
Best Local Similarity 35.0°
Matches 171; Conservative
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LISGKLAA 486
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P54971;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 RIMLERLYRVQMRRFID---ANPDS------PFQLVHPDLAR----LAALGGFGRLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349 SLYLHAPCVTDPSLAPEGCGSYYVLAPVPH--LGTANLDWAVEGPRLRDRIFDYLEQHYM
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01-MAY-1991 (Rel. 18, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4B6DEFC076D51CB5 CRC64;
                                                                                                                                                                                         EMBL, DSS723; BAA09537.1; -.
InterPro; IPR000759; Adrndx_reductase.
InterPro; IPR0012937; Amino_oxidase.
InterPro; IPR008150; Bac_phytoene_dh.
InterPro; IPR008150; NAD_BY.
InterPro; IPR008151; Phytn_dehydro.
Pram; PR01593; Amino_oxidase; 1.
PRIMTS; PR00419; ADXRDTASE.
ProDom; PD139017; Phytn_dehydro; 1.
PROSITE; PS00982; PHYTOENE DP; 1.
Carotenoid biosynthesis; Oxidoreductase; PAD; E
NP_BIND
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Best Local Similarity 34.77
Matches 173; Conservative
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408 GLR-SQLVTHRMF-TFFDFRDELNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVGA
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                                                                                                                                                                                                                                                                                                                                                          Myxococcus xanthus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 FLDYSRAVFNEGYLXLGTVPPLSFKOMLRAA-PQLA-----KLQAWRSVYSKVAGYIEDE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 HLRQAFSFHSLLVGGNPFATSSIYTLIHALERZWGVWPPRGGTGALVNGMIXLFQDLGGE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 RMORVFTFATWYMGMSPFDAPATYSLLQYSELAEGIWYPRGGFHKVLDALVXIGERMGVK 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVLNARVSHMETVG-----DKIQAVQLEDGRRFETCAVASNADVVHTYRD1LSQHPAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.4%; Score 635; DB 1; Length 595;
31.3%; Pred. No. 1e-43;
ive 97; Mismatches 226; Indels 24; Gaps
                                                                      SEQUENCE FROM N.A.

STRAIN=74-0R23-1A / FGSC 987;

MEDLINE=90377195; PubMed=2144609;

Schmidhauser T.J., Lauter F.-R., Russo V.E.A., Yanofsky C.;

"Cloning, sequence, and photoregulation of al-1, a carotenoid biosynthetic gene of Neurospora crassa.";

Mol. Cell. Biol. 10:5064-5070(1990).

-!- FUNCTION: This enzyme converts phytoene into zeta-carotene via intermediary of phytofluene by the symmetrical introduction of double bonds at the C-11 and C-11' positions of phytoene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probom; PD139017; Phytn dehydro; 1.
PROSITE; PS00982; PHYTOENE DH; 1.
Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD;
Sordariomycetidae, Sordariales; Sordariaceae, Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                 INDUCTION: By photoinduction.
SIMILARITY: Belongs to the phytoene dehydrogenase family.
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OFF3DF07328ED784 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                              COFACTOR: FAD (Probable).
PATHWAY: Carotenoid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002937; Amino oxidase.
InterPro; IPR00815; Bac phytoene_dh.
InterPro; IPR000205; NAD-BS.
InterPro; IPR008151; Phytn dehydro.
Pfan; PF01593; Amino_oxidase; 1.
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578 595 PC
595 AA; 66367 MW;
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Best Local Similarity 31.3%
Marches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A35919; A35919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane
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SEQUENCE
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465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 TDPSAIEELFALAGKQLKDYVELLPVTPFYRLCWESGKVFNYDNDQAQLEAQIQQFNPRD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
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                                                                428 ĞLSLSPLITERIVNTPYTWETKFNLSKGAILGLAHDFFNVLAFRPRTKAQGMDNAYFVGA
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Pontes M., Ruiz-Vazquez R.M., Murillo F.J.;

Fontes M., Ruiz-Vazquez R.M., Murillo F.J.;

Forwth plase dependence of the activation of a bacterial gene for carotenoid synchesis by blue light.";

EMBO J. 12:1265-1275(1993).

-!-FUNCTION: This enzyme converts phytoene into lycopene via the intermediaries of phytofluene, zeta-carotene and neurosporene b the introduction of four double bonds (By similarity).

-!-COPACTOR: PAD (Probable).

-!-COPACTOR: PAD (Probable).

-!- PATHWAY: Carotenoid biosynthesis.

-!- RATHWAY: Belongs to the phytoene dehydrogenase family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Myxococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NP BIND 12 45 FAD (ADP PART) (POTENTIAL). SEQUENCE 529 AA; 58420 MW; 53536A8DFD0D248C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    CRII MYXXA STANDARD; PRI; 529 AA.
002861;
01-UDN-1994 (Rel. 29, Created)
01-UDN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 529
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30.2%; Pred. No. 3.1e-42;
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InterPro; IPR0009159; Adrndo oxidase.
InterPro; IPR000150; Bac piytoene_dh.
InterPro; IPR000205; NAD ES.
InterPro; IPR0008151; Phytn_dehydro.
Pfam; PP01593; Amino oxidase; I.
PRINTS; PR00419; ADXEDTASE.
ProDom; PD139017; Phytn_dehydro; I.
PROSITE; PS00982; PHYTOENE_DH; I.
                                                                                                                                                                                      #88 STHPGTGVPIVLAGAKITAEQILEE 512
                                                                                                                                             GTHPGAGIPGVIGSAKATAGLMLED 490
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FAD (ADP PART) (POTENTIAL)
          41 FAD (ADP PART) (POT
551 POTENTIAL.
65983 MW; BOE8F682B12FB591
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene
PDH
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MEDLINE=94368091; PubMed=8085820;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cercospora nicotianae.
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531
583 AA;
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 Transmembrane.
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TRANSMEM
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                               SALRQWWEDGREKYGIAYQKFICTSADNLGYYAPWRLAPTL-RFXFWQTLYRQLDGFFF 186
                                                                                                                                                                                              304 RETDAALERAKYSCSTFMAYYGLDTVYADLPHHLIYLSESARRT----DRDALEDRHVD
                                                                                                                       GEVVI.NARVSHMETVGDXIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAK
                                                                                                                                                                                                                                                  VAGYRAFLDYSRAVENEGYLKL--GTVPFLSFKDMLRAAPQLAKLQAWRSVYSKVAGYIE
                                                                                  247 ATFRMGTPVEKVRVDAGRAVGVKLVGGEVLDADAVVVNADLAYAARSLI---PAEAREGS
                                                                                                                                                                                                                                   345 AEDFSLYLHAPCVTDPSLAPEGCGSYYVLAPVPHLGTANLDWAVEGPRLRDRIFDYLEQH
                                                                                                                                                                                                                                                                                          405 YMPGLRSQLVTHRMFTPFDFRDELNAWQGSAFSVEPILFQSAWFRPHNRDKHIDNLYLVG
                                                                   DEHLROAFS FHSLLVGGNPFATSSIYTLIHALEREWGVWFPRGGTGALVNGMIKLPQDLG
                                                                                                                                                                              K-----LOSKRMSNSLFVLYFGLMHHDQLAHHTVCFGPRYRBLIHBIFNHDGL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruiz-Hidalgo M.J.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This enzyme converts phytoene into zeta-carotene via
intermediary of phytofluene by the symmetrical introduction of
double bonds at the C-11 and C-11' positions of phytoene.
-!- COFACTOR: PAD (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD139017; Phyth dehydro; 1.
PROSITE; PS00982; PHYTOENE DH; 1.
Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD;

    -!- PATHWAY: Carotenoid biosynthesis.
    -!- SIMILARITY: Belongs to the phytoene dehydrogenase family.

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01-0CT-1996 (Rel. 34, Last sequence update)
28-F3B-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99,-) (Phytoene desatuxase)
CARB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                583 AA
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InterPro; IPR008150; Bac_phytoene_dh.
InterPro; IPR002055; NAD_BS.
InterPro; IPR008151; Phytn_dehydro.
Pfam; PP01593; Amino_oxidase; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=NRRL 1555;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 KOAKKLOSKRMSNSLFVLYPGLAHHDQLAHHTVCFGPRYRELIHRIFNHDGLAEDFSLY
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                                                    27; Gaps
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"Isolation, sequence, and characterization of the Cercospora
"Isolation, sequence, and characterization of the Cercospora
"Isolation, sequence, and characterization of the Cercospora
Appl. Environ. Microbiol. 66:2766-2773 (1994).
-1- FUNCTION: This enzyme converts phytoene into zeta-carotene via intermediary of phytofluene by the symmetrical introduction of double bonds at the C-11 and C-11' positions of phytoene.
-1- COFACTOR: PAD (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Fungi; Ascomycota; Pezizomycotina;
Dothideomycetes et Chaetothyriomycetes incertae sedis;
Mycosphaerellaceae; mitosporic Mycosphaerellaceae; Cercospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       desaturase)
   Length
                                                        Indels
Query Match 22.9%; Score 595.5; DB 1; Best Local Similarity 29.1%; Pred. No. 1.6e-40; Matches 146; Conservative 103; Mismatches 225;
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CONFLICT
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                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYRAFLDYSRAVFNEGYLKLGTVPFLSFKD----MLRAAPQ----LAKLQAWRSVYSKVAG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 SAIEELFALAGKQL-KDYVELLPVTPFYRLCWESGKVFNYDNDQAQLEAQIQQFNPRDVA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 GLEHRTFAELGTSLEQEGVKLLKCEPNYMIHFSDGEKFTLSSDLSVMKTEVEKWEGKE- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YIEDEHLRQAFSFHSLLVGGNPFATSSIYTLIHALEREWGVWFPRGGTGALVNGMIKLFQ 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   413 SPPDQPGLTPTEKQDWPAMISLARKTILSTIQSRTNVDLTPLIIHESTNSPLSWKQTFNL 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 WOGSAFSVEPILTQSAWFRP------------HNRDKHIDN 459
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                                                                                                                                                                                      InterPro; IPR008150; Bac_phytoene_dh.
InterPro; IPR008151; Phytn dehydro.
ProDom; PD139017; Phytn dehydro; 2.
PROSITE; PS00982; PHYTOENE DH; 1.
Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD;
                                                                                                                                                                                                                                                                                                                                                                                       96;
SIMILARITY: Belongs to the phytoene dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                       Length 621;
                                                                                                                                                                                                                                                                                                                                                    Ouery Match
20.3%; Score 530; DB 1; Length 621
Best Local Similarity 26.1%; Pred. No. 3.7e-35;
Matches 145; Conservative 90; Mismatches 224; Indels
                                                                                                                                                                                                                                                                                       (ADP PART) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                       61B9EA7784963CA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 LAEDFSLYLHAPCVTDPSLAPEGOGSYYVLAPVPHL
                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                     44 FA
556 PO
69529 MW;
                                                                                                                                                         EMBL; U03903; AAB86988.1; -.
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                                                                                                                                                                          T48646; T48646.
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536 5
621 AA;
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TRANSMEM
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CRTD_RHOSH STANDARD; PRT; 495 AA Q01671; 01-JUL-1993 (Rel. 26, Created) 16-OCT-2001 (Rel. 40, Last sequence update)

SSULT 13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 LFALAGKOLKDYVELLPVTPFYRLCWESGKVFNYDND-QAQLEAQIQQFNPRDVAGYRAF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
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PIR; 523633; 523633.

InterPro; IPR002937; Amino oxidase.

InterPro; IPR008150; Bac_phytoene_dh.

InterPro; IPR008150; Bac_phytoene_dh.

InterPro; IPR008153; Amino oxidase; 1.

PROSITE; PS00982; PHYTOENE_DH; 1.

PROSITE; PS00982; PHYTOENE_DH; 1.

PROCINCHARSIS; Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sphaeroides.";
J. Bacteriol. 177:2064-2073(1995).
J. Bacteriol. 177:2064-2073(1995).
-!- FUNCTION: CONVERTS HYDROXYMEUROSPORENE TO DEMETHYLSPHEROIDENE METHOXYNEUROSPORENE TO SPHEROIDENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
MEDLINE=92238278; Pubmed=7721699;
Lang H.P., Cogdell R.J., Takaichi S., Hunter C.N.;
"Complete DNA sequence, specific Th5 insertion map, and gene assignment of the carotenoid biosynthesis pathway of Rhodobacter
                                                                                                                           Bacteria; Proveobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
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                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAINS-ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
STRAINS-BATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
MEDILINS-92307398; PubMed=1612412;
Gari E., Toledo J.C., Gibert I., Barbe J.;
"Nucleotide sequence of the methoxyneurosporene dehydrogenase from Rhodobacter sphaeroides: comparison with other bacterial carotenoid dehydrogenases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- PATHWAY: Carotenoid and chlorophyll biosynthesis.
-i- SIMILARITY: Belongs to the phytoene dehydrogenase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 495;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAD (ADP PART) (POTENTIAL)
                                                                                                      Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 A -> G (IN REF. 2).

157 T -> P (IN REF. 2).

170 L -> M (IN REF. 2).

273 L -> I (IN REF. 2).

443 PHGA -> ATGP (IN REF. 1).

52900 MW, 62227931415B253E CRC64;
28-FEB-2003 (Rel. 41, Last annotation update)
Methoxyneurosporene dehydrogenase (EC 1.14.99.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEMS Microbiol, Lett. 72:103-108(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AJ010302; CAB38743.1; ALT_SEQ.
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170
170
273
240
495 AA;
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                                                                                                                                                                                                    NCBI_TaxID=1063;
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                                          ----YIEDEHLROAFSFHSLLVGGNPFATSSIYTLIHALEREWGVWFPRGGTGALVNGMI 228
                                                                                                                                                                                                                                            289 AAAKQAKKLQSKRMSNSLFVLYFGLNHHHDQLAHHTVCFGPRYRELIHRIFNHDGLAEDF 348
                                                                                                                                                                                                                                                                                                                                                                   406
                                                                                                                                                                                                                                                                                                                                                                                                          354 TLYI---CAEDRSGGQLPDGPERPEIIMNGPPGRPAKPE---DPAQCRSRTFDRLROFGL 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----PGLRSQLVTHRMFTPFDFRDELNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLY 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 QDAVPEDRIHPR--SLSAWVWSYAARASGPPLVHHNVFFADDPRREFGPIAAGQ-MPEDA 353
                                                                                                                       229 KLFQDLGGEVVLNARVSHMETVGDKIQAVQLEDGRRFBTCAVASNADVVHTYRDLLSQHP
                                                                                                                                                                           237 RLADDOGVRLRYGAPVAGILRQGGRPTGVQLADGRTLPADHIVFNGDPAALLAGCLGDGP
                                                                                                                                                                                                                                                                                                                                                                349 SLYLHAPCVTDPS--LAPEGCGSYYVLAPVPHLGTANLDWAVEGPRLRDRIFDYLEQHYM
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STRAIN=SB1103 / St Louis, and BEC404;
MEDLINE=8931363; Pubmed=2747617;
Armstrong G.A., Alberti M., Leach F., Hearst J.E.;
"Nucleotide sequence, organization, and nature of the protein products of the carotenoid biosynthesis gene cluster of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90368827; PubMed=2144293;
Bartley G.E., Schmidhauser T.J., Yanofsky C., Scolnik P.A.;
Scarcenoid degaturages from Rhodobacter capsulatus and Neurospora crassa are structurally and functionally conserved and contain domains homologous to flavoprotein disulfide oxidoreductases.";
J. Biol. Chem. 265:16020-16024(1990).
-i. FUNCTION: CONVERTS HYDROXYNEUROSPORENE TO DEMETHYLSPHEROIDENE CMETHAXYNEUROSPORENE TO SPHEROIDENE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRID.

Rhodobacter capsulatus (Rhodopseudomonas capsulata).

Rhodobacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;

Rhodobacteraceae; Rhodobacter.

NCBI_TaxID=1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COFACTOR: FAD (Probable).
PATHWAY: Carotenoid and chlorophyll biosynthesis.
SIMILARITY: Belongs to the phytoene dehydrogenase family.
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01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Methoxyneurosporene dehydrogenase (RC 1.14.99.-).
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InterPro; IPR002937; Amino_oxidase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z11165; CAA7754
S04406; S04406.
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RTD_RHOCA
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                                                                                                                                                                                                                                                                                                                                                 69 LFAACGTRABEHLTLIFLPLPRLARHFWPDGSSLDLFTDTEANIEA-IRAFAGDKEAAAFRR 127
                                                                                                                                                                                                                                                                                                                                                                                  124 FLDYSRAVFNEGYLKLGTVPFLSFKDMLR-AAPQLAKLQAW-----RSVYSKVAGYIED 176
                                                                                                                                                                                                                                                                                                                                                                                                         177 EHLRQAFSFHSLLVGGNPFATSSIYTLIHALEREWGVWFPRGGTGALVNGMIKLFQDLGG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 PRLAÓLFGRYATYVGGRPGATPAVLSLÍMOAEVO-GVWAIREGMHGVAAALARVAEAKGV 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 SPRPAPSLSAWWAFGATPIGVDLAHHNVFFTADPELEFGP------IGAGEMPEEP 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 RFHYGAKAKRIVRKEGRVTAVEIETGVSIPCGACIFNGDPGALRDGLLGD--AARASMEK
                                                                                                                                                                                                                                           6 VIGAGEGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITDPSAIRE
                                                                                                                                                                                                                                                                            9 VICARMGGLAAAIGAAAAGLRVIVVEAGDAPGGKARAVPIPGGPADIGPIVLIMRHVLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353 TLYI---CAQDREMQ------APVPRI--ERFEIIMNGPACHQPFPQEEAQCRART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      398 PDYLEQ---HYMPGLRSQLVTHRMFTPFDFRDELNAWGGSAFSVEPILTQSAWFRPHNRD
                                                                                                                                                                                                          Gabs
InterPro; IPR000150; Bac_phytoene_dh.
InterPro; IPR00151; Phytn_dehydro.
Probom; PP01593; Amino oxidase; IPR001593; Amino oxidase; IPR050m; PD139017; Phytn_dehydro; I.
Probom; PD139017; Phytn_dehydro; I.
PROSTIE; PS009982; PHYTORNE DH; I.
Photosynthesis; Chlorophyll blosynthesis; Carotenoid blosynthesis; Oxidoreductase; RAD; Flavoprotein; NAD.
                                                                                                                                                                                                          67;
                                                                                                                                                                        DB 1; Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=66 / 1326;
MEDLINE=87231086; PubMed=3453116;
Burnett W.V., Henner J., Eckhardt T.;
"The nucleotide sequence of the gene coding for XP55, a major secreted protein from Streptomyces lividans.";
Nucleic Acids Res. 15:3926-3926(1987).
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Streptomycineae, Streptomycetaceae, Streptomyces.
NCBL TaxID=1916;
                                                                                                                                                                        14.2%; Score 369.5; DB 1; Length 26.8%; Pred. No. 2.9e-22; ive 76; Mismatches 236; Indels
                                                                                                                      AD (ADP PART) (POTENTIAL)
D1180A023FFEB5A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 SLYLHAPCVTDPSLAPEGCGSYYVLAPVPHLGTANLDWAVEGP-
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Last sequence update)
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                                                                                                                          PAD
                                                                                                                                       494 AA; 52312 MW;
                                                                                                                                                                                           Local Similarity 26.8 es 139; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute in There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 TVITDPSALEELPALAGKQLKDY-VEL----LPVT-PFYRLCWESGKVFNYDNDQAQLEA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 QIQQ----FNPRDVAGYRAFLDYSRAVFNEGYLKLGTVPFLSFKDM-LRAAPQ----LAK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 SVGETAASFGARDAGPYRRLI-----ERFLPRWDTLARDFMSLPLTALPRDPVTLAR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 L------QAWRSVYSKVAGYIEDEHLRQAFS---FHSLL-VGGNPFATSSIYTLIHAL- 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 FGLVGLPPSTW-----LMRRFRDEXAKTLFAGLVAHVMAPLGG--FATGAI-GLVPALA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --EREWGVWFPRGGTGALVNGMIKLFQDLGGEVVLNARVSHMETVGDKIQAVQLEDGRRF 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 AHARGWPV--ARGGSQSISDALTAYIKDLGGAVHTDYSVRRLD-------DLPPARAY 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 ETCAVASNADVVHTYRDILISQHPAAAKQAKKLQSK----RMSNSLFVLYFGLNHHHDQLA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------VLDTSPTALARIAGLGSHYANYRYGPSVFKIDYALDGPVPWTA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 HH-----TVCFGPRYREL---IHEIFNHDGLAEDFSLYLHAPCVTDPSLAPEGCGSYYVL 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 APVPHLGTANLDWAVEGPRIRDRIPDYLEQHYMPGIRSQLVTHRMFTPFFDFRDELNAWQG 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LGINSP-----PDGSAAVLENTHPGLPMAHPF------PDGSAAVLSR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 SAFS------VEPILTQSAMFRPHNRDKHIDNLYLVGAGTHPGAGIPGVIG--SAK 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKPTTVIGAGFGGLALAIRLQAAGIPVLLIRQRDKPGGRAYVYQ--BQGFTFD----AGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.6%; Score 171.5; DB 1; Length 469;
23.3%; Pred. No. 3.1e.06;
tive 64; Mismatches 212; Indels 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      o; 1.
C2AE7533C7C701CB CRC64;
                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000759; Adrndx reductase.
InterPro; IPR00205; NAD BS.
InterPro; IPR008151; Phyrn dehydro.
PRINTS; PR00419; ADXRDTASE.
PRODOM; PD139017; Phyrn dehydro; I.
SEQUENCE 469 AA; 49740 MW; C2AE753
                                                                                                                                                                                                                                                                      EMBL; Y00142; CAA68336.1;
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Best Local Similarity 23.33
Matches 126; Conservative
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arch completed: February 29, 2004, 14:45:12 b time : 10.2921 secs

Page 1

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	, model	<pre>February 29, 2004, 14:34:14 ; Search time 13.6946 Seconds (without alignments) 3455.835 Million cell updates/sec</pre>	
enCore) 1993	ws buis	004, 14	-32
G Copyright (c	protein - protein search, using sw model	February 29, 2	US-09-941-947A-32
	protein -	n on:	tle:

tle: rfect score: 2606 quence: 1 MKPTTVIGAGFGGLALAIRi.....IPGVIGSAKATAGLMLEDLI 492

table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues

arched:

tal number of hits satisfying chosen parameters: 283366

nimum DB seq length: 0
ximum DB seq length: 2000000000
st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

tabase : PIR 78:* 1: pir1:* 3: pir2:* 4: pir4:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2	Description	phytoene dehydroge		_							probable diapophyt		probable phytoene	squalene synthase	phytoene dehydroge	zeta-carotene desa	phytoene dehydroge		phytoene dehydroge	phytoene desaturas			phytoene dehydroge	crtN protein - Sta	phytoene dehydroge	hypothetical prote	phytoene desaturas	phytoene dehydroge	methoxyneurosporen	methoxymeurosporen
SUMMERTES	ΙD	\$52586	D37802	A33120	T50910	C75466	A32617	S49620	T50745	832169	T31463	A35919	T36968	B90061	535306	AG2509	S43139	843324	AH1199	T46822	E69108	H84320	m	B55548	AF1557	E90061	T51119	B84327	σ	823633
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	Length	492	492	492	511	548	524	518	518	517	517	595	523	502	529	499	583	499	490	582	514	512	621	448	488	497	528	536	486	495
ok	Query Match	94.1	93.6	77.6		40.3	38.7	36.8		29.1		24.4	24.2	23.9	23.6	23.2	22.9	22.7	21.8	21.6	21.1	20.8	20.3	18.9	18.8	18.5	17.9	16.6	16.4	16.3
	Score	2453	2438	2023	1099.5	1051	1007.5	959.5	952.5	757.5	752	635	629.5	624	919	604	595.5	592	567	562	549.5	541.5	530	493	489	482	S	433.5		423.5
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hydroxyneurosporen	methoxyneurosporen	hypothetical prote	hypothetical prote	methoxyneurosporen	phytoene dehydroge	hypothetical prote	hypothetical prote	probable phytoene	methoxyneurosporen	hypothetical prote	hypothetical prote	phytoene dehydroge	phytoene dehydroge	probable carotenoi	hypothetical prote
S32171	T50749	S76617	AI2273	S04406	A99470	H83880	AB2064	E75561	T50893	875951	A86203	GB7635	G90413	T34971	AI2185
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411 15.	388.5 1	380.5	375	369.5	343	342.5	322	316	313	311	292.5	289	276.	274.5	259

ALIGNMENTS

RESULT 1

S52586 phytoene dehydrogenase (EC 1.3) - Erwinia herbicola C;Species: Erwinia herbicola C;Date: 15-Jul-1995 #secuence revision 01-Sep-1995 #text change 29-Sep-1999	C; Accession: S52586 R; Lin, Y.P.; Lai, E.M.; To, K.Y.; Chang, Y.S.; Liu, S.T. Wol. Gen. Genet. 245, 417-423, 1994	A;Title: Transcriptional activation of ilanking sequences by injour insertion. A;Reference number: S52583; MuiD:95107237; PMID:7808390 A;Accession: S52586	A.Status: preliminary, nucleic acid sequence not shown; translation not shown A.Molecule type: DNA A.Residues: 1-492 <lin></lin>	A.Cross-references: EMBL:M90698; NID:g148393; PIDN:AAA21263.1; PID:g148397 A.Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1992 C.Superfamily: phytoene dehydrogenase C.Keywords: oxidoreductase
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C;Keywords: oxidoreductase

Query Match

Best Local Similarity 93.7%; Pred, No. 5.9e-189;

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		GPT	GPT	FNPI	FNPI	YIEI	XIEI	9510	DIG.	OAKG	SSK	HAPC	HAPC		- <u>F</u>	I PG1
	0	FEDA	FPDA	2100	-8	CVAG-	CVAS	Q.F.O.	-9 -8	AAK -	-8 -8	17.7. 	-17.	RSO	RSQ	GAG
4	l.s	SGF.	-8	LEAC	LEAC	VYS	- K.	GMI	- E	ZAHO	OHP?	EDFS		MPGI	MPGI	STHE
Lengen 492;	Indels	VYOB		0040	-0 -0 -0 -0	SWRS	WRT	T CAN	TVK	STTC	11.LS	GILA -	GILA	SOHY	- KHOS	VGA
		RAY	RAY	NO.	- 2 - 2 - 2	χ. Σ-	-9 -13	GTG	GTG	TYRI	TYRI	HNH	HALL	DYL	EYL	NLYI
יו קר	17;	XP = 28	KPGC	KVF	- K	00-		PPRG	PPRG	EAAG	- E	IHEI	IHEI	DRIF	DRIF	KHID
- G	16.5 16.5 1	SORD	- QE	VESG	ÆSG	EAA.	-RA-	₩. 	GVW	SNA	SNA	REL	REL	RLR	RIER	NRD)
Score 2453; DB 2;	14; Mismatches	7.1.1.	-11-	RIC	RIG-	Ď-	. P. C. M.	ERE	ERES	S. S.	RAV	GPR	GPR	VEGI	VEGI	FRP
אינ ט אינו	Misa Misa	GIPV		Yagi	APPY	FLSF	FLSF	THAL	HAL	RFBT	RFPT	IVCF	IVCF.	LDWA	-MOS	SAW
S S	υ	APO-	-0 -0	PV-	LPV	TVP	-Y		- F	DGR	- 100 - 100	AHH		TAN	TAN	ILI
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	vat	GFG 	-GPG	AGK.	-K-	SAVE:	-A	P.GG-	- 5 - 5 - 6	WGD]	- <u>1</u>	E E	- K	Z.	- <u>\$</u>	AWO
i	nse	7517	- Z	LFAI	LFT	DYSE	DYSE	HSILI	HSIT	HME1	EWE!	LPVI	LF.	8006	- 9008 8008	DELL
;	8	KPTT	- E	AIEE	AIEE	SAFL	ZOFI.	AFSF	FSF	RVS	-KVS	SNS	SNS	APE	APE	PDFR
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phytoene dehydrogenase [imported] - Rubrivivax gelatinosus
C;Species: Rubrivivax gelatinosus
C;Species: Rubrivivax gelatinosus
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
C;Accession: T60910
C;Accession: Boll Data Library, November 1999
A;Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photosynt
A;Reference number: Z55270
A;Accession: T50910
A;Accession: T50910
A;Accession: T50910
A;Accession: Lype: DNA
A;Residues: 1-511 kNAG>
A;Cross-references: EMBL:AB034704; PIDN:BAA94063.1
                                                                            carotenoid biosynthesis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NARVSHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQSK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: A39273; A33120
R;Armatrong, G.A.; Ablerti, M.; Hearst, J.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 9975-9979, 1990
A;Title: Conserved enzymes mediate the early reactions of carotenoid biosynth A;Reference number: A39273; MUID:91088634; PMID:2263648
A;Accession: A39273
A;Accession: A39273
A;Accession: A39273
A;Readues: 1-492 ARWA
A;Readues: 1-492 ARWA
A;Cross-references: GB:M38423; NID:g148401; PIDN:AAA24820.1; PID:g148402
A;Note: strain Bhol0; ATCC 39368
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: phytosne dehydrogenase
C;Keywords: carotenoid biosynthesis; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TALEALPTLAGRRMEDYVRILLPVKPFYRLCWESGKTLDYANDSAELEAQITQFNPRDVEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKPTTVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITDP
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                                                                                                                                                                                                                                                                                                                                                                                                            77.6%; Score 2023; DB 2; Length 4 76.8%; Pred. No. 2e-154; ive 42; Mismatches 72; Indels
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Best Local Similarity 76.8
Matches 377; Conservative
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Jaces 13-may-1991 #sequence_revision 31-may-1991 #text_change 20-Jun-2000
Jaces 13-may-1991 #sequence_revision 31-may-1991 #text_change 20-Jun-2000
Jaces 100: D37802
Macawa, N.; Nakagawa, M.; Kobayashi, K.; Yamano, S.; Izawa, Y.; Nakamura, K.; Harashim Bacteriol. 172, 6704-6712, 1990
Title: Blucidation of the Erwinia uredovora carotemoid biosynthetic pathway by function Reference number: A37802; MuID:91072214; PMID:2254247
Jacession: D37802
Status: preliminary
Molecule type: DNA
Residues: 1-492 <MIS>
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Alternate names: phytoene desaturase
;Species: Erwinia herbicola
;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 29-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: GB:D90087; NID:g216681; PIDN:BAA14127.1; PID:g216685; Superfamily: phytoene dehydrogenase; Keywords: oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 492;
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RESULT 6
A32617
phydrogenase (BC 1.3...) - Rhodobacter capsulatus
N;Alternate names: phytoene desaturase
C;Species: Rhodobacter capsulatus
C;Sacession: A32617; 804402
R;Bartley, G.E.; Scolnik, P.A.
J. Biol. Chem. 264, 13109-13113, 1989
A;Fitle: Carotenoid biosynthesis in photosynthetic bacteria. Genetic characterization of
A;Reference number: A32617; WUID:89327279; PMID:2546948
A;Reference number: A32617; WUID:89327279; PMID:2546948
A;Residues: 1-524 cBAR>
A;Residues: 1-524 cBAR>
A;Residues: 1-524 cBaR>
A;References: GB:J04969; NID:340554; PIDN:AAA50313.1; PID:9556397
A;Armstrong, G.A.; Alberti, M.; Leach, F.; Hearst, J.E.
Mol. Gen. Genet. 216, 254-268, 1989
A;Title: Nucleotide sequence, organization, and nature of the protein products of the ca:
A;Accession: S04401; MUID:89313663; PMID:2747617
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                            17 KTALVIGAGFGGLALGIRLQSLGFDTTILBRLDGPGGRAYQKRTPDGYVFDMGPTVLTVP
                                                                                                                                                                                                           94 GKVFNYDNDQAQLEAQIQQFNPRDVAGYRAFLDYSRAVFNBGYLKLGTVPFLSFKDMLRA
                                                                                                                                                                                                                                                                                                                    154 APQLAKLQAWRSVYSKVAGYIBDEHLRQAFSFHSLLVGGNPPATSSIYTLJHALERBWGV
                                                                                                                                                                                                                                                                                                                                                                                                                         214 WFPRGGTGALVNGMIXLFQDLGGEVVLNARVSHMETVGD-----KIQAVQLEDGRRFETC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 HYAMGGTGALVRGLVQKFEELGGAIRYGAGVDEVLVDGNLPGKRTARGVRLESGEELRAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         386 WAVEGPRIRDRIFDYLEOH-YMPGLRSQLVTHRMFTPFDFRDELNAWQGSAFSVEPILTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434 WDVEGPKLARAALADIERRGLIPGLRERLTHFEFITPDYFAGTLDSYLGNAFGPEPRLVQ
2 KPTTVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQ-EQGFTFDAGPTVITDP
                                                                                                                                                                                                                                                                                                                                                    197 VPDLLKLDAVRTLFSFTSKYFQSDKLRQVFSFFTLLVGGNPLSVPAIYAMIHFVBKTWGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 AVASNADVVHTYRDLLSQHPAAAKQAKKLQSKRMSN--SLFVLYFGLNHHHD-QLAHHTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 CFGPRYRELIHEIFNHDGLAEDFSLYLHAPCVTDPSLAPEGCGSYYVLAPVPHLGTANLD
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A;Note: translation of codons 1-33 is not given
A;Note: the authors translated the codon GTG for residue 34 as Met.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445 SAWFRPHNRDKHIDNLYLVGAGTHPGAGIPGVIGSAKATAGLMLED 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     494 SAFFRPHNRSEDLHNFYLVGAGAQPGAGTPSVMMSANMTARLIAED 539
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C,Keywords: carotenoid biosynthesis; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-524 <ARM>
                                                                                                    61 SAIEELFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 204
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Cross-references: GB:AE001940; GB:AE000513; NID:g6458577; PIDN:AAF10439.1; PID:g645858
Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ytoene dehydrogenase - Deinococcus radiodurans (strain R1)
Species Deinococcus radiodurans
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
Accession: C75466
Accession: C75466
M.; Shen, J.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, Smith, H.O.; Venter, J.C.; Praser, C.M.
Tience 286, 1571-1577, 1999
Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans Reference number: A75250; MUID:20036896; PMID:10567266
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                                                                                                                                                                                                                                                                                                                                                                                203 QSELIGGNPESVISMYALINALERQWGVHWAMGGTGELIRGLVDVFEGWGGTMRLKAEVK 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323 LFVWYPGTDRRYEDVPHHMWVLGPRYRELLDDIFRKKKKLASDFSIYLHRPTATDPSMAPA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 LFALAGKOLKDYVELLPVTPFYRLCWESGKVPNYDNDQAQLEAQIQQPNPRDVAGYRAFL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 DYSRAVFNEGYLKLGTVPFLSFKOMLRAAPQLAKLQAWRSVYSKVAGYIEDEHLRQAFSF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSELVGGNPFATSSIYILIHALEREWGVWFPRGGTGALVNGMIKLFQDLGGEVVLNARVS 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 HMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQSKRMSNS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 LEVLYFGLMHHHDQLAHHTVCFGPRYRELIHEIFNHDGLAEDFSLYLHAPCVTDPSLAPE 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 GCGSYYULAPVPHLGTANLDWAVEGPRLRDRIFDYLEQHYMPGLRSQLVTHRMFTPFDFR 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   426 DELNAWOGSAFSVEPILTOSAWFRPHNRDXHIDNLYLVGAGTHPGAGIPGVIGSAKATAG 485
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                                                                                                                                                                                                                                                                                           82
                                                                                                                                                                                                                                                                    23 VVGSGFGGMAAAVRLAAKGYRVTVLEKLDAPGGRAYVHRREGHVEDAGFTIVTVFYLFDE
                                                                                                                                                                                                                                       6 VIGAGFGGLALAIRLQAAGIPVLLLEQRDKFGGRAYVYQEQGFTFDAGPTVITDPSAIBE
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                                                                                                                                                                                    1;
                                                                                                                                Length 511;
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                                                                                                                                                                                    Indels
                                                                                                                                DB 2;
                                                                                                                             Query Match 42.2%; Score 1099.5; DB 2; Best Local Similarity 42.3%; Pred. No. 38-80; Matches 204; Conservative 100; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
40.3%; Score 1051; DB 2;
Best Local Similarity 43.5%; Pred. No. 2.6e-76;
Matches 229; Conservative 72; Mismatches 185;
                                             Gene: crtl
Superfamily: phytoene dehydrogenase
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Experimental source: strain IL144
                                                                                                                          Query Match
Best Local Similarity
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Status: preliminary
Molecule type: DNA
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Gene: DR0861
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C;Accession: T50745
R;Choudhary, M.; Kaplan, S.
Rxichoudhary, M.; Kaplan, S.
Rxichoudhary, M.; Kaplan, S.
Rxiches Sales 28, 862-867, 2000
A;Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides in A;Reference number: Z25222; MUID:20115911; PMID:10648776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQSKRMSNS 305
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                                                                                                                                                                       315 LFVWYRGTKGTKGMWPDVGHHTIVNAPRYKGLVBDIFLKGKLAKDMSLYIHRPSITDPTV 374
                                                                                                                                                                                                                                                                                                                                      LPALAGKOLKDYVELLPVTPPYRLCWESGKVFNYDNDQAQLEAQIQOFNPRDVAGYRAFL 125
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                                                                                                                                                                                                                                  APEGCGSYYVLAPVPHLGTAN-LDWAVEGPRLRDRIFDYLEQHYMPGLRSQLVTHRMFTP 421
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Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
                                                                                                    ELLVEKGTATGVRLASGEVLRAGLVVSNADAGHTYMRLLRNHPRRRWTDAHVKSRRWSMS
                                                                                                                                                                                                                                                            ||||| ::| |:||||| | :||
APBGDDTFYALSPVPHLKQAQPVDWQAVAEPYRESVLEVLEQS-MPGIGERIGPSLVFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 VIGSGLGGLAAAMRLGAKGWRVTVIDKLDVPGGRGSSITQBGHRFDLGPTIVTVPQSLCD
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                                                                                                                                                 LFVLYFGLMHHH----DQLAHHTVCFGPRYRELIHEIFNHDGLAEDFSLYLHAPCVTDPSL
                                                                                                                                                                                                                                                                                                                    422 FDFRDE-LNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVGAGTHPGAGIPGVIGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 VICAGEGGLALAIRLOAAGIPVILLEQRDKEGGRAYVYQEQGFTFDAGPTVITDPSAIBE
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40.9%; Pred. No. 1.9e-68;
iive 78; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary; translated from GB/EMBL/DDBJ; Molecule type: DNA
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A;Cross-references: EMBL:AF195122; PIDN:AAF24289.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: crtI
C,Superfamily: phytoene dehydrogenase
C,Keywords: oxidoreductase
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Best Local Similarity 40.9
Matches 199; Conservative
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Jiang, H.P.; Cogdell, R.J.; Takaichi, S.; Runter, C.N.
Jubmitted to the EMBL Data Library, November 1994
Description: The complete DNA sequence, specific TNS insertion map and gene assignment
PREFerence number: S49619
                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                           KRWSMGLFVWYPGTKGTAXMWKDVGHHTVVVGPRYKEHVQDIFIKGELAEDMSLYVHRPS 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HRMFTPFDFRDELNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVGAGTHPGAGIPG 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPALAGKQLKDYVELLPVTPFYRLCWESGKVFNYDNDQAQLEAQIQQFNPRDVAGYRAFL 125
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                                                                                                                                 YRAFLDYSRAVFNEGYLKLGTVPFLSFKDMLRAAPQLAKLQAWRSVYSKVAGYIEDEHLR 180
                                                                                                                                                                            187
                                                                                                                                                                                                                                                                                                     NARVSHMETVGD-KIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQS 299
                                                                                                                                                                                                                                                                                                                                         NTEVDRILVSRDGKATGIRLMDGTBLPAQVVVSNADAGHTYKRLLRNRDRWRWTDEKLDK 307
                                                                                                                                                                                                                                                                                                                                                                                        KRMSNSLFVLYPGLN---HHHDQLAFHTVCFGPRYRELIHBIFNHDGLABDFSLYLHAPC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIDPSLAPEGCGSYYVLAPVPHLGTAN-LDWAVEGPRLRDRIFDYLEQHYMPGLRSQLVT 415
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           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alternate names: phytoene desaturase
Species: Rhodobacter sphaeroides
Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 13-Sep-1998
        MGRAVVIGAGLGGLAAAMRLGAKGYKVTVVDRLDRPGGRGSSITKGGHRFDLGPTIVTVP
                                                 SAIBELPALAGKOLKDYVELLPVTPFYRLCWESGKVFNYDNDQAQLEAQIQ2FNPRDVAG
                                                                              QAFSFHSLLVGGNPPATSSIYTLIHALEREWGVWFPRGGTGALVNGMIKLFQDLGGEVVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 36.8%; Score 959.5; DB 2; Length 518; Best Local Similarity 40.9%; Pred. No. 5.3e-69; Matches 199; Conservative 79; Mismatches 201; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hytoene dehydrogenase (EC 1.3.-,-) - Rhodobacter sphaeroides
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yResidues: 1-518 <LAN>
yCross-references: EMBL:X82458; NID:9575405; PID:9575407
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',Superfamily: phytoene dehydrogenase
',Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIGSAKATAGLM 487
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probable diapophytoene dehydrogenase crtN - Heliobacillus mobilis
C;Species: Heliobacillus mobilis
C;Species: Heliobacillus mobilis
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000
C;Accession: T31463
R;Xiong, J.; Inoue, K.; Bauer, C.E.
R;Xiong, J.; Inoue, K.; Bauer, C.E.
A;Ticle: Tracking molecular evolution of photosynthesis by characterization of a major p
A;Reference number: Z21036; MUID:99061957; PMID:9843979
A;Accession: T31463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
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                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residuee: 1.517 < XIO>
A;Residuee: 1.517 < XIO>
A;Cross-references: EMBL:AF080002; NID:g3820536; PID:g3820561; PIDN:AAC84034.1
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C;Date: 09-Nov-1990 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C;Accession: A35919
K;Schmidhauser, T.J.; Lauter, F.R.; Russo, V.B.A.; Yanofsky, C.
Mol. Cell. Biol. 10, 5064-5070, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 LFALAGKQLKDYVELLPVTPFYRLCWESGKVFNYDNDQAQLBAQIQQFNPRDVAGYRAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 HIRQAPSFHSLLVGGNPPATSSIYTLI----HALEREWGVWPPRGGTGALVNGMIKLPQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 LGGEVVLNARVSHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 FGGSLRVNAEVEQILIBQGRAVGVRLANGEVLKADVVISNADFPYTMENLVPASHRGKYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 AKKLQSKRMSNSLFVLYPGLNHHHDQLAHHTVCFGPRYRBLIHEIFNHDGLAEDFSLYLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 APCVTDPSLAPEGCGSYYVLAPVPHLGTANLDWAVEGPRLRDRIFDYLEQHYMPGLRSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 RPTKYDDSVAPPGKDIIYVLVPVPNL-SSGIDWKKETHRYRELVIKKLRRQGVTDLSKHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414 VTHRMFTPFDFRDELNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVGAGTHPGAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 VIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITDPSAIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----DYSRAVFNEGYLKLGTVPPLSFK-DMLRAAPQLAKLQAWRSVYSKVAGYIEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 AQIHRRYQVAREKFIE---KSFIKPSDPPNIDTLIGMMQLRTL---NNMYDDIARFIKDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91; Mismatches 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28.9%; Score 752; DB 2; 34.2%; Pred. No. 2.4e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: crtN
C;Superfamily: phytoene dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        474 PGVIGSAKATAGLMLED 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    483 PVVLVCCKLVSEQVLAD 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 34.2
Matches 170; Conservative
    482 ATAGLM 487
                                                 487 VTERLM 492
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                                                                                                                     RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                      Species: Myxococcus xanthus
Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 29-Sep-1999
Accession: S32169, S67952
Botella, J.; Murillo, F.; Ruiz-vazquez, R.
Botella, J.; Murillo, F.; Ruiz-vazquez, R.
Botella, J.; Murillo, F.; Ruiz-vazquez, R.
Bestription: Nucleotide and deduced protein sequences of a carotenoid gene cluster
Reference number: S32168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                 433
                                                                                       132 AQGRVQYRTSLDHLVGRNYAGLRDYLSPRVLARIFQVRAHRRAYADVSRFFQDERLRAAM 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 SFHSLLVGGNPFATSSIYTLIHALEREWGVWFPRGGTGALVNGMIKLFQDLGGEVVLNAR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGGYMLYLGMKRRYPELLHHNVVPGRDYKGSFDDIFEF-RVPEDPSFYVNAPTRTDASLA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 LPALAGKOLKDYVELLIPVTPFYRLCWESGKVFNYDNDQAQLEAQIQQFNPRDVAGYRAFL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 TFRAVGRRIEDYLTLLRCDPNYRVHFRDRSDVTFTSBLCAMGRBLBRVEPGSYARYLAFL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .26 DYSRAVFNEGYLKLGTVPFLSFKDML.--RAAPQLAKLQAWRSVYSKVAGYIBDEHLRQAF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 VSHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQSKRMS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSLFVLYFGLNHTHDQLAHHTVCFGPRYRELIHEIFNHDGLAEDFSLYLHAPCVTDPSLA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 PEGKDALYVIJVPVPH-QHPDLDWKVEGPKVRAKFFARMAELGFPSLESDIEVERRSSTPD 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFRDELNAWQGSAFSVEPILTQSAWFRPHNRDXHIDNLYLVGAGTHPGAGIPGVIGSAK- 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92
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                                6 VIGAGFGGLALAIRLQAAGIPVLLLEQRDKRGGRAYVYQEQGFTFDAGPTVITDPSAIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 VVGAGVGGLAAARLAHQGPDVQVFEKTQGPGGRCNRLQVDGFTWDLGPTIVIMPEVFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: EMBL:Z21955, NID:g577589; PIDN:CAA79956.1; PID:g288221 Experimental Source: strain DK1050
30tella, J.A.; Murillo, F.J.; Ruiz-Vazquez, R.
r. J. Biochem. 233, 238-248, 1995
Title. A clusteer of structural and regulatory genes for light-induced ca: Reference number: S67950; MUID:96061955; PMID:7588751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 PEGCGSYYVLAPVPHLGTANLDWAVEGPRLRDRIFDYLEQHYMPGLRSQL-VTHRMFTPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.1%; Score 757.5; DB 2; 35.6%; Pred. No. 8.8e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88; Mismatches 216;
                                                                                                                                                                                                                                                                                                                                                     pothetical protein 2 - Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: DNA
Residues: 9-37,462-488 <BOW>
Superfamily: phytoene dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 35.6
Matches 173; Conservative
                                                                                                                                                                                     481 KATAGL 486
                                                                                                                                                                                                                                  EVMAKL 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Residues: 1-517 <BOT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecule type: DNA
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295

355 357 413

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squalene synthase [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 02-Aug-2002
C;Accession: B90061
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
R;Kuroda, M.; Ohta, T.; Hattori, M.; Gasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Reterence number: A89768; MUID:21311952; PMID:11418146
A;Reterence number: A89768; MUID:21311952; PMID:11418146
A;Reterence number: A89768; MUID:21311952; PMID:1418146
A;Reterence number: A89768; MUID:21311952; PMID:213702511; PIDN:BAB43652.1; GSPDB:GN00149
A;Cross-references: GB:BAA000018; PID:213702511; PIDN:BAB43652.1; GSPDB:GN00149
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                                                                                          3 PT---TVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITD
                                                                                                                                                              60 PSAIEELFALAGKOLKDYVELLPVTPFYRLCWESGKVFNYDNDQAQLEAQIQQF-NPRDV
                                                                                                                                                                                                                                                                                                                                                                                  67 PHLADRAFAAVGDSLRRRVELTALDPAYRAČFADGSALDVHTDGEAMRAEVRRFAGPAQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGYRAFLDYSRAVFNEGYLKLGTVPFLSPKDMLRAAPQLAKLQA---WRSVYSKVAGYIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 DEHLROAFSFHSLLVGGNPPATSSIYTLIHALEREWGVWFPRGGTGALVNGMIKLPQDLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 GEVVINARVSHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 KLOSKRMSNSLFVLYFGLNHHHDQLAHHTVCFGPRYRELIHEIFNHDGLAEDFSLYLHAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356 CVTDPSLAPEGCGSYYVLAPVPH--LGTANLDWAVEGPRLRDRIFDYLEQHYMPGLRSQL
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Gaps
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23.9%; Score 624; DB 2; Length 50
Best Local Similarity 31.7%; Pred. No. 4.4e-42;
Matches 159; Conservative 98; Mismatches 221; Indels
76; Mismatches 235; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: phytoene dehydrogenase
     161; Conservative
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                                                                                                                                                                                                                                                                                        Cross-references: GB:M57465, GB:M33867, NID:g168746, PIDN:AAA33555.1, PID:g168747, Note: the authors translated the codon CTC for residue 157 as Glu, and GAG for residue 180 as Glu, and GAG 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.A.
     'Title: Cloning, sequence, and photoregulation of al-1, a carotenoid biosynthetic gene, Reference number: A35919; MUID:90377195; PMID:2144609; Accession: A35919; Accession: A35919; Accession: A35919; Accession: Preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Seeger, K.J.; Harris, D.; Thomson, N.R.; Parkhill, J.; Barrell, B.G.; Rajandream, ubmitted to the BMBL Data Library, September 1999 ;Reference number: Z21607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIDN: CAB53153.1; GSPDB:GN00070; SCOEDB:SCJ1.35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KQ-AKKLQSKRMSNSLFVLYFGLAHHHDQLAHHTVCFGPRYRBLIHEIFNHDGLAEDFSL 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YLHAPCVIDPSLAPEGCGSYYVLAPVPHL --- GTANLDWAVEGPRLRDRIFDYLEQHYMP 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 YIHVPSRVDPSAAPPDRDAVIALVPVGHLLQNGQPBLDWPTLVSKARAGVLATIQAR--T 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELFALAGKOL-KDYVELLPVTPFYRLCWESGKVFNYDNDQAQLEAQIQQFNPRDVAGYRA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 FLDYSRAVFNEGYLKLGTVPFLSFKDMLRAA-PQLA----KLQAWRSVYSKVAGYIEDE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 VVLNARVSHMETVG-----DKIQAVQLEDGRRFETCAVASNADVVHTYRDELSQHPAAA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 VIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGR-AYVYQEQGFTFDAGPTVITDPSAIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 24.4%; Score 635; DB 2; Length 595; Best Local Similarity 31.3%; Pred. No. 7.4e-43; Matches 158; Conservative 97; Mismatches 226; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary, translated from GB/EMBL/DDBJ:
Molecule type: DNA;
Residues: 1-523 <SEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTHPGAGIPGVIGSAKATAGLMLED 490
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Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.2%;
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                                                                                                                                                                                                              Molecule type: DNA;Residues: 1-595 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: T36968
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278]

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72

310 351

292

408

466

488

Query Match

Genetics:

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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA. Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; WUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (strain PCC 7120) plasmid pCC7120alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                         zeta-carotene desaturase [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7:
C,Species: Nostoc sp. PCC 7120
A;NOte: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AG2509
                               304 RLTDAALERAKYSCSTFWAYYGLDTVYADLPHHLIYLSESARRT-----DRDALEDRHVD 358
                                                                                                                                               417
                                                                                                                                                                                              464
                                                                                                                                                                                                                             345 AEDFSLYLHAPCVTDPSLAPEGCGSYYVLAPVPHLGTANLDWAVEGPRLRDRIFDYLEQH 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:BA000020; PIDN:BAB78339.1; PID:g17135793; GSPDB:GN00180
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 LYKELFEEAGLNPADYVQLKRLEPYTRLKF------WDGTQLDITSDLQSFKTQLATLR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 AIBELFALAGKOLKDYVELLPVTPFYRLCWESGKVFNYDNDQAQLEAQIQQFNPR---- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 -DV------AGYRAFL-DYSRAVFNEGYLKIG-TVPFLSFKDMLRAAPQL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKLOAWRSVYSKVAGYIEDEHLROAFSFHSLLVGGNPFATSSIYTLIHALEREWGVWPPR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTCALVNGMIKLFQDLGGEVVLMARVSHMETVGDKIQAVQLEDGRRFBTCAVASNADVV 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 WVDDSALDETDPPFYVCNPTIIDPSNAPAGHSTLFVLVPIPNTSYA-VDWDIXQXSYTDF 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IFDYLEQHYMPGLRSQLVTHRMFTPFDFRDELNAWQGSAFSVEPILTQSAWFRPHNRDKH 456
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                                                                                                                               405 YMPGLRSQEVTHRMFTPFDFRDELNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVG
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  296 K----LOSKRMSNSLFVLYFGLNHHHDQLAHHTVCFGPRYRELIHEIFNHDGL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
23.2%; Score 604; DB 2; Length 49
Best Local Similarity 29.8%; Pred. No. 1.8e-40;
Matches 153; Conservative 89; Mismatches 224; Indels
                                                                                                                                                                                                                                                                                               465 AGTHPGAGIPGVIGSAKATAGLMLED 490
                                                                                                                                                                                                                                                                                                                           478 GGTHPGSGLLTIMESANIAADYLTRE 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Genome: plasmid
C;Superfamily: phytoene dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-499 <KUR>
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Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 29-Sep-1999
Accession: S35306; S27594
Fontes, M.; Ruiz-Vazquez, R.; Murillo, F.J.
BO J. 12, 1255-1275, 1993
Title: Growth phase dependence of the activation of a bacterial gene for carotenoid Reference number: S35306; MUID:93223667; PMID:8467787
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-----DYSRAVFNEGYLKLGTVPFLSFKDMLRAAPQLAKLQAWRSVYSKVAGYIEDEH 178
                               125 TDVYKKYELARRYFLERTYRKPS----DFYNM-TSLVQGAKLKTLNHADQLIEHYIDNEK 179
                                                                                                LRQAFSFHSLLVGGNPFATSSIYTLIHALEREWGVWFPRGGTGALVNGMIKLFQDLGGEV 238
                                                                                                                             357 VPAVADKSLAPEGKTGIYVLMPTPELKTGSGIDWSDEALTQQIKELITKRLATIEVFEDI 416
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                                                                                                                                                                                                                                                                                            295 KKLQSKRMSNSLFVLYFGLN-HHHDQLAHHTVCFGPRYRELIHEIFNHDGLAEDFSLYLH 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 QLPGVLEQIFRRAARRLEDYVKLLPLDVNTRVHFWDGTHLDTTRHLDRWEAELAKFGPRQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 VAGYRAFLDYSRAVFNEGYLKL--GTVPFLSFKDMLRAAPQLAKLQAWRSVYSKVAGYIE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 ATFRMGTPVEKVRVDAGRAVGVKLVGGEVLDADAVVVNADLAYAARSLI---PAEAREGS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 TDPSAIRELPALAGKQLKDYVELLPVTPFYRLCWESGKVFNYDNDQAQLEAQIQQFNPRD 117
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Molecule type: DNA
Residues: 1-529 <PON's
Cross-references: EMBL:M94727; NID:g150079; PIDN:AAA25390.1; PID:g150080
                                                                                                                                                                                                                                                                                                                                                                                             354 APCVTDPSLAPEGCGSYYVLAPVPHLGT-ANLDWAVEG--PRLRDRIFDYLEQ-HYMPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410 RSQLVTHRMFTPFDFRDELNAWQGSAFSVEPILIQSAWFRPHNRDKHIDNLYLVGAGTHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ytoene dehydrogenase (BC 1.3...-) - Myxococcus xanthus
Alternate names: phytoene desaturase
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Keywords: carotenoid biosynthesis; oxidoreductase
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Best Local Similarity 30.2%;
Matches 153; Conservative 99
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126
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400 ILKRLHLIGYHNIEQHIVTQSCYTAQSWLDDYRVHLGAVPNLYBHNLYQLGPFRPPIRSEN 459

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earch completed: February 29, 2004, 14:52:52 ob time : 15.6946 secs

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Pebruary 29, 2004, 14:51:24 : Search time 32.666 Seconds
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3180.293 Million cell updates/sec
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(Ggn2_6/prodate/2/pubpaa/US07_NEW_PUB.pep:*

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enCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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ximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	•	Description	Sequence 32, Appl	Sequence 8, Appli	Sequence 234, App	Sequence 5, Appli	Sequence 4, Appli	Sequence 10579, A	Sequence 17830, A	Sequence 20438, A	Sequence 540, App	Seguence 19248, A	Sequence 7750, Ap	Sequence 19519, A	Sequence 16, Appl	Sequence 76, Appl	Semiance 22 Anni
	;	10	US-09-941-947A-32	US-10-218-118-8	US-10-369-493-234	US-09-547-267-5	US-09-920-923-4	US-10-369-493-10579	US-10-369-493-17830	US-10-369-493-20438	US-10-369-493-540	US-10-369-493-19248	US-10-369-493-7750	US-10-369-493-19519	US-09-934-903-16	US-09-934-868-76	118-09-941-9478-22
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		Score	2606	2606	1802	1595	1595	1464	1461	1183.5	1051	1014	962.5	793.5	703.5	703.5	703.5
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Seguence 4, Appli		•	Sequence	Sequen	Sequence	Sequence	Sequence 8562	Sequence	Sequence	Sequence 3769,		Sequence 18644	Sequence 14,				Sequence 3, Appli				Sequence 4194, Ap		Seguence 20440,	Seguence 1	Sequence 5		Sequence 2	Sequence 188	Compression
US-10-358-917-4	US-09-934-903-18	US-09-934-868-78	US-09-941-947A-24								US-10-369-493-21541									Þ		US-10-369-493-19518	US-10-369-493-20440	US-10-369-493-19986	US-10-438-784-5	US-10-209-372-6	US-10-369-493-2831	US-10-369-493-1887B	US-10-369-493-17259
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511	497	497	497	497	494	502	513	905	499	618	514	512	497	530	404	495	1268	536	498	439	548	485	496	537	469	542	542	539	498
27.0	26.4	26.4	26.4	26.4	24.3	23.9	23.7	23.6	23.2	23.1	21.1	20.8	18.6	17.7	17.1	16.7	16.7	16.6	16.1	15.9	25.8	15.7	25.5	15.0	14.9	14.6	14.6	14.4	13,1
703.5	687	687	687	687	633	624	616.5	614.5	604	602	549.5	541.5	484	461.5	444.5	434.5	434.5	433.5	420.5	415	410.5	410	403.5	390	388.5	380.5	380.5	375	342.5
16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	හ හ	40	41	42	43	44	45

ALIGNMENTS

Sequence 32, Application US/09941947A

PUblication No. US20030003528A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cheng, Qiong
APPLICANT: Dicosimo, Deana J.
APPLICANT: Dicosimo, Deana J.
APPLICANT: Dicosimo, Deana J.
APPLICANT: Miller, Edward S. Jr.
APPLICANT: Miller, Edward S. Miller, Ed

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61 SAIEBLFALAGKQLKDYVELLPVTPFYRLCWESGKVFNYDNDQAQLBAQIQQFNPRDVAG 120

1 MKPITVIGAGFGGIALAIRLQAAGIPVILLEQRDKPGGRAYVYQEQGFTFDAGPTVITDP 60

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US-10-369-493-234

Sequence 234, Application US/10369493

Publication No. US20030233675A1

Fublication No. US20030233675A1

APPLICANT: Cao, Yongwei

APPLICANT: Galdman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: PLANS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10 (52022) B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-28

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 234

LENGTH: 491
                                                                                                                                                                                                                                                                            361 SLAPEGCGSYYVLAPVPHLGTANLDWAVEGPRLRDRIFDYLEQHYWPGLRSQLVTHRMFT 420
                                             NARVSHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQSK 300
                                                                241 NARVSHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQSK 300
                                                                                                                      RMSNSLFVLYPGLMHHDQLAHHTVCPGPRYRBLIHEIFNHDGLAEDFSLYLHAPCVTDP 360
                                                                                                                                                     301 RMSNSLFVLYFGLNHHHDQLAHHTVCFGPRYRBLIHBIFNHDGLABDFSLYLHAPCVTDP 360
                                                                                                                                                                                                   SLAPEGCGSYYVLAPVPHLGTANLDWAVEGPRLRDRIFDYLEQHYMPGLRSQLVTHRMFT 420
        181 QAFSFHSLLVGGNPPATSSIYTLIHALEREWGVWFPRGGTGALVNGMIKLFQDLGGEVVL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SAIRELFLIAGKKWSDYIELLPISPFYRLOWQSGEIFDYGGDQVKLEKQIARFNPGDVQG 120
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67.4%; Pred. No. 4.5e-173;
tive 66; Mismatches 94;
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                                                                                                                                                                                                                                                                                                                                                           KATAGLMLEDLI 492
                                                                                                                                                                                                                                                                                                                                                                                            481 KATAGLMLEDLI 492
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Best Local Similarity 67.4
Matches 331; Conservative
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Publication No. US2030148319A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bricategio, Patricia
APPLICANT: Picateggio, Stephen
APPLICANT: Picateggio, Stephen
APPLICANT: Cheng, Qiong
TITLE OF INVENTION: Genes Encoding Carotenoid Compounds
FILE REFERENCE: CL1876 US NA
CURRENT PELICATION NUMBER: US/10/218,118
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: 60/312,646
NUMBER OF SEQ ID NOS: 14
SOFTWARRE: Microsoft Office 97
SEQ ID NOS: 14
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100.0%; Score 2606; DB 14;
Best Local Similarity 100.0%; Pred. No. 2.2e-254;
Matches 492; Conservative 0; Mismatches 0;
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S-10-218-118-8
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APPLICANT: Tsygankov, Yuri
TITLE OF INVENTION: Improved Permentative Carotenoid Production
FILS REFERENT Improved Permentive Carotenoid
CURRENT APPLICATION NUMBER: US/09/920,923
CURRENT FILING DATE: 2001-08-02
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PRIOR FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.1
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Publication No. US20030022273A1
GENERAL INFORMATION:
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                                        SLAPEGCGSYYVLAPVPHLGTANLDWAVEGPRIRDRIFDYLEQHYMPGLRSQLVTHRMFT
                                                             PPDFRDELNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVGAGTHPGAGIPGVIGSA
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APPLICANT: Pasamontes, Luis
APPLICANT: Pessier, Michel
APPLICANT: van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SUCURNES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , DB 9;
3.9e-152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: POKTAS, Bruce A.
REGISTRATION NUMBER: 32,748
REGISTRATION NUMBER: RAN 6002/170
TELECOWUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
TELEPRICON: (201) 235-363
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 494 amino acids
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/660,645
                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09547267
Patent No. US20020147371A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340 Kingsland Street
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amino acid
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Matches 304; Conservative
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KITANLMIEDL 491
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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STREET: 340 K
CITY: Nutley
STATE: NJ
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RESULT 7

US-10-369-493-17830

i Sequence 17830, Application US/10369493

j Fublication No. US20030233675A1

j GENERAL INFORMATION:
   APPLICANT: Cao, Yongwei
   APPLICANT: Goldman, Barry S.
   APPLICANT: WINNERNER: US/10/369,493
   CURRENT APPLICATION NUMBER: US/10/369,493
   CURRENT PILING DATE: 2003-02-28
   PRIOR PRILING DATE: 2003-02-21
   NUMBER OF SEQ ID NOS: 47374
   SEQ ID NO 17830
   LENGTH: FOL
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                               421 PFDFRDELNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVGAGTHPGAGIPGVIGSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKPTTVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RMSNSLFVLYFGLNHHHDOLAHHTVCFGPRYRBLIHEIFNHDGLABDFSLYLHAPCVTDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.1%; Score 1461; DB 15; 56.8%; Pred. No. 1.4e-138; ive 75; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity 56.8
279, Conservative
                                                                                                                                                                  487 KATARLMLEDL 497
                                                                                                           481 KATAGLMLEDL 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KATAGLMLEDL 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: SPHINGOMONAS
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Best Local Si
Matches 279;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10579, Application US/10369493
Sequence 10579, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Calcal Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Gloman, Barry S.
APPLICA
301 RMSNSLFVLYFGINHHHDQLAHHTVCFGPRYRELIHEIFNHDGLAEDFSLYLHAPCVTDP 360
                               SLAPEGCGSYYVLAPVPHLGTANLDWAVEGPRLRDRIFDYLEQHYMPGLRSQLVTHRMFT 420
                                                                                                                                        PFDFRDELNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVGAGTHPGAGIPGVIGSA 480
                                                                                                                                                                                                                                             120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Sphingomonas arcmaticivorans
S-10-369-493-10579
                                                                                                                                                                                                                                                                                                                                                                               491
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KATAQVMLSDL
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APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFETIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICANTON NUMBER: US 10/369,493
PRIOR PELLING DATE: 2003-02-28
PRIOR PELLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO S40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19248, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                LENGTH: 548
TYPE: PRT
ORGANISM: Deinococcus radiodurans
Einkle, Gregory J.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 229; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-10-369-493-19248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 DYSRAVFNEGYLKLGTVPFLSPKDMLRAAPQLAKLQAMRSVYSKVAGYIEDEHLRQAFSF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 HSLLVGGNPFATSSIYTLIHALEREWGVWFPRGGTGALVNGMIKLFQDLGGEVVLNARVS 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 HPLLIGGNPEWSSSVYCLITYLEKQWGVHSAMGGTGALVTGLVNLIEGGGNTIRYNQDVR 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 QIVVENGTACGVKLADGEVIKADIVVSNADSASTYRYLLPPETRKRWTDAKIEKSRYSMS 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306 LFVLYFGLAHHDQLAHHTVCFGPRYRELIHEIFNHDGLAEDFSLYIHAPCVTDPSLAPE 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 LFVWYEGTKRRYEDVKHHTILLGPRYKELISDIFSRKVVAEDFSLYLHRPTATDPSLAPQ 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGSYYVLAPVPHLGTANLDWAVEGPRLRDRIFDYLEQHYMPGLRSQLVTHRMFTPFDFR 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DELNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVGAGTHPGAGIPGVIGSAKATAG 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 VIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITDPSAIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 HMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQSKRMSNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.4%; Score 1183.5; DB 15; Lengt
47.5%; Pred. No. 1.6e-110;
tive 84; Mismatches 169; Indels
                                                                                                                                  APPLICANT: Con. Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewen C.
APPLICANT: Slater, Stewen C.
APPLICANT: Slater, Stewen C.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-18
NUMBER OF SEQ ID NOS: 47374
                                SULT 8
3-10-360-493-20438
5-quence 20438, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Rhodopseudomonas palustris-10-369-493-20438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -10-369-493-540
Sequence 540, Application US/10369493
Publication No. US20030233675A1
ETRIREAL INFORMATION:
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 47.53
Matches 230; Conservative
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LVPE 497
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Blatter, Steven C.
APPLICANT: Slatter, Steven C.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10 (52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
                                                                                                                                                                                                                                                77 HFIEELFALERDRAGLDAPDYPPEVLSGERVKEGVSGCPHTSRYVTLVPILPFYRIVFHD 136
                                                                                                                                                                                                                                                                                                                                                      137 GTYFDYDGDPESTRROIAELAPGDLAGYERFHADAEAIFRRGFLELGYTHFGDVPTMLRV 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 AVASNADVVHTYRDLLSQHPAAAKQAKKLQSKRMSN--SLFVLYFGLMHHHD-QLAHHTV 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 LVASNGDWANTY--LKRVRPSARLVNSDLRVKAASESMSLLVVYFGFRGGDDLPLKHHNI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326 CFGPRYRELIHRIFNHDGLAEDFSLYLHAPCVTDPSLAPEGCGSYTVLAPVPHLGTANLD 385
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                                                                                                                                                                 96
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                                                                                                                                                154 APQLAKLQAWRSVYSKVAGYIEDEHLRQAFSFHSLLVGGNPFATSSIYTLIHALEREWGV
                                                           Gaps
                                                        40;
     Length 548;
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40.3%; Score 1051; DB 15;
43.5%; Pred. No. 4.8e-97;
tive 72; Mismatches 185;
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us-09-941-947a-32.rapb

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0uery Match
Best Local Similarity 41.23
Matches 200; Conservative
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US-10-369-493-7750
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Publication No. US20030233675A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gan', Yongwei
APPLICANT: Glater, Steven C.
AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 LEALAGKOLKDYVELLEPVTPFYRLCWESGKVFNYDNDQAQLEAQIQQFNPRDVAGYRAFL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 SHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQSKRMSN 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.9%; Score 1014; DB 15; Length 44.0%; Pred. No. 2.3e-93; tive 80; Mismatches 185; Indels
                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(498)
O'THER INFORMATION: unsure at all Xaa locations
S-10-369-493-19248
                              PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 19248
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ORGANISM: Rhodobacter sphaeroides
   2003-02-28
                                                                                                                                                                                           TYPE: PRT ORGANISM: Myxococcus xanthus
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   CURRENT FILING DATE:
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Matches 210; Conserv
                                                                                                                                                                LENGIH: 498
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Sequence 19519, Application US/10369493

Sequence 19519, Application US/10369493

Fublication No. US20030233675A1

Fublication No. US20030233675A1

FUBLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)8

FILE REFERENCE: 38-10(52052)8

FURNERY TAPLICATION UNMBER: US 60/360,039

PRIOR APPLICATION UNMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 19519

LENGTH: 517
                                                       'n,
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                                                                                                                                                                                                                                                         195 HPLFIGGDPFNVTSMYILVSQLEKEPGVHYAIGGVAALAAAMAKVIEGQGGSPRMNTEVD 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 BILVEKGTATGVRLASGEVIRAGLVVSNADAGHTYMRLIRNHPRRRWIDAHVKSRRWSMG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||| ::| |:||||| | :|| ||| || 315 APEGDDIFYALSPVPHIKQAQPVDWQAVAEPYRESVLEVLEQS-MPGIGERIGPSLVFTP 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 HMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQSKRMSNS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 APEGCGSYYVLAPVPHLGTAN-LDWAVEGPRLRDRIFDYLEQHYMPGLRSQLVTHRMFTP 421
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                                                                                                                                                              15 VIGSGLGGLAAAMRLGAKGWRVTVIDKLDVPGGRGSSITQEGHRFDLGPTIVTVPQSLRD
                                                                                                                                                                                                                                                                                                                                   126 DYSRAVFNEGYLKLGTVPPLSFKDMLRAAPQLAKLQAWRSVYSKVAGYIEDEHLRQAFSF
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                                                          Gaps
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30.4%; Score 793.5; DB 15; Length 517;
Best Local Similarity 36.1%; Pred. No. 4.8e-71;
Matches 175; Conservative 89; Mismatches 214; Indels 7;
  518;
  Length
36.9%; Score 962.5; DB 15; Length
41.2%; Pred. No. 3.9e-88;
tive 78; Mismatches 201; Indels
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ORGANISM: Myxococcus xanthus
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---LKLGTVPFLSFKUMLRAAPQLAKLQAWRSVYSKVAG 172
                                                                                                                                                                                                                                                                                                                           Q--AKKLQSKRMSNSLFVLYFGLNHHHDQLAHHTVCFGPRYRELIHBIFNHDGLAEDFSL 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 YLHAPCVTDPSLAPEGCGSYYYLAPVPHLGTANLDWAVEGPRLRDRIFDYLEQHY-MPGL 409
                                                                                                                                                                                                                                                                                                                                                                                                                                     122 RAFLDYSRAVFNEGY-----LKLGTVPFLSFKDMLRAAPQLAKLQAWRSVYSKVAG 172
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                                                                                                                                                   YIEDEHLROAPSFHSLLVGGNPFATSSIYTLIHALEREWGVMFPRGGTGALVNGMIKLFO
                                                                                                                                                                                                                                       DLGGEVVLNARVSHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAK
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APPLICANT: Cofon, James M
APPLICANT: Cofon, James M
APPLICANT: Cofon, James M
APPLICANT: Cofon, James M
TITLE OF INVENTION: DEMINISTRYING METHANOTROPHIC BACTERIAL STRAIN
PILE REFERENCE: CL1596 US NA
CURRENT PPLINGATION NUMBER: US/09/934,868
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Microsoft Office 97
SEQ ID NO 76
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US-09-934-868-76
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Patent No. US20020137190A1
GENERAL INFORMATION:
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                                                                 RAFLDYSRAVFNEGY-
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ORGANISM: Methylomonas 16a
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US-09-934-868-76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRDELNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVGAGTHPGAGIPGVIGSAK-A 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAGTENLARGSAFGLSONFTOIGPFRPSNODARVKNIFFVGASTOPGTGLPTVLISARLY 487
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      12 VVGAGVGGLAAAARLAHQGFDVQVFEKTQGPGGRCNRLQVDGFTWDLGPTIVLMPEVFEE
                                               LPALAGKQLKDYVELLPVTPFYRLCWESGKVFNYDNDQAQLEAQIQQFNPRDVAGYRAFL
                                                                                      TFRAVGRRIEDYLTLLRCDPNYRVHFRDGSDVTFTSBLCAMGRELERVBPGSYARYLAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/09934903
Patent No. US20020102690A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Koffas, Mattheos APPLICANT: Odom, J. Martin
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ORGANISM: Methylomonas 16a
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                                                                                           Q--AKKLQSKEMSNSLFVLYFGLNHTHDQLAHHTVCFGPRYRELIHEIFNHDGLAEDFSL 350
                                                                                                                                                             351 YLHAPCVIDPSLAPEGCGSYYVLAPVPHLGTANLDWAVEGPRLRDRIFDYLEQHY-MPGL 409
                                                                                                                                                                                                                                            410 RSQLVTHRWFTPFDFRDELNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVGAGTHP 469
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APPLICANT: Cheng, Olong
APPLICANT: Dicosimo, Deana J.
APPLICANT: Offes, Mattheos
APPLICANT: Miler, Edward S. Jr.
APPLICANT: Oden, J. Martin
APPLICANT: ON NUMBER: US/09/941,947A
CURRENT APPLICATION NUMBER: US/09/941,947A
CURRENT APPLICANTION NUMBER: 00/229,907
PRIOR PILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 60
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GSGLPTIYESARISAKLI 489
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SEQ ID NO 22
LENGTH: 511
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ORGANISM: Methylomonas 16a
IS-09-941-947A-22
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Sequence 8, Appli Sequence 7549, Ap Sequence 15, Appli Sequence 24944, A Sequence 27, Ap Sequence 22, Appli Sequence 1, Appli Sequence 1, Appli Sequence 4, Appli

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COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDITUM TYPE: Diskette, 3.50 inch, 720Kb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: N/A CURRENT APPLICATION NUMBER: US/07/783,705A PLILNG DATE: 19911023 CLASSIFICATION NUMBER: US/07/783,705A PLILNG DATE: 19911023 CLASSIFICATION NUMBER: US 07/519,011 APPLICATION NUMBER: US 07/519,011 FILING DATE: 05-MR-1990 APPLICATION NUMBER: US 07/519,011 FILING DATE: 05-MR-1990 APPLICATION NUMBER: US 07/519,011 FILING DATE: 19-ARR-1990 APPLICATION NUMBER: US 07/519,011 FILING DATE: 19-ARR-1990 APPLICATION NUMBER: US 07/519,011 TELERBACTION NUMBER: 33,778 TELECOMMUNICATION NUMBER: 33,778 TELERBACTION NUMBER: 33,778 TELERBACTION NUMBER: 212-246-5559 TELERBACTION NUMBER: 212-246-5559
US-09-191-998-8
US-09-497-698-8
US-09-28-352-7549
US-09-067-626-4
US-09-650-942-15
US-09-522-991A-24944
US-09-567-003C-22
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US-09-690-942-10
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US-08-08-323-4
US-09-102-420B-4
US-09-102-420B-4
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US-09-102-420B-4
US-09-102-420B-4
US-09-102-420B-4
US-09-071-296-4
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Patent No. 5429939
GENERAL INPORMATION
APPLICANT: Misawa, No. 5429939ihiko
APPLICANT: Mobayashi, Kazuo
APPLICANT: Nakamura, Katsumi
APPLICANT: Vamano, Shigeyuki
TITLE OF INVENTION: DNA SEQUENCES USEFUL FOR THE
TITLE OF INVENTION: SYNTHESIS OF CARCTENOIDS
INUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSER: Ladas & Parry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 492 amino acids
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MOLECULE TYPE: protein
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1 MKPITVIGAGFGGLALAIRL......IPGVIGSAKATAGLMLEDLI 492
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Sequence 32,
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.: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                    GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-096-613A-10
US-08-096-623A-10
US-08-096-63A-10
US-08-096-63A-10
US-08-096-63A-10
US-09-298-718-5
US-09-298-718-5
US-09-298-718-5
US-09-934-903-18
US-09-944-903-18
US-09-944-903-18
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US-09-944-903-18
US-08-132-168A-32
US-08-132-168A-32
US-08-08-31-8
US-08-08-31-8
US-08-08-31-8
US-09-071-256-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nimum DB seq length: 0
ximum DB seq length: 200000000
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Match Length
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1849. S
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rfect score:
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                                                                                                                                                                                                                                                                                                                                         guence:
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Length 492;

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TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-095-726-8
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                                                                        TELEPHONE:
TELEFAX: 3
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                                                                                                                                                                                                                                                                     121 YRQFLDYSRAVFKEGYLKLGTVPFLSFRDMLRAAPQLAKLQAWRSVYSKVASYIEDEHLR 180
                                                                                                                                                                                                                                                                                                                            181 QAFSFHSLLVGGNPFATSSIYTLIHALEREWGVWFPRGGTGALVNGMIKLFQDLGGEVVL 240
                                                                                                                                                                                                                                                                                                                                                 NARVSHMETVGDKIQAVQLEDGRRFEICAVASNADVVHTYRDLLSQHPAAAKQAKKLQSK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 PPDFRDQLNAYHGSAFSVEPVLTQSAWFRPHNRDKTITNLYLVGAGTHPGAGIPGVIGSA 480
                                                                                                                                                           61 SAIBELFALAGKOLKDYVELLPVTPFYRLCWESGKVFNYDNDQAQLEAQIQQFNPRDVAG 120
                                                                                                                  9
                                                                                                               1 MKPTTVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYEDQGFTFDAGPTVITDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ausich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Michari, Indrani
APPLICANT: Yanger, John H
APPLICANT: Yanger, James G
APPLICANT: Yen, Huei-Che B
TITLE OF INVENTION: Beta-Carotene Biosynthesis in
TITLE OF INVENTION: Genetically Engineered Hosts
NUMBER OF SEQUENCES: 79
Pred. No. 1e-234;
          93.5%; Pred. ...
tive 13; Mismatches
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APPLICATION NUMBER: US/08/095,726
FILING DATE: 21-UUL-1993
CLASSIPICATION A73:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,566
FILING DATE: 30-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP. 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5530188
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Matches 460; Conservative
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200 E Randolph St
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APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Brinkhaus, Indrani
APPLICANT: Proffitt, Indrani
APPLICANT: Proffitt, John H
APPLICANT: Yarger, James G
APPLICANT: Yarger, James G
APPLICANT: Yarger, John H
TITLE OF INVENTION: Genetically Engineered Hosts
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
AMONO COLP., Patents and Licensing Dept
                                                                                                                                                                                                                                                                                                                        71.0%; Score 1849.5; DB 1;
72.3%; Pred. No. 6.1e-176;
iive 44; Mismatches 89;
ATTORNEY/AGENT INFORMATION:
MAME: Galloway, No. 5530188val
TELECOMMUNICATION INFORMATION:
TELEPHOKE: 3128567180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08096043; Patent No. 5530189; GENERAL INFORMATION:
                                                                                        TELEFAX: 3128664972
INFORMATION FOR SEG ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 489 amino acids
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 72.3
Matches 355; Conservative
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478 ESTASLMIEDL 488
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TALEALFTLAGREMEDYVELLPVXPFYRLCWESGKTLDYANDSFELEAQITQFNPRDVEG 120
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72.3%; Pred. No. 6.1e-176;
tive 44; Mismatches 89;
                                                                                   COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTHWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,043
FILING DATE: 22-UUL-1993
CLASSIFFICATION PATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/785,568
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5530189val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1218671180
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acids
TYPE: amino acid
                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 72.3 Matches 355; Conservative
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ESTASLMIEDL 488
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MOLECULE TYPE: protein
:-08-096-043-8
                    ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COUNTRY:
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Sequence 8, Application US/08096623A Patent No. 5684238 GENERAL INFORMATION:

SSULT 4 3-08-096-623A-8

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APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H.
APPLICANT: Yarger, James
APPLICANT: Yarger, James
APPLICANT: Yarger, James
TITLE OF INVENTION: Blosynthesis of Zeaxanthin and
TITLE OF INVENTION: Glycosylated Zeaxanthin in Genetically Engineered Hosts
NUMBER OF SEQUENCES: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TALEALFTLAGRRWBDYVRLLPVKPFYRLCWBSGKTLDYANDSFELBAQITQFNPRDVBG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 YRAFLDYSRAVFNEGYLKLGTVPFLSFKDWLRAAPQLAKLQAWRSVYSKVAGYIEDEHLR 180
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72.3%; Pred. No. 6.1e-176;
viematches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
CURRALING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US 07/805,061
FILING DATE: 22-JUL-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/662,921
FILING DATE: 09-DEC-1991
FILING DATE: 28-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/525,551
FILING DATE: 10-MAY-1990
ATTORNER: US 02-MAR-1990
                                                                                                                                                                                                                                                                       3: Welsh & Katz, Ltd.
120 S. Riverside Plaza, 22nd Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 29,381
REPERENCE/DOCKET NUMBER: AMO-006.1
TELECOMMUNICATION:
TELEPHONE: (312) 655-1500
TELEPAX: (312) 655-1501
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH. A.
Ausich, Rodney L.
Brinkhaus, Friedhelm
Mukharji, Indrani
Proffitt, John H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Gamson, Edward P
REGISTRATION NUMBER: 23
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Matches 355; Conservative
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                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Korristrer: 120 S. Riveri
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181 QAFSFHSLLVGGNPFTTSSIYTLIHALBREWGVWFPEGGTGALVNGMVKLFTDLGGEIEL 240
                                                                                                                                                                                                                                                                                                                                            241 NARVSHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQSK 300
                                                                                                                                                                                                                                                                                                                                                                    61 SAIBELFALAGKOLKDYVELLPVTPFYRLCWESGKVFNYDNDQAQLEAQIQQFNPRDVAG
                                                                                                                                                                          121 YRAFLDYSRAVFNEGYLKLGTVPFLSFKDMLRAAPQLAKLQAWRSVYSKVAGYIEDEHLR
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                                                61 TALEALFTLAGRRAEDYVRLLPVKPFYRLCWESGKTLDYANDSFELRAQITQFNPRDVBG
                                                                                                                                                                                                                                                             QAFSFHSLLVGGNPFATSSIYTLIHALEREWGVWPPRGGTGALVNGMIKLPQDLGGEVVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Ausich, Rodney L

APPLICANT: Mukharji, Indrani

APPLICANT: Mukharji, Indrani

APPLICANT: Yarger, James G

APPLICANT: Yarger, James G

APPLICANT: Yen, Huei-Che B

TITLE OF INVENTION: Lycopene Biosynthesis in

TITLE OF INVENTION: Genetically Engineered Hosts

NUMBER OF SEQUENCES: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONDUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
CONFAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
RILING DATE: 22-JUL-1993
CIASSIPICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,568
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Galloway, No. 5530189val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 10, Application US/08096043; Patent No. 5530189
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478 ESTASLMIEDL 488
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: IL
COUNTRY:
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                                                                                                                                              301 RMSNSLFVLYFGLNHHHDQLAHHTVCFGPRYRBLIHBIFNHDGLAEDFSLYLHAPCVTDP 360
                                                                                                                                                                                                                                                       241 NARVSHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQSK 300
                                                                                     301 SMSNSLFVLAFGLNQPHSQLAHHTICFGPRYRELIDEIFTGSALADDFSLYLHSPCYTDP 360
                                                                                                                                                                                                                               361 SLAPEGCGSYYVLAPVPHLGTANLDWAVEGPRLRDRIFDYLEQHYMPGLRSQLVTHRMFT 420
                                                                                                                                                                                                                                                                                                                421 PFDFRDELNAWQGSAFSVEPILTQSAWFRPHNRDXHIDNLYLVGAGTHPGAGIPGVIGSA 480
                                                                                                                                                                                                                                                                                                                                                 421 ROISKHAWIAILGSLFIBPPSLTQGLF--AANATRH-SNLYLVAAGTHPGAGIPGVVGLA 477
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APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Brinkhaus, Indrani
APPLICANT: Proffitt, John H
APPLICANT: Yarger, James G
APPLICANT: August G
ADPRESSEE: Amoco Corp., Patents and Licensing Dept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Amoco Corp., Patents and Licensing Dept 200 E Randolph St
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70.8%; Score 1845.5; DB 1
Best Local Similarity 72.1%; Pred. No. 1.5e-175;
Matches 354; Conservative 45; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA

ZIP: 60680-0703

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
FILING DATE: 21-UUL-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DITA:
APPLICATION NUMBER: US 07/785,566
FILING DATE: 30-007-1991
ATTONNEY/AGENT INPORMATION:
NAME: Galloway, No. 5530188val B
TELECHONE: 312856180
TELECHONE: 312856180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08035726
Patent No. 5530188
GENERAL INFORMATION:
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'FROGHE 489 amino acids
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478 ESTASLMIEDL 488
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STREET: 200 -
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IS-08-095-726-10
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COMPUTER REALMALL

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/096,623A
FILING DATE: 22-JUL-1993
CLASSIFICATION NUMBER: US 07/805,061
FILING DATE: 09-DEC-1991
PRIOR APPLICATION NUMBER: US 07/805,061
FILING DATE: 28-FEB-1991
PRIOR APPLICATION NUMBER: US 07/662,921
FILING DATE: 09-DEC-1991
PRIOR APPLICATION NUMBER: US 07/562,674
FILING DATE: 03-AUG-1990
PRIOR APPLICATION NUMBER: US 07/562,674
FILING DATE: 18-MAY-1990
PRIOR APPLICATION NUMBER: US 07/562,674
FILING DATE: 18-MAY-1990
PRIOR APPLICATION NUMBER: US 07/562,674
FILING DATE: 18-MAY-1990
PRIOR APPLICATION NUMBER: US 07/563,613
FILING DATE: 02-MAR-1990
PRIOR APPLICATION NUMBER: US 07/487,613
FILING DATE: 18-MAY-1990
PRIOR APPLICATION NUMBER: US 07/487,613
FILING DATE: 02-MAR-1990
PRIOR APPLICATION NUMBER: 29-381
REPERENCE/DOCKET NUMBER: 29-381
REPERENCE/DOCKET NUMBER: 29-381
REPERENCE/DOCKET NUMBER: 29-381
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 NARVEELVVADNRVSQVRLADGRIFDTDAVASNADVVNTYKKLIGTIPVGQKRAARLERK 300
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                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                               89:
                                                                                                                                                                                                                                                                                         70.8%; Score 1845.5; DB 1
72.1%; Pred. No. 1.5e-175;
iive 45; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ausich, Rodney L. APPLICANT: Brinkhaus, Friedhelm L. APPLICANT: Brinkhaus, Friedhelm L. APPLICANT: Mukharji, Indrani APPLICANT: Yarger, James G. APPLICANT: Yarger, James G. APPLICANT: Yen, Huei-Che B. TITLE OF INVENTION: Biosynchesis of TITLE OF INVENTION: Glycosylated Zeau NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Litd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S-08-096-623A-10
Sequence 10, Application US/08096623A
Patent No. 5684238
GENERAL INFORMATION:
             TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128567180
                                                                                           10:
                                                                                                                                        LENGTH: 489 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                    Best Local Similarity 72.1%
Matches 354; Conservative
                                                             TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ESTASLMIEDL 488
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489 amino acids amino acid

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                                                                                                                                                                                                                                                     301 RMSNSLFVLYFGLANHHDQLAHHTVCFGPRYRELIHBIFNHDGLAEDFSLYLHAPCVTDP
                                                                                                                 1 MKPTTVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQFFTFDAGPTVITDP
                                                                                    Gaps
                                                       Length 489;
                                                                                  Indels
                                                       DB 1;
                                                                       5e-175;
                                                      70.8%; Score 1845.5;
72.1%; Pred. No. 1.5e
Live 45; Mismatches
                                                           Query Match
Best Local Similarity 72.1%
Matches 354; Conservative
TOPOLOGY: linear MOLECULE TYPE: protein
                            US-08-096-623A-10
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of Zeaxanthin and Zeaxanthin in Genetically Engineered Hosts

E: Welsh & Katz, Ltd. 120 S. Riverside Plaza, 22nd Floor

STREET: 120 CITY: Chicago STATE: IL COUNTRY: USA ZIP: 60606

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241 NARVTRIDTEGDRATGVTLLDGRQLRADTVASNGDVMHSYRDLLGHTRRGRTKAAILNRQ 300
                                                                                                                                           241 NARVSHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQSK 300
                                                                                                                                                                                                              SLAPEGCGSYYVLAPVPHLGTANLDWAVEGPRLRDRIPDYLEQHYMPGLRSQLVTHRMFT 420
                                                                                                                                                                                                                                       361 SLAPEGASTHYVLAPVPHLGRADVDWEAEAPGYAERIFEELERRAIPDLRKHLTVSRIFS 420
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                                                                                                                     RMSNSLFVLYFGLMHHHDQLAHHTVCFGPRYRELIHEIPNHDGLAEDFSLYLHAPCVTDP
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APPLICANT: Pasamontes, Luis
APPLICANT: Pasamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: Van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
WOMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,718
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CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/660,645
FILING DATE:
ATYONEN'AGENT INFORMATION:
NAME: POKEAS, Bruce A.
REGISTRATION NUMBER: 32,748
REGISTRATION NUMBER: 32,748
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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340 Kingsland Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 494 amino acids
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amino acid
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Best Local Similarity 61.9<sup>3</sup>
Matches 304; Conservative
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STATE: NJ
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421 RQTSRHAWIAILGSLFIEPPSLTQGLF--AANATRH-SNLYLVAAGTHPGAGIPGVVGLA 477
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                                                                                                                                                                                                                                                                                                   APPLICANT: Hohmann, Hans-Peter
APPLICANT: Pseamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: van Loon, Adolphus
APPLICANT: van Loon, Adolphus
TITLE OF INVENTION: FREMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: PIOPPY disk
COMPUTER READABLE FORM:

MEDIUM TYPE: PIOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,645A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: EP 9510888.9
FILING DATE: 09-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: POKRAS, BTUCE A.
RESTSATION NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
TELEPHONE: (201) 235-5801
TELEPACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                  Sequence 5, Application US/08660645A Patent No. 6087152 GENERAL INFORMATION:
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478 ESTASLMIEDL 488
                                                                        481 KATAGLMLEDL 491
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STATE: NJ
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STREET: 34
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S-08-660-645A-5
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INFORMATION FOR SEQ ID NO:
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Best Local Simi
Matches 304;
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US-08-980-832-4
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LENGTH: 494
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PFDFRDELNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVGAGTHPGAGIPGVIGSA
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APPLICANT: Tessier, Michel
APPLICANT: Tessier, Michel
APPLICANT: van Loon, Adolphus
TITLE OF INVENTION: PERMENTATIVE CAROTEMOID PRODUCTION
NUMBER OF SECURNES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Pokras, Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCZ/DOCKET NUMBER: RAN 6002/170
TELECOMUNICATION INFORMATION:
TELEPHONE: (201) 235-2861
TELEFAX: (201) 235-2363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Hoffmann-La Roche Inc
340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
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Patent No. 6207409
GENERAL INFORMATION:
APPLICANT: HOLMANN, HANS-Peter
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KATAQVMLSDL 491
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ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CITY: Nutley
STATE: NJ
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Patent No. 6291204
GRAKEAL INFORMATION:
APPLICANT: Pasamontes, Luis
APPLICANT: Tsygankov, Yuri
TITLE OF INVENTION: Improved Fermentative Carotenoid Production
FILE REFERENCE: Improved Fermentive Carotenoid
CURRENT APPLICATION NUMBER: US/08/980,832B
CURRENT FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                    Length 494;
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                                                                                                                                                                                                           Query Match 61.2%; Score 1595; DB 3; Length 4
Best Local Similarity 61.9%; Pred. No. 1.6e-150;
Matches 304; Conservative 65; Mismatches 122; Indels
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SEQUENCE CHARACTERISTICS:
LENGTH: 494 amino acids
TYPE: amino acid
STRANDEDNESS: single
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481 KATAOVMLSDL 491
                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-546-969-5
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                                                                                                                61 DSLRELWALSGQPMERDVTLLPVSPFYRLTWADGRSFEVVNDDDELIRQVASFNPADVDG 120
                                                                                                                                                        121 YRAPLDYSRAVFNEGYLKLGTVPFLSFKDMLRAAPQLAKLQAWRSVYSKVAGYIEDEHLR 180
                                                                                                                                                                             NARVSHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQSK 300
                                                                                                                                                                                                                                                                                                                                          301 RMSNSLFYLYPGLNHHHHDQLAHHTVCFGPRYRELIHEIFNHDGLAEDFSLYLHAPCVTDP 360
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9
                     421 PFDFRDELNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVGAGTHPGAGIPGVIGSA
MKPTTVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITDP
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APPLICANT: Pasamontes, Luis
APPLICANT: Pasamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: Tessier, Michel
APPLICANT: PERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-ia Roche Inc.
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIF: 0710
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Pokras, Bruce A.
REGISTRATION NUMBER: 32,748
REPERBENCE/DOCKET NUMBER: RAN 6002/170
TELECOMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 340 Kingsland Street CITY: Nutley STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/09547267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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IS-09-547-267-5
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                                                                                                                                                                                                                                                    Length 494;
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Patent No. 6677134

GENERAL INFORMATION:

APPLICANT: Pasamontes, Luis

APPLICANT: Taygankov, Yuri

TITLE OF INVENTION: Fermentative Carotenoid Production
FILE REFERENCE: 15464 US (C38435/125944)

CURRENT PILING DATE: 2001-08-02

PRIOR PILING DATE: 1997-12-01

PRIOR APPLICATION NUMBER: 08/980,832

PRIOR PILING DATE: 1997-12-01

PRIOR PILING DATE: 1997-12-01

PRIOR PILING DATE: 1997-12-01

PRIOR PILING DATE: 1997-12-01

PRIOR PILING DATE: 1097-12-01

                                                                                                                                                                                                                                                   61.2%; Score 1595; DB 4;
61.9%; Pred. No. 1.6e-150;
ive 65; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.2%; Score 1595;
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                                                                      LENGTH: 494 amino acids
TYPE: amino acid
STRANDEDNESS: single
TELEFAX: (201) 235-2363
INPORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 494 amino acids
                                                                                                                                                                                                                                                                               Best Local Similarity 61.9
Matches 304, Conservative
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                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                               linear
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                                                                                                                                                                                                US-09-547-267-5
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294 KYTPENLKQREYSCSTFMLYLGLDKIYD-LPHHTIUVFAKDYTTNIRNIFDNKTLTDDDFSF 352
                                                                                                                                                                                       122 RAFLDYSRAVFNEGY-----LKLGTVPFLSFYDMLRAAPQLAKLQAWRSVYSKVAG 172
                                                                                                                                                                                                                                     124 EQFWEQERKRFNALYPCITRDYSSLK----SFLSL-DLIKALPWLA---FPKSVFNNLGQ 175
                                                                                                                                                                                                                                                                                                                                                                              233 DIGGEVVIMARVSHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293 Q--AKKLQSKRMSNSLFVLYFGLMHHHDQLAHHTVCFGPRYRELIHEIFNHDGLAEDFSL 350
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                                                                                                62 AIEELFALAGKOLKDYVELLPVTPFYRLCWESGKVFNYDNDQAQLEAQIQQFNPRDVAGY 121
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                                  65 VLDEMPELCERRSEDYLEFLPLSPMYRLLYDDRDIFVY-SDRENMRAELQRVFDEGTDGY
                                                                                                                                                                                                                                                                                                                                                                                                              353 YVQNASASDDSLAPAGKSALYVLVPMPN-NDSGLDWQAHCQNVREQVLDTLGARLGLSDI
       KPTTVICAGFGCLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITDPS
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TITLE OF INVENTION: Genes Involved in Isoprenoid Compounds Production
FILE REFERENCE: CL1646 US NA
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33.3%; Pred. No. 8e-60;
tive 87; Mismatches 229; Indels
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CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR FILING DATE: September 1, 2001
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Koffas, Mattheos
APPLICANT: Odom, J. Martin
APPLICANT: Schenzle, Andreas J.
APPLICANT: No. 6660507con, Kelley C.
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Patent No. 6660507
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APPLICANT: No. 6660507con, Kell
APPLICANT: Tomb, Jean-Francois
APPLICANT: Rouviere, Pierre
APPLICANT: Picataggio, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 33.34
Matches 164; Conservative
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ORGANISM: Methylomonas 16a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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-09-934-903-18
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                                                                                                                                                                                                                                                         YRAFLDYSRAVFNEGYLKLGTVPFLSFKOMLRAAPQLAKLQAWRSVYSKVAGYIEDEHLR 180
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                                                                                                361 SLAPEGMSTHYVLAPVPHLGRADVDWEAEAPGYAERIFBELERRALPDLRKHLTVGRES
                                                                       1 MKPTTVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITDP
                                                                                                                                                                                                                                                                                                      121 YRRFHDYAEEVYREGYLKLGTTPFLKLGOMLNAAPALMRLQAYRSVHSMVARFIQDPHLR
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APPLICANT: Tomb, Jean-Francois
APPLICANT: Rouviere, Pierre
APPLICANT: Cheng, Joing
TITLE OF INVENTION Genes Involved in Isoprenoid Compounds Production
FILE REFERENCE: CLIEGG US NA
CURRENT APPLICATION NUMBER: US/09/934,903
CURRENT FILING DATE: 2001-22
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR APPLICATION NUMBER: 1, 2001
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
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; Pred. No. 1.6e-150;
65; Mismatches 122; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KOffas, Mattheos
APPLICANT: Odom, J. Martin
APPLICANT: Schenzle, Andreas J.
APPLICANT: No. 6660507con, Kelley C.
APPLICANT: Tomb, Jean-Francois
APPLICANT: Rouviere, Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/09934903
Patent No. 6660507
GENERAL INFORMATION:
  61.9%;
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ORGANISM: Methylomonas 16a
                           304; Conservative
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||KATAQVMLSDL 491
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  Best Local Similarity
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LENGTE: 511
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                                                                           188 VEILNYFIKYVGSSPYDAPALMNILPYIQYHYGLMYVKGGMYGMAQAMEKLAVELKVER 247
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SUMMARIES

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ALIGNMENTS

RESULT 1

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Carotenoid; isopentenyl pyrophosphate; antheraxanthin; astaxanthin; diet; anti-oxidant; steroid; flavour; fragrance; electro-optic application; aquaculture; enzyme; phytoene desaturase; CrtL.
                                        Pantoea stewartii phytoene desaturase (CrtL) enzyme.
     AAE22314 standard; protein; 492 AA
                            (first entry)
                            25-JUL-2002
                 AAE22314;
AAE223
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Pantoea stewartii.

WO200218617-A2.

07-MAR-2002.

04-SEP-2001; 2001WO-US027420.

01-SEP-2000; 2000US-0229858P. 01-SEP-2000; 2000US-0229907P.

(DUPO) DU PONT DE NEMOURS & CO E I.

Miller ES; Koffas M, Dicosimo DJ, Rouviere PE; ò Brzostowicz PC, Cheng Q, Odom JM, Picataggio SK,

WPI; 2002-351711/38. N-PSDB; AAD35512 Producing carotenoid compounds e.g. antheraxanthin and astaxanthin, by using microorganisms having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolize single carbon substrates.

Claim 19; Page 141-143; 156pp; English.

The invention relates to a method for producing carotenoid compounds. The method comprises a transformed metabolising host cell, comprising suitable levels of isopentenyl pyrophosphate and a nucleic acid molecule encoding an enzyme in the carotenoid blosynthetic pathway, under the control of regulatory sequences, and contacting the host cell with carbon substrate to produce a arotenoid compound. The method is useful for producing carotenoid compounds such as antheraxanthin and astaxanthin, by using microorganism having a nucleic acid molecule encoding enzymes in

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the carotenoid biosynthetic pathway and which metabolise single carbon substrates. The carotenoids have potent anti-oxidant properties useful in diet, and aquadvaulture elements. The carotenoids are also useful as intermediates in the synthesis of steroids flavours and fragrances and compounds for potential electro-optic applications. The present sequence is Pantoea stewartii phytoene desaturase (Crtl) enzyme used in the
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                                                                                                                                                                                                                     The invention comprises the amino acid and coding sequence of a number carotenoid (crt)-related proteins. The crt-related DNA and protein sequences of the invention are useful for engineering cells which are able to produce carotenoids. The present amino acid sequence represents crt-related protein of the invention
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The present invention describes Pantoea stewartii carotenoid biosynthetic enzymes (I). More specifically described are the geranylgeranyl pyrophosphate synthase (GrEB), zeazanthin glucosyl transferase (GrEX), lycopene cyclase (GrEY), phytoene desaturase (GrI), phytoene synthase (GrEB) and beta-carotene hydroxylase (GrEZ) enzymes (see ABP96685 to CAPP90 encoded by ACC44769 to ACC44764. (I) can be used for regulating carotenoid biosynthesis in an organism, by over-expressing (I) in an organism, such that the carotenoid biosynthesis is altered in the phytoene to the carotenoids (for creating recombinant organisms that have the ability to produce various carita compounds, and also for the carotenoids compounds, and also for the carotenoids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enhancing or manipulating carotenoid compounds. (I) can also be used for producing gene products having enhanced or altered activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acid molecule isolated from Pantoea stewartii encoding a carotenoid biosynthetic enzyme, useful for regulating carotenoid biosynthesis in an organism.
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Pantoea stewartii; carotenoid biosynthetic enzyme; crtE; crtX; crtY; crtI; crtE; crtZ; phytoene desaturase; enzyme; phytoene; carotenoid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rouviere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Picataggio SK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheng Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-268323/26
                                                                                                         Pantoea stewartii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brzostowicz PC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
             Gene products are useful for the synthesis of carotenoids, useful as food coloring, vitamin A precursor, and possibly in prevention of cancer. See also AAQ06293-9. (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                       Polypeptide with enzymatic activity for the conversion of phytoene into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA sequences encoding enzymes for carotenoid biosynthesis - for prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAIBELFALAGKQLKEYVELLPVTPFYRLCWESGKVFNYDNDQTRLEAQIQQFNPRDVEG
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PFDFRDELNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVGAGTHPGAGIPGVIGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of carotenoid cpds. e.g. beta-carotene, lycopene, phytoene, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 492;
                                                                                                                                                                                                                                                               Carotenoid biosynthesis; vitamin A; cancer; food coloring
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.6%; Score 2438; DB 2; 93.5%; Pred. No. 4.3e-237;
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                                                                                                                                      AAR07466 standard; protein; 492 AA.
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                                                                                                                                                                                                                                                                                          Pantoea anamatis
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                                                                                                                                                                                                                                                                                                                                                                                                        05-MAR-1990;
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                                                                                                                                                                                       24-0CT-2003
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Best Local S
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                                                                                                                             AAR07466
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SAIEELFALAGKQLKEYVELLPVTPFYRLCWESGKVFNYDNDQTRLEAQIQQFNPRDVEG 120
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                                                                                                                                                                                                                                                                                                     SLAPEGCGSYYVLAPVPHLGTANLDWAVEGPRLRDRIFDYLEQHYMPGLRSQLVTHRMFT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a protein involved in carotenoid blosynthesis. The specification describes astaxanthin diglucosides and adontanthin-3-iglucosides. The specification also describes a method for the preparation of a carotenoid glycoside, in which all, or part of, carotenoid blosynthesis genes crtE, crtE, crtY, crtZ, crtX or crtW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carotenoid biosynthesis; astaxanthin diglucoside; crtE gene; crtI gene; crtI gene; crtI gene; crtI gene; crtI gene; carotenoid glycoside; crtY gene; crtZ gene; crtX gene; crtW gene; food additive.
                                                                                                                                                                                                                                                                                                                                                                QAFSFHSILVGGNPFATSSIYTLIHALEREWGVWFPRGGTGALVNGMIKLFQDLGGEVVL
                                                                                                                                241 NARVSHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAXXLQSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein encoded by the carotenoid biosynthesis gene crtI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - used as food additives
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KIRI ) KIRIN BREWERY KK. (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO
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N-PSDB; AAV84081.
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10-MAR-1999
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        NARVSHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQSK 300
                          241 NARVSHMETTGNKI EAVHLEDGRRFLTQAVASNADVVFTYRDLILSQHPAAVKQSNKLQTK 300
                                                                                     RASNSLFVLYFGLNHHHDQLAHHTVCFGFRYRELIDEIFNHDGLAEDFSLYLHAPCVTDS 360
                                                                                                                                 SLAPEGCGSYYVLAPVPHLGTANLDWAVEGPRLRDRIFDYLEQHYMPGLRSQLVTHRMFT 420
                                                                                                                                                    SLAPEGCGSYYVLAPVPHLGTANLDWTVEGPKLRDRIFAXLEQHYMPGLRSQLVTHRMFT 420
                                                                                                                                                                                              PPDFRDBLMAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVGAGTHPGAGIPGVIGSA 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel method for the preparation of carotenoids using genes and proteins isolated from Candida utilis. The invention specifically describes the isolation of a 3-hydroxy-3-methylightary1 coenzyme A (HMG-COA) reductase protein. This sequence represents the Candida utilis crtl protein which is used in the method the invention. (Updated on 17-0CT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RMSNSLFVLYFGLNHHHDQLAHHTVCFGPRYRZLIHBIFNHDGLABDFSLYLHAPCVTDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene useful for increase in carotenoid production - and preparation carotenoid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HMG-CoA; 3-hydroxy-3-methylglutaryl coenzyme A reductase; crtI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.6%; Score 2438; DB 2; Length 492;
Larity 93.5%; Pred. No. 4.3e-237;
Conservative 13; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Fig 11-14; 54pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                          492 AA
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                                                                                                                                                                                                                                                                                                                                                                        AAW82257 standard; protein;
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 utilis crtI protein.

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N-PSDB; AAV73181.
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                                                                  Beta-carotin hydroxylase
their metabolites.
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                                                                                                     Disclosure; Page 13-15;
           (KIRI ) KIRIN BREWERY
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                                 WPI; 1999-208113/18.
N-PSDB; AAX19119.
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13-JAN-2000
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are introduced to a microbe or plant and expressed. The transformed organism is cultured and astaxanthin diglucosides, adonixanthin-3'-glucosides, and/or astaxanthin monoglucoside are collected. The carotenoid glucosides are used as food additives. (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                           19; Indels
                                                                                                     Length
                                                                                                  93.6%; Score 2438; DB 2;
93.5%; Pred. No. 4.3e-237;
iive 13; Mismatches 19;
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                                                                                                  Query Match
Best Local Similarity 93.5
Matches 460; Conservative
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                                                                               Sequence 492 AA;
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                                                                                                       The present invention describes beta-carotin hydroxylase. Beta-carotene can be used in the preparation of xanthophylls and their metabolites. The present sequence represents an Brwinia uredovora crtl protein sequence from the present invention. (Updated on 17-OCT-2003 to standardise OS
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                                                                                                                                                                                                                                                                                          93.6%; Score 2438; DB 2; 93.5%; Pred. No. 4.3e-237; ive 13; Mismatches 19;
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AC AAY2
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DX 13-C
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KW PDS
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Shipton CA, Bryan IB;
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N-PSDB; AAX90713.
                                      (ZENE ) ZENECA LTD.
        Pantoea ananatis.
                                                                                                             Sequence 492 AA;
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                          37-APR-1999;
              W09953081-A1
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                                       KATAGLMLEDLI 492
                                                        Photorhabdus luminescens.
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                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the Phytoene desaturase (PDS) enzyme, isolated from Erwinia uredovora, that can inhibit 4-hydroxy-phenylpyruvate pidoxygenese (4HPPD) in vitro. This peptide sequence is used in the production of plants having resistance or tolerance to herbicides of the isoxazoles family. The plasmid pyPIET4 is constructed using plant operable promoters like CaMV 355 and chloroplast transit peptide resulting in a transgenic tp-crt1 gene. This plasmid is transformed and over-expressed in tomato and tobacco plants. This sequence is specifically used to transform plants like banana, cotton, maize, tomato or vines. It is also applied to plants that allow selective weed control in fields. (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                    Producing plants, especially banana, cotton, maize, tomato or vine, resistant to herbicides.
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93.6%; Score 2438; DB 2; Length 492;
Best Local Similarity 93.5%; Pred. No. 4.3e-237;
Matches 460; Conservative 13; Mismatches 19; Indels
            promoter; CaMV 35S; tp-crtI gene;
             plasmid pYPIET4; operable promoter; CaMv 3 chloroplast transit peptide; over-express.
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The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primars for detecting the genome of P. luminescens and related species, to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that companies or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. compinest production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The carpentically vectors containing the genes are useful for theratemic vectors containing the genes and Ab are also useful chere are sensitive to P. luminescens-encoded toxins or antibiotics) and as are sensitive to P. luminescens-encoded toxins or antibiotics and as bioperticides. Other uses of the genes and the proteins are as virulence factors and for identifying targets of human diseases for which P. ceptons of the isolated P. luminescens proteins
                                                                           Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides
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Photorhabdus luminescens protein sequence #3220
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WPI; 1996-308823/31
          N-PSDB; AAT40792.
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LFVLYPCINFHHTQLAHHTVCRGPRYXELIEDIFYHDRLSEDFSLYLHAPSVTDPSLAPR
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                                                                          DYSRAVPNEGYLKLGTVPFLSFKDMLRAAPQLAKLQAWRSVYSKVAGYIEDEHLRQAFSF
                                                                                                               HSLLVGGNPFATSSIYTLIHALEREWGVWPPRGGTGALVNGMIKLFQDLGGEVVLNARVS
                                                                                                                                                  HMETVGDKI QAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQSKRMSNS
                                                                                                                                                               LFVLYFGLNHHHDQLAHHTVCFGPRYRBLIHEIFNHDGLAEDFSLYLHAPCVTDPSLAPE
                                                                                                                                                                                                                          GCGSYYVLAPVPHLGTANLDWAVEGPRLRDRIFDYLEQHYWPGLRSQLVTHRMFTPFDFR
                                                                                                                                                                                                                                    DELINAWQGSAFSVBPILIQSAWFRPHNRDKHIDNLYLVGAGTHPGAGIPGVIGSAKATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGPP synthase; lycopene cyclase; phytoene synthase; beta-carotene; phytoene dehydrogenase-4H; carotenoid; C40; zeaxanthin; diglucoside; pigment; food colourant; chloroplast transit peptide; increase yield; tobacco ribulose bis-phosphate carboxylase-oxygenase.
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90US-00525551.
90US-00562674.
91US-00662921.
91US-00785566.
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(revised)
(first entry)
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25-MAR-2003
11-DEC-1996
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28-FEB-1991;
30-OCT-1991;
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18-MAY-1990;
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Ausich R
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The present sequence is that of the Erwinia herbicola phytoene dehydrogenase-4H which produces lycopene biosynthetically from phytoene through four sequential dehydrogenations controls. Other enzymes involved in the carctenoid biosynthesis pathway include geranylgeranyl prophosphate (AAW01118), phytoene synthase (W01121) and lycopene cyclase gene (AAM01125), whinjulation of, in partic., lycopene cyclase gene (AAM01125), by in frame linkage to the chloroplast transit peptide (AAW01124) of the tobacco ribulose bis-phosphate carboxylase-oxygenase gene can lead to increased production of total carotenoids in the chloroplast of transformed plants as compared to native, non-transformed plants of the same type. Beta-carotene is an effective and apparently harmless food colourant and is also in the pathway for biological cycle surface (Updated on 25-MAR-2003 to correct PF field.) (Updated on 16 corr-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TALEALFTEAGRRAEDYVRLLEVKPFYRLCWESGKTLDYANDSFELEAGITGFNFRDVBG
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Increasing prodn. of total carotenoid(s) in a higher plant - by transforming with vector encoding chloroplast transit peptide opelinked to the Erwinia herbicola lycopene cyclase structural gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.0%; Score 1849.5; DB 2
72.3%; Pred. No. 1.4e-177;
ive 44; Mismatches B9;
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                                                                                                                   Example 10; Fig 11; 99pp; English
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Best Local Similarity 72.3
Matches 355; Conservative
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(revised)
(revised)
(first entry)

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This sequence represents Erwinia herbicola phytoene dehydrogenase4H encoded by DNA from the plasmid pARC376. Phytoene dehydrogenase-4H has a encoded by DNA from the plasmid pARC376. Phytoene dehydrogenase-4H has a molified by DNA from the structural gene, presuming an average amino acid residue of about 100 bp for the structural gene, presuming an average amino acid residue of about 109. The native phytoene dehydrogenase-4H gene is located between positions 749 and 6380 of plasmid pARC376. Phytoene checknose and phytosenese of the phytosenese of the phytosenese of the prosphosphate. In E. herbicola, phytoene has been found to be formed prosphosphate. In E. herbicola, phytoene has been found to be formed prosphosphate in a two-step process. The initial step is the condensation of farnesyl pyrophosphate (FPP) and isopentyl pyrophosphate (FPP) and isopentyl pyrophosphate (FPP) and isopentyl pyrophosphate is produced from phytoene synthese, to form phytoene is produced from phytoene by the catalysed by the enzyme phytoene by the catalysed by the longent in the catalysed by the sensome phytoene by the catalysic action of phytoene is produced from phytoene by the catalysic action of phytoene is produced from phytoene by the catalysic action of phytoene commercial production of lycopene which is used as a food colourant.

Thanks transformed with the phytoene dehydrogenase-4H coding sequence are protected from the herbicide norfluxazon. (Updated on 25-MAR-2003 to standardise OS field)
                                                                                                                            E. herbicola, geranylgeranyl pyrophosphate synthase; pARC376; GGPP synthase; blosynthesis; carotenoid; lycopene; farnesyl pyrophosphate; phytoene; FPP; isopentyl pyrophosphate; IPP; tail to tail dimerisation; phytoene synthase; phytoene dehydrogenase-4H; food colourant; herbicide; norflurazon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding Erwinia herbicola phytoene dehydrogenase-4H - used for
in. of lycopene, and to produce transgenic plants resistant to
                                                                                        Phytoene dehydrogenase-4H encoded by DNA derived from pARC376.
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N-PSDB; AAT37094.
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03-AUG-1990;
28-FES-1991;
30-OCT-1991;
                16-OCT-2003
25-MAR-2003
17-OCT-1996
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Ausich R
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Mukharji I,

Proffitt J,

Brinkhaus FL,

90US-00525551. 90US-00562674. 91US-00662921. 91US-00785568. 90US-00487613. 93US-00096043

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241 NARVSHMETVGDKIQAVQLEDGRRFETCAVASNADVVHTYRDLLSQHPAAAKQAKKLQSK 300
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lycopene cyclase; recombinant enzyme; transgenic organism; beta-carotene;
yeast; plant; vitamin A; cancer.
SAIBELFALAGKOLKDYVELLPVTPFYRLCWESGKVFNYDNDQAQLEAQIQQFNPRDVAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         477
                                                                                                                                QAPSFHSLLVGGNPFATSSIYTLIHALERSWGVWFPRGGTGALVNGMIKLPQDLGGBVVL
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                                61 TALEALFTLAGRRANEDYVRLLPVK?FYRLCWESGKTLDYANDSFELEAQITQFNPRDVBG
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90US-0052551.
90US-00562674.
91US-00662921.
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{revised}
{first entry}
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Brinkhaus FL;
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28-PEB-1991;
21-JUL-1993;
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18-MAY-1990;
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25-MAR-2003
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Gaps

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71.0%; Score 1849.5; DB 2; Length 489; 72.3%; Pred. No. 1.4e-177; ive 44; Mismatches 89; Indels 3;

Query Match Best Local Similarity 72.3\$ Matches 355; Conservative

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1 MKPTTVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITDP 1 MKKTVVIGAGFGGLALAIRLQAAGIPTVLLEQRDKPGGRAYVWHDQGFTEDAGPTVITDP Phytoene_dehydrogenase-4H from pARC146D

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A novel DNA molecule has been isolated which encodes an Erwinia herbicola lycopene cyclase enzyme that converts lycopene to beta-carotene. The DNA molecule comprises at 1825 bp and is present in the plasmids pARC1510, pARC1510. The present in the plasmids the amino acid sequence corresponding to the structural gene for phytosne dehygrogenase-4H. The new DNA molecule can be used to produce the recombinant enzyme and transgenic organisms, e.g. yeasts or plants, with increased beta-carotene levels. Beta-carotene is used as a colourant in margarine and butter and as an intermediate for vitamin A, and may prevent cancer. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                   DNA encoding Erwinia herbicola lycopene cyclase - for producing recombinant enzyme, and transgenic organisms with increased beta-carotene
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N-PSDB; AAT91544
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Sequence 489 AA;

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240
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                                                                                               YRAFLDYSRAVFNEGYLKLGTVPFLSFKDMLRAAPQLAKLQAWRSVYSKVAGYIEDEHLR
                                                                           1 MKPTTVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITDP
                                             Gaps
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       Length 489;
                                           89; Indels
         DB 2;
         71.0%; Score 1849.5; DB 2
72.3%; Pred. No. 1.4e-177;
ive 44; Mismatches 89;
Query Match
Best Local Similarity 72.39
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489 AA.

AAR13985 standard, protein;

ESULT 13 AR13985 AAR13985;

(revised)
(revised)
(first entry)

24-OCT-2003 25-MAR-2003 26-NOV-1991

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coli cells to produce GGPP and the carotemoids phytoene through seaxanthin diglucoside, which is the final prod. identified in the carotemoid pathway contd. in plasmid pARG376 (contg. a ca. 13 Kb chromosomal DNA fragment isolated by Perry et al., J. Bacteriol., i68:607 (1986). The genes for geranylgaranyl pyrophosphate (GGPP) synthase, phytoene synthase, phytoene dehydrogenase-4H, lycopene cyclase, beta-caroteme hydroxylase, and zeaxanthin glycosylase are represented in AAQ1316, AAQ1318, AAQ13712, AAQ13724 and AAQ13726 respectively. Recombinant expression plasmids can be used to produce large ants. of the enzymes and hence large ants. of the carotemoids which they synthesise. Carotemoids are pigments with a variety of applications (Updated on 25-MAR-2003 to correct PP field.) (Updated on 25-MAR-2003 to correct PP field.) (Updated on 25-MAR-2003 to correct PP field.)
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                                                       Pantoea agglomerans; BHO-10 (E. vulneris - ATCC 39368)
                                                                                                                                                                                                                                                                                      Mukharji I, Proffitt JH,
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ilarity 72.1%; Pred. No. 3.5e-177;
Conservative 45; Mismatches 89;
                          GGPP; carotenoid; phytoene; zeaxanthin; lycopene.
                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 15(1-4); 313pp; English
                                                                                                                                                                            90US-00487613.
90US-00525551.
90US-00562674.
91US-00662921.
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354; Conser
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                                                361 SLAPPPCASFYVLAPVPHLGNAPLDHAQEGPKLRDRIFDYLBERYMPGLRSQLVTQRIFT 420
                                                                                         421 PFDFRDELNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVGAGTHPGAGIPGVIGSA 480
                                                                                                          RQTSRHAWIAILGSLFIEPPSLTGGLF--AANATRH-SNLYLVAAGTHPGAGIPGVVGLA 477
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SMSNSLFVLYFGLNQPHSQLAHHTICFGPRYRELIDBIFTGSALADDFSLYLHSPCVTDP 360
                               SLAPEGCGSYYVLAPVPHLGTANLDWAVEGPRLRDRIFDYLEQHYWPGLRSQLVTHRMFT
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Yen HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biosynthesis of carotenoid(s) in genetically engineered hosts encoding enzymes from Erwinia herbicola.
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90US-00525551.
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N-PSDB; AAQ13719.
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18-MAY-1990;
03-AUG-1990;
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Length 489

DB 2;

70.8%; Score 1845.5;

Match

Query

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                                                                                       61 SAIEELFALAGKOLKDYVELLPVTPFYRLCWESGKVFNYDNDQAQLEAQIQQFNPRDVAG 120
                                                                                                                                           121 YRAFLDYSRAVFNEGYLKLGTVPFLSFKDMLRAAPQLAKLQAWRSVYSKVAGYIEDEHLR 180
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                                                    1 MKPŢŢVIGAGFGGLALAIRLQAAGIPVLLLEQRDKFGGRAYVYQEQGFTFDAGPŢVITDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGPP synthase; lycopene cyclase; phytoene synthase; beta-carotene; phytoene dehydrogenase-4H; carotenoid; C40; zeaxanthin; diglucoside; pigment; food colourant; chloroplast transit peptide; increase yield; tobacco ribulose bis-phosphate carboxylase-oxygenase.
            Gaps
            3
            Indels
 Pred. No..3.5e-177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW01123 standard; protein; 489 AA.
al Similarity 72.1%; Pr
354; Conservative 45;
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90US-0052551.
90US-00562674.
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91US-00785566.
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ESTASLMIEDL 488
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28-FEB-1991;
30-OCT-1991;
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25-MAR-2003
11-DBC-1996
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18-MAY-1990;
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  Best Local
Matches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
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Proffitt J, Mukharji I, Yarger J; Brinkhaus FL,

N-PSDB; AAT40793

Increasing prodn. of total carotenoid(s) in a higher plant - by transforming with vector encoding chloroplast transit peptide operably linked to the Erwinia herbicola lycopene cyclase structural gene.

Example 12; Col 97-100; 99pp; English

The present sequence is that of a recombinant Brwinia herbicola phytoene dehydrogenase-4H (from pARC146D) which produces lycopene biosynthetically from phytoene through four sequential dehydrogenation reactions. Other enzymes involved in the carotemoid biosynthesis pathway include geranylgeranyl pyrophosphate (AAM01119), phytoene synthase (Wol121) and lycopene cyclase (AAM01125). Manipulation of, in partic., lycopene cyclase (PAM01125), Manipulation of, in partic., lycopene cyclase gene (AAM01125), by in frame linkage to the chloroplast transit peptide (AAM01124) of the tobacco ribulose bis-phosphate carboxylase-oxygenase gene can lead to increased production of total carotemoids in the chloroplast of transformed plants as compared to native, nontransformed plants of the same type. Beta-carotene is an effective and apparently harmless food colourant and is also in the pathway for biological synthesis of further C40 carotemoids such as zeaxanthin and zeaxanthin diglucoside. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 489 AA;

DB 2; Length 489; 70.8%; Score 1845.5; DB 2 72.1%; Pred. No. 3.5e-177; ive 45; Mismatches 89; Best Local Similarity 72.18 Matches 354, Conservative Query Match

60 1 MKPTTVIGAGFGGLALAIRLQAAGIPVLLLEQRDKPGGRAYVYQEQGFTFDAGPTVITDP

121 YRAFLDYSRAVFNEGYLKLGTVPFLSFKDMLRAAPQLAKLQAWRSVYSKVAGYIEDEHLR 180

181 QAFSFHSLLVGGNPFATSSIYTLIHALEREWGVWFPRGGTGALVNGMIKLFQDLGGEVVL 240

181 QAFSFHSLLVGGNPFTTSSIYTLIHALEREMGVWFPEGGTGALVNGMVKLFTDLGGBIEL 240

301 RMSNSLFVLYFGLNHHHDQLAHHTVCFGPRYRELIHBIFNHDGLAEDFSLYLHAPCVTDP 360

301 SMSNSLFVLYFGLNQPHSQLAHHTICFGPRYRELIDBIFTGSALADGFSLYLHSPCVTDP 360

361 SLAPEGCGSYYVLAPVPHLGTANLDWAVEGPRLRDRIFDYLEQHYMPGLRSQLVTHRMFT 420

::|| ||:||| 478 ESTASLMIEDI 488

arch completed: February 29, 2004, 14:44:02 ptime : 60.2706 secs

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famiunten H.C., Hirata R.;
fasolation and characterization of carotenoid biosynthesis genes from Parioea agglomerans pv. milletiae Wist 801.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB076662; BAB79602.1; -..
GO; GO:0045145; F:19copene beta cyclase activity; IEA.
GO; GO:001517; P:carotenoid biosynthesis; IEA.
InterPro; IPR008461; CttY;
FFam; PF05897; CttY; 1.
SEQUENCE 386 AA; 43674 MW; IB7DB42C08447AE7 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                       NGYRFVYTLPLSATALLIEDTHY1DXANLQAERARQNIRDYAARQGWPLQTLLREEQGAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dycopene cyclase.

CRTY.

Pantoea agglometria.

Bacteria, Proteobacteria; Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae; Pantoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94236237; PubMed=8180698;
MEDLINE=94236237; PubMed=8180698;
To K.Y., Lai E.M., Lee L.Y., Lin T.P., Hung C.H., Chen C.L.,
Chang Y.S., Liu S.T.
"Analysis of the gene cluster encoding carotenoid biosynthesis is
Erwind a herbicola Bhol3.";
Microbiology 140:313-1339 (1994).
EMBL: M90698; AAA21262.1;
PIR, S52585; S52585.
GO; GO:0045416; Plycopene beta cyclase activity; IEA.
GO; GO:0016117; P:carotenoid biosynthesis; IEA.
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SEQUENCE 382 AA; 43248 MW; A3A3197C91BB1D64 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.9%; Score 1715; DB 2;
83.8%; Pred. No. 1.2e-134;
iive 31; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 ILSGKPPVPVFAALQAIMTTHR 382
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01-NOV-1996 (TræMBLrel. 01,
01-NOV-1996 (TræMBLrel. 01,
01-OCT-2003 (TræMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 83.8 tes 320; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    301
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Matches
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125 ADGRIHASTVIDGRGYTPDSALRVGFQAFIGQEWQLSAPHGLSSPIIMDATVDQQNGYR 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 EGGRILRAPCVIDARGGRPVPGLALGFOKFLGLEVRLAAPHGLDVPIVMDATVAQSDGYR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 VVHHWPDYQVRFPQRRRHVNSGYYCVTSRHFAGILRQQFGQHLWLH-TAVSAVHAESVQL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 TGDNRQFWQQ---QPQACSGLRAGLFHPTTGYSLPLAVALAD----RLSALDVFTSSSVH 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|| : : |:::|::| ||||| || || || ETIDGYGRIIWRRGYYRFINRMLFKAAEPSERHRILARFYGLDQALIERFYAARIQPQD 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QTIAHFAQQRWQQQGFFRMLNRMLPLAGPAESRWRVMQRFYGLPEDLIARFYAGKLTVTD 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FVYTLPLSATALLIEDTHYIDXANLQABRARQNIRDYAARQGWPLQTLLREEQGALPITL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 DLILVGAGLANGLIALRLQQQHPDMRILLIBAGPEAGGNHTWSFHEEDLTLNQHRWIAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 DVIVIGGGLAGCLIALRITDARPDLRVVIIEGSASIAGNHTWSFRGTDISSDQHAWLGRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 394;
                    Sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flavobacterium sp. ATCC 21588.
Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
Flavobacteriaceae; Flavobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.8%; Score 804; DB 2; Length 39 43.9%; Pred. No. 1.2e-58; ive 63; Mismatches 138; Indels
genes from the photosynthetic bacterium Bradyrhizobium ORS278. ^{\circ} ,
                                                                                                                                                                                                                                                                                                                                                                                ROKAR_LIPOPROTEIN; 1,
43435 MW; 8BDDD59304EB194A CRC64;
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                                                                                                                             activity; IEA
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Last annotation update)
                                                              U. Bacteriol. 102.00.1; -. Grolase activit GO, GO:004543; F:lycopene beta cyclase activit GO, GO:0015491; F:oxidoreductase activity; IEA. GO; GO:0015117; P:carctenoid biosynthesis; IEA. GO; GO:0015118; P:electron transport; IEA. GO; GO:006118; P:electron transport; IEA.
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InterPro; IPR00172; GMC oxred.
InterPro; IPR000437; Prok_lipoprot_S.
Pfam, PF005897; Crry.
Pfam, PF00732; GMC oxred N; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RLRI---LSGKPPVPVFAALQAI 377
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MEDLINE=97186694; PubMed=9034310;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al Similarity
168; Conserv
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CRTY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S:
Matches 168
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 VVIHIWPDYQVRFPQRRRHVNSGYYCVTSRHFAGILRQOFGQHLWLHTAVSAVHAESVQLA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 QSYLWAGHGVHFPAFSRTLKGGYATISSERMAEVMNERLCAAIRTNARVAHVAPDHVVLE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDNRQFWQQQPQ--ACSGLRAGLFHPTTGYSLPLAVALADRLSALDVPTSSSVHQTLAHF 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 DLILVGAGLANGLIALRLQQQHPDMRILLIEAGPEAGGNHTWSFHEEDLTLNQHRWIAPL
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MEDLINE=20309720; PubMed=10851005;
Hannibal L., Lorquin J., Angles d'Ortoli N., Garcia N.,
Chaincreuil C., Masson-Boivin C., Dreyfus B., Giraud E.;
"Isolation and characterization of the canthaxanthin biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
                                                                                                                       Xanthobacter sp. (strain Py2).
Batteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Hyphomicrobiaceae, Xanthobacter.
NCDI_TaxID=78245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.5%; Score 899; DB 2; Length 385; 48.3%; Pred. No. 1.4e-66; ive 57; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bradyrhizobium sp. ORS278.
Bracteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
NCBI_TaxID=114615;
                                                                                                                                                                                                                                                                                                                    Larsen R.A., Metcalf W.W.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF408848; AAL01999.1; -.
GO, GO:0046436; F:lycopene beta cyclase activity; IEA.
GO, GO:0016117; P:carotenoid biosynthesis; IEA.
InterPro; IPR008461; CrtY.
Pfam; PPGS897; CrtY; 1.
SEQUENCE 385 AA, 41442 MM; EPB9C80ECFGE09FE CRC64;
              Last sequence update)
Last annotation update)
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GRPPVSVFRALSCLVET 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 182; Conservative
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           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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SEQUENCE FROM N.A
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                                                                    Lycopene cyclase
           01-DEC-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                               STRAIN-Py2;
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MEDLINE=97311406; PubMed=9168123;
Matsumura H., Takeyama H., Husakabe E., Burgess J.G., Matsumaga T.;
Matsumura H., Takeyama H., Husakabe E., Burgess J.G., Matsumaga T.;
"Cloning, sequencing and expression the carotenoid biosynthesis gene,
lycopene cyclase and phytoene desaturase, from the aerobic
photosynthetic bacterium Erythrobacter longus sp.strain Och 101 in
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                                                                                                                                                                                            2; Length 382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harker M., Hirschberg J.; "Carotenoid biosynthesis genes in the bacterium Paracoccus
                                                                                                                                                                                         38.8%; Score 783.5; DB 2; Length 343.7%; Pred. No. 5.7e-57; ive 64; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 36.4%; Score 735.5; DB 2; Length Best Local Similarity 41.5%; Pred. No. 5.9e-53; Matches 158; Conservative 69; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42283 MW; 91952F0F33F36800 CRC64;
                                                                                                                       6DB5452F45D9RF4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y15112; CABS6061.1; -. GO; GO:0045436; F:lycopene beta cyclase activity; IEA. GO; GO:0016117; P:carotenoid biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
           GO:0016117; P:carotenoid biosynthesis; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386 AA
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RIVTGRPPIPLSOAVRCL 372
                                          InterPro; IPR008461; CrtY.
Pfam; PP05897; CrtY; 1.
SEQUENCE 382 AA; 42369 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBirel. 13, 0
(TrEMBirel. 13, 1
(TrEMBirel. 25, 1
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Pfam; PF05897; CrtY; 1.
SEQUENCE 386 AA; 42283 )
                                                                                                                                                                                                                                                                  Matches 165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                           Similarity
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01-MAY-2000
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Best Local S
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4081;
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                                                                      Q9FV32
Q9FV32;
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              RESULT 10
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                                          Q9FV32
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                                                                                                         315 ------PDISGEQLAAFFDSRARRHWSKTGYYRLLARFLFFAAKPEKRVKVFQRFYGLR 367
                                                               233 IREEQGALPITLIGDNRQFWQQQPQ----ACSGLRAGLFHPTTGYSLPLAV----ALADR 284
                                                                                                                                                                                                 285 LSALDVFTSSSVHQTIAHF---AQORWQQQGFFRMLNRMLFLAGPABSRWRVMQRFYGLP 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265
196 QLAPHGNGSSYRFVYVLPLGSHDVPIEDTYYADDPLLDRNALSGRIDQYARANGWENGTP 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 FDVIIIGAGPA----GLRLAEHVSKYGIKVCCVDPSPLSWPNNYGVWVDEFENGLEDC 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 QHLWLHTAVSAVHAE---SVQLADGRIIHASTVIDGRGYTP-----DSALRVGFQAPIGQ 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
lamids, Solanales, Solanaceae, Solanum.
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"Identification of a novel gene coding for neoxanthin synthase from Solanum tuberosum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-cv. Desiree; TISSUE-Tuber;
MEDLINE-20547529; PubMed-11094161;
Al-Babili S., Hugueney P., Schledz M., Welsch R., Frohnmeyer H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.7%; Score 156.5; DB 10; Length 498; Best Local Similarity 22.1%; Pred. No. 0.00016; Matches 71; Conservative 59; Mismatches 128; Indels 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dene Cycl; 1.
56336 MW; 0CAB552D958C6F26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                   SDLIARFYAGKLTVTDRLRILSGKPPVPVFAALQAI
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WHELL, AJS72136, CASS2977.1;

InterPro, IPR008671; Lycopene_cycl.
InterPro, IPR000205; NAD_BS.
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SEQUENCE 498 AA, 5635
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                                                                                                                                                                                                                                                                                                                                   342
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82 FDVIIIGAGPA----GLRLAEQVSKYGIKVCCVDPSPLSMWPNNYGVWVDBFBNLGLENC 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57
                                                                                                                          Chromoplast-specific lycopene beta-cyclase.
Lycopersicon esculentum (Tomato).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 -QHRWIAPLVVHHWPDYQVRF---PQRR-----RHVNSGYYCVTSRHFAGILRQQFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 EWQL-SAPHGLSSPIIMD------ATVDQQNGYRFVYTLPLSATALLIEDTHYID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 AKVW-----KVEHEEFESSIVCDDGKKIRGSLVVDASGFASDFIEYDRPRNHGYQIAHGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Citrus paradisi (Grapefruit).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids;
eurosids II; Sapindales; Rutaceae; Citrus.
                                                                                                                                                                                                                                                                                                                                            MEDINE=20461502; PubMed=10995464;
Ronen G., Carmel-Goren L., Zamir D., Hirschberg J.;
"An alternative pathway to beta-carotene formation in plant
chromoplasts discovered by map-based cloning of Beta and old-gold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Costa M.C., Moreira C.D., Melton J.R., Otoni W.C., Moore G.A., "Developmental expression of carotenoid genes in Citrus.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF05834; Lycopene_Cycl; 1.
SEQUENCE 498 AA; 56448 MW; 2C21D3480746D5AA CRC64;
                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   color mutations in tomato.";
Proc. Natl. Acad. Sci. U.S.A. 97:11102-11107(2000)
EMBL, RPS4793; AAG21133.1;
InterPro; IPR008671; Lycopene_cycl.
InterPro; IPR000205; NAD_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.5%; Score 152.5; DB 10;
22.1%; Pred. No. 0.00034;
cive 59; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                524 AA
498
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFHPTTGYSLPLAVALADRLS 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, 01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 22.13
les 71; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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61 WIAPLVVHHWPDYQVRFPQRRRHVNSGYY-----CVTSRHFAGILRQQFGQHLWLHTA 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 VSAVHAESVQLA---DGRIIHASTVIDGRGYTP----DSALRVGFQAFIGQEWQLSA-P 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IKVIHEESKSILICNDGVTIQAAVVLDATGPSRCLVQYDKPYNPGYQVAYGILAEVEEHP 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGLSSPIIMD-----ATVDQQNGY--RFVYTLPLSATALLIBDTHYIDKANLQAER 213
69 DIAVVGGGPAGLAVAQRVAE--AGLSVCAIDPSPAV----VW-----PNNYGVWVDEF 115
                                                                                                110 -LHTA--VSAVHAESVQLA---DGRIIHASTVIDGRGYTP-----DSALRVGFQAFIGQE
                                                                                                                                                                                                                          169 VFFQAKVAKAVHYDASSLLICDDGVAVPASVVLDATGFSRCLVQYDKPYNPGYQVAYGIL
                                                                                                                                                                                                                                                                                                                                       ----LPEDL---I
                                                                                                                                                                                                                                                                                                    159 WOLSA-PHGLSSPIIMD-----ATVDQQNGY--RFVYTLPLSATALLIEDTHYIDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 PGLAMDDIQERMAARLRHLGIRVRSVEEDERCVIPMGGPLPVL-------PORVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GL--RAGLFHPTTGY----SLPLAVALADRL-SALDVFTSSSV----HQTIAHFAQQRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            397 PANRRRQREFF-CFGMDVLLKLDLEGTRRFFDAFFDLEPHYWHGFLSSRLFLPELLMFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLAVVGGGPAG--LAVAQOVSEAGLSVCSIDPSPKLIWPNNYGVWVDEFBAMDLLDCLDT
                                                                                                                                                                                                                                                                                                                                                                                                                           207 ANLQAERARQNIRDYAARQGWPLQTLLREEQ-----GALPITLFGDNRQFWQQQPQACS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 DLILVGAGLANGLIALRLQQQHPDMRILLIEAGPB---AGGNHTW--SFHEEDLTLNQHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopene beta-cyclase.
Citrus sinensis (Sweet orange).
Citrus sinensis (Sweet orange).
Bukaryota, Viidiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids,
euromids II; Samindales; Rutaceae, Citrus.
NCBI_TaxID=2711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Citrus
                                                             63 APLVVHH-----WPDYQVRFPQRRRHVNSGYYCVTSRHFAGILRQQFGQHLM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ku C.J., Zhang S.L.;
"Molecular cloning of lycopene beta-cyclase gene from orange
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sinensis).";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF240797; AAF4400.2;
InterPro; IPR008671; Lycopene_cycl.
InterPro; IPR00205; NAD_BS.
Pfam; PF05534; Lycopene_cycl. 1.
SEQUENCE_S04_AA; S6460 MW; 7C12B2BFB464481C_CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----QQQGFFRMLNRMLFLAGPAESRWRVMQRFYG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 ARFYAGKLTVTDRLRILSGKPPVPV 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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nes 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RWIAPLVVHHWPDYQVRFPQRRRHVNSGYYCVTSRHF-AGILRQQFGQHLWLHTA--VSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 TWSGAVV--HIDD-----NTKKDLNRFYGRVNRKLLKSKMLQKCITNGVKFHQAKVIKV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 APHGLSSPIIMD-----ATVDQQNGY--RFVYTLPLSATALLIEDTHYIDKANEQA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BRARONIRDYAAROGWPLQTLIREEQ-----GALPITLIGDNRQFWQQQPQACSGL--R 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGLFHPTTGYSLPLAVALADRIS-----ALDVPTSSSVHQTIAHFAQQRW-----QQQGF 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 KDIQERMVARLKHLGIKVKSIBEDEHCVIPMGGPLPVL-------PORVVGIGGT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                           6 DLILVGAGLANGLIALRLQQQHPDMRILLIEAGPE---AGGNHTW--SFHEED-LTLNQH 59
                                                                                                                                                                                                                                                                                                                                                                              DLILVGAGLANGLIALRLQQQHDDMRILLIBAGPRAGGNHTWSFHEEDLTINQHRWI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 VHAESVQLA---DGRIIHASTVIDGRG------YTPDSALRVGFQAFIGQEWQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IHEESKSLLICNDGVTIQAAVVLDATGFSRCLVQYDKPYNPGYQVAYGILAEVEQH----
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                                                                                                                                                                                                                                                                                 Gaps
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STRAIN=CV. W22;
SINGTH M., Lewis P.E., Hardeman K., Bai L., Rose J.K., Mazourek M.,
Chomet P., Brutnell T.P.;
"Activator Mutagenesis of the Pink scutelluml/viviparous7 Locus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSI...
Zea mays (Maize).
Bukaryots; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
NCBL_TaxID=4577;
                                                                                                                                                                                                                                                                                 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 490;
                                                                                                                                                                                                                7.4%; Score 150; DB 10; Length 524;
Larity 21.9%; Pred. No. 0.00058;
Conservative 66; Mismatches 162; Indels 8
   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFI52246; AAD38049.2; -.
InterPro; IPR008671; Lycopene_cycl.
InterPro; IPR008051; NAD_BS.
Pfam; PF09834; Lycopene_cycl, 1.
SEQUENCE 524 AA; 58553 MW; 51823CF5B3B9208C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRM-LARMLFLAGPAESRWRVMQRFYGLPEDLIARFYAGKLT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AY206862; AA018661.1; -.
InterPro; IPR000205; NAD BS.
SEQUENCE 490 AA; 53360 MW; 05456FE5D355D1A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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7.4%; Score 149; DB 10; 1
Best Local Similarity 21.6%; Pred. No. 0.00064;
Matches 96; Conservative 69; Mismatches 164;
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01-UUN-2003 (TrEMBLrel. 24,
01-UUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
Lycopene beta-cyclase.
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                                                                                                                                                                                                                                          Local Similarity
nes 88; Conserv
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SEQUENCE FROM N.A.
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256 FDLDKAVEWDWARDSHLANANSELKEANSKIPTFLYAMPFSSNRIFLEETSLVARPGVEWKD 315
                                                                                                                    265
                                                                                                                                                                        316 IQERMVARLKHLGIKVRSIBEDEHCVIPMGGPLPVL------PQRVVGIGGTAG 363
                                                                                                                                                                                                                                                            266 LFHPTTGYSLPLAVALADRLS----ALDVFTSSSVHQTIAHFAQQRW-----QQQGFFR 315
                                                                                                                                                                                                                                                                                                                                    364 WYHPSTGYMVARTLAAAPIVANAIVRSLSSDRSISGHKLSAEVWKDIMPIERRRQREFFC 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 QOFGQH---LMLHTAVSAVHAES-----VQLADGR--IIHASTVIDGR-GYTPDSAL 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 RVGFQAFIGQEWQLSAPHGLSSP---IIMD-ATVDQONGYRFVYTLPLSATALLIEDTHY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 TTLLQHFTG--WFVRTERPVFDPGTADLMÖFRTPQPARGLSFGYVLFLDPHTALVBYTEF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 IDKANLQAERARQNIRDY---AARQGWPLQTLLREEGGALFITLTGDNRQFWQQQPQAC- 259
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                                                                                                            214 ARQNIRDYAARQGWPLQTLLREEQ-----GALPITETGDNRQFWQQQPQACSGL--RAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=JA1933;
MEDLINE=97074881; PubMed=8917308;
Schumann G., Nuernberger H., Sandmann G., Kruegel H.J.;
"Activation and analysis of silent carotenoid biosynthetic genes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MQPHYDLILVGAGLANGLIALRLQQQHPD--MRILLIEA--GPEAGGNHTWSFHEE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces griseus.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycinaes, Streptomycetaceae, Streptomyces.
NCBI_TaxID=1911;
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Mol. Gen. Genet. 253:658-666(1996).
EMBL. X95596, CAM640855.1;
GO; GO:0016117; P:carotenoid biosynthesis; IEA.
InterPro; IPR0008461; CrtY.
Pfam; PF05897; CrtY; 1.
SEQUENCE 418 AA; 46239 MW; 77698BE02FCF6FF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            424 FGMDILLKLDLPA-----TRRFFDAFFDLEPRYWHGFLS 457
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Last annotation update)
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Best Local Similarity 23.99
Matches 99; Conservative
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01-0CT-2003
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147 TWSGAVV--HIDD-----NTKXDLDRPYGRVNRKLLKSKMLQKCITNGVKFHQAKVIKV 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 RWIAPLVVHHWPDYQVRFPPQRRRHVNSGYYCVTSRHF-AGILRQOFGQHLWLHTA--VSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 VHAESVQLA----DGRIIHASTVIDGRGYTP-----DSALRVGFQAFIGQEWQLSA-PHGL 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 DLAVVGGGPAG--LAVAQOVSEAGLSVCSIDPSPKLIWPNNYGVWVDEFEAMDLLDCLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CV. Red flesh navel orange;

Xu J., Meng H.J.; Deng X.X.;

"Molecular cloning of lycopene beta-cyclase gene from Red flesh navel orange by using Tail-PCR.";

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AY094582; AAM21152.1; -.

InterPro; IPR008611; Lycopene_cycl.

InterPro; IPR0080205; NAD BS.

Pfam; PP05834; Lycopene_cycl: 1.

SEQUENCE 504 AA; 56470 MM; E15495367378B6B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168 SSPIIMD-----ATVDQQNGY--RFVYTEPLSATALLIEDTHYIDKANLQABRARQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 DLILVGAGLANGLIALRLQQQHPDMRILLIBAGPE---AGGNHTW--SFHEED-LTLMQH
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Sapindales; Rutaceae; Citrus.
NCBI_TaxID=2711;
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                                                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Job time : 35.41nf Fear
                                                                                                                                                                                                   PRELIMINARY;
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androctonus bacillus su synechococc

salmonella

P72835 P72833 P73460 P32139 P74879 P80476 P20692 P59109

yersinia pe

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Q8ve73 P22105

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us-09-941-947a-30.rsp

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 WIAPLVVHHWPDYQVRPPQRRRHVNSGYYCVTSRHFAGILRQQFGQHLWLHTAVSAVHAB 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 WIAPLVVHHWPDYQVRPPTRRKEINSGYPCITSQRFABVLQRQPGPHLWMDTAVAEVNAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=20D3;
MEDDLINE=91072214; PubMed=2254247;
Misawa N., Nakagawa M., Kobayashi K., Yamano S., Izawa Y.,
Nakamura K., Harashima K.,
"Elucidation of the Erwinia uredovora carotenoid biosynthetic pathway
by functional analysis of gene products expressed in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MQPHYDLI1VGAGLANGLIALRLQQQHPDMRILLIEAGPEAGGNHTWSFHEEDLTLNQHR
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                                                                                                                                                                                                                                                                                                                                                                                               Pantosa ananas (Erwinia uredovora).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantosa.
NCBI_TaxID=553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Bacteriol. 172:6704-6712(1990).
-!- FUNCTION: Catalyzes the cyclization reaction which converts
-!vcopene to beta-caractene.
-!- PATHWAY: Carotenoid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.0%; Score 1678; DB 1; Length 3
82.2%; Pred. No. 8.7e-132;
ive 31; Mismatches 37; Indels
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PIR; C37802; C37802.
InterPro; IPR008461; CrtY.
Pafan, PF05897; CrtY; 1.
Pafan, PF05897; CrtY; 1.
Sarotenoid biosynthesis.
SEQUENCE 382 AA; 43047 MW; 62A94222A95B6D45 CRC64;
                                                                                                                                                                                                                                                                                                                                     01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                        382 AA
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                                            YD00 SYNY3
SOXA CORSI
MRAW SYNY3
YIHR ECOLI
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HCY6_ANDAU
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GID_SYNEL
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Matches 314; Conservative
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055276 synechococc
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038932 arabidopsis
931575 escherichia
091768 deinococcus
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001331 erwinia her
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1 MQPHYDLILVGAGLANGLIA.....SGKPPVPVFAALQAIMTTHR 382
                                                                                                             2004, 14:27:18 ; Search time 6.4382 Seconds
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(c) 1993 - 2004 Compugen Ltd.
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    protein search, using sw model

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                243 GDIQALWADAPGVPRSGWRAGLFHPTTGYSLPLAVALADAIADSPRLGSVPLYQLTRQFA 302
                                                                                                                                                                                                                                                                                                                                                                                303 ERHWRRQGFPELLINRMIFLAGREENRWRVWQRFYGLPSPTVERFYAGRESLFDKARIIJG 362
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                                                                     186 VYTLPLSATALLIEDTHYIDKANLQAERARQNIRDYAARQGWPLQTLLREEQGALPITLT 245
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123 NGEALLAGAVIDGRGVTASSAMQTGYQLFLGQQWRLTQPHGLTVPILMDATVAQQQGYRF 182
                                                                                                                                   183 VYTLPLSADYLLIEDTRYANVPORDDNALRÖTVTDYÄHSKGMOLAQLEREETGCLPITLA 242
                                                                                                                                                                                                     246 GDNRQFWQQQPQA-CSGLRAGLFHPTTGYSLPLAVALADRLSALDVFTSSSVHQTIAHFA 304
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J. Bacteriol. 177:6575-658(1995).

J. Bacteriol. 177:6575-658(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agrobacterium aurantiacum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
VCBI_TaxID=44155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.6%; Score 759.5; DB 1; Length 3 43.0%; Pred. No. 1.4e-55; ive 65; Mismatches 137; Indels
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01-0CT-1996 (Rel. 34, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 KPPVPVFAALQAIM 378
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CRTY.
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CRTY AGRAU
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                                                                                NGYRFVYTLPLSATALLIEDTHYIDKANLQAERARQNIRDYAARQGWPLQTLLREEQGAL 240
                                                                                                                                                                                                                   PITLIGDNRQFWQQQPQACSGLRAGLFHPTIGYSLPLAVALADRLSALDVFTSSSVHQFI 300
                                                                                                                                                                                                                                                               301 AHFAQQRWQQQGFFRYLNRMLFLAGPAESRWRVMQRFYGLPEDLIARFYAGKLTVTDRLR 360
                                                                                                                                                                                                                                                                                                                                                                                    301 THFARERWQQQGFFRALARMLFLAGPADSR#RVWQRFYGLPEDLIARFYAGKLTLTDRLR 360
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              121 SVRLKKGQVIGARAVIDGRGYAANSALSVGFQAFIGQEWRLSHPHGLSSFIIMDATVDQQ 180
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                                                                                                                                                 NGYRPVYSLPLSPTRIL IEDTHY I DNATLDPECARONI CDYAAQQGWQLQTLLREEQGAL
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Enterobacteriaceae; Pantoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEBS Lett. 315:329-334(1993).
-!- FUNCTION: Catalyzes the cyclization reaction which converts
lycopene to beta-carotene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hundle B.S., O'Brien D.A., Beyer P., Kleinig H., Hearst J.E., "In vitro expression and activity of lycopene cyclase and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    386 AA; 43341 MW; F4A40563BFCFA980 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 beta-carotene hydroxylase from Erwinia herbicola.";
FEBS Lett. 315:329-334(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created}
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: Carotenoid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILSCKPPVPVFAALOAIMTTHR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 ILSGKPPVPVLAALQAIMTTHR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93138098; PubMed=8422926;
Hundle B.S., O'Brien D.A., Beyer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M87280; AAA64980.1; -
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InterPro; IPR008461; CrtY.
Pfam; PF05897; CrtY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 58.3
Matches 218; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carotenoid biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25,
01-APR-1993 (Rel. 25,
10-OCT-2003 (Rel. 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Erwinia herbicola.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lycopene cyclase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERWHE
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                                    140 -VDCLDKTWPMTCVFINDHKTKYLDRP-----YGRVSRNILKTKILLENCVSNGVKFHK 191
                                                                                                                                                                                          SAPHGLSSPIIMDATVDQQNGYR-----FVYTLPLSATALLIEDTHYIDKANL 209
                                                                                                                                                                                                                                    252 SHPFDLDRWVLMDWR-DSHLGNEPYLRASNLKLPTFLYAMPFDSNLVFLEETSLVSRPVL 310
                                                                                                                                                                                                                                                                                                             : : : | | : : | | : : : : | 311 SYKEVKSRWARLRHWGIRVKRVIEDEKCLIPWGGPLPVI-------PQSVWAIG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----DYQVRFPQRRRHVNSGYYCVTSRHF--AGILRQQFGQHLWLHT 112
                                                                                                                                         192 AKVWHVNEQEFESSIVCDDGNEIKASLIVDASGFASSFVEYDKPRNHGYQIAHGILAEVE 251
                                                                                                                                                                                                                                                                                  210 QAERARQNIRDYAARQGWPLQTLLRBEQ-----GALPITLTGDNRQFWQQQPQA--CSG 261
                                                                                                                                                                                                                                                                                                                                                                           262 LRAGLFHPTTGY----SLPLAVALADR----LSALDVFTSSSVHQTIAHFAQQRWQQQGF 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 F---RMINRMLFLAGPAESRWRV----MORFYGLPEDLIARPYAGKLTVTDRLRILSG-- 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum (Tomato).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; asterids;
Jamiids, Solanales, Solanacese, Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WHICH CONVERTS
                                                                                                  113 AV--SAVHAE---SVQLADGRIIHASTVIDGRGYTP-----DSALRVGFQAFIGQEWQL-
                                                                                                                                                                                                                                                                                                                                                                                                                       359 GTSGLIHPATGYMVARTMALAPALADAIAECLGSTRMIRGRPLHOKV-----W--NGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAINSON. VF36; TISSUE=Leaf;
Ronen G., Cohen M., Zamir D., Hirshberg J.;
Ronen G., Cohen M., Zamir D., Hirshberg J.;
Regulation of expression of the gene for lycopene epsilon cyclase during fruit ripening of tomato.";
Submitteed (Mar.1988) to the EMBL/Genenk/DDBJ databases.
-!- PUNCTION: CATALYZES THE SINGLE CYCLIZATION REACTION WHICH CONVERT INCOPENE TO DELTA-CAROTENE AND NEUROSPORENE TO ALPHA-ZEACAROTENE.
-!- SATHMAY CARCHAION: Chloroplast.
-!- SUBCELLULAR LOCATION: Chloroplast.
-!- SIMILARITY: Belongs to the lycopene cyclase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lycopene epsilon cyclase, chloroplast precursor (EC 1.14.-.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase; NAD; Carotenoid biosynthesis; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                526 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KPPVPV 370
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         62 IAPLVVHHWP-
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ONGYRFVYTLPLSATALLIEDTHYIDKANLQAERARQNIRDYAARQGWPLQTLLREEQGA 239
                                                                                                                                                                  LPITLIGDNROFWOOOP--QACSGLRAGLFHPTTGYSLPLAVALADRLSALD-VFTSSSV 296
                                                                                                                                                                                               296 RGAIRDYAIDRARRDRFIRLIANRMLFRGCAPDRRYTTLQRFYRMPHGLIERFYAGRLSVA 355
                                                                                                                                                                                                                                                          297 HOTIAHFAQQRWQQQGFFRMLNRMIFLAGPAESRWRVMQRFYGLPEDLIARFYAGKLTVT 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 ODGYRFIYLLPFSPTRILIEDTRYSDGGDLDDDALAAASHDYARQQGW-TGAEVRRERGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEBE-2003 (Rel. 41, Last annotation update)
Capsanthin/capsorubin synthase, chloroplast precursor.
CCS.
Citrus sinensis (Sweet orange).
Bukaryota, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; edicocyledons; core eudicots; rosids; eurosids II; Sapindales; Rutaceae; Citrus.
NCBL TaxID=2711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY: Carotenoid biosynthesis. SUBCELLULAR LOCATION: Chloroplast; chromoplast (By similarity). SIMILARITY: Belongs to the lycopene cyclase family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAPSANTHIN/CAPSORUBIN SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.7%; Score 156; DB 1; Length 503; 21.2%; Pred. No. 2.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF05834; Lycopene cycl, 1.
Oxidoreductase; NAD; Carotenoid biosynthesis; Chloroplast;
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DQLRIVTGKPPIPLGTAIRCL 376
                                                                                                                                                                                                                                                                                                                                                       DRLRILSGKPPVPVFAALQAI 377
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503 CP
117 NP
56663 NW;
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TRANSIT
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us-09-941-947a-30.rsp

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EMBL: X74599; CAA52677.1;
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                                                                                                                                                                                                                                                                                                   209 SKVDRIVBATNGOSLVECEGDVVIPCRFVTVASGAASGKFLQYELGSP-RVSVQTAYGVE 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 VEVDNNPFDPSLMVFMD------YRDYLRHDAQSLEAKYPTFLYAMPMSPTRVFFEST 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376 AAASWVHPATGYSVVRSLSEAPKCASVLANILRQHYSKNMLTSSSIPSISTQAWNTLWPQ 435
                                                                                                                                                                                                                                                                                                                                                                         63 APLVVHHWPDYQVRFPQRRRHVNSGYYCVTSRHF------AGILRQQFGQHLWLH 111
                                                                                                                                                                                                                                                                                                                                                                                                                         158 -ACIEHVWRDTIVYLDDDBPILIGRAYGRVSRHFLHEELLKRCVEAGV------LYLN 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 T----AVSAVHAESVQLADGRII----HASTVIDGRG-----YTPDSALRVGFQAFIGQE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 WQL-SAPHGLSSPIIMDATVDQQNGYR--------FVYTLPLSATALLIEDT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 HYIDKANLQAERARQNIRDYAARQGWPLQTLLREEQGALPITLTGDNRQFWQQQPQACSG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 CLASKDAMPFDLLKKKLALRINTLGVRIKEIYBEBWSYIPVGGSLPN----TBOKTLAFG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 LRAGLFHPTTGYSLPLAVALADRLSAL------DVFTSSSVHQTLAH-----FAQ 305
                                                                                                                                                                                                                                                                    6 DILLVGAGLANGLIALRLQQQHPDMRILLIEAGPE---AGGNHTWSFHEEDLTLNQHRWI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95093701; PubMed=7919981; Mirschberg J., Gannt B.; Cunningham FX. Jr., Sun Z., Chamovitz D., Hirschberg J., Gannt B.; Cunningham FX. Jr., Sun Z., Chamovitz D., Hirschberg J., Gannt B.; Molecular structure and enzymatic function of lycopene cyclase from the cyanobacterium Synechococcus sp strain PCC7942."; Plant Cell 6:1107-1121(1994).

-:- FUNCTION: Catalyzes the double cyclization reaction which converts lycopene to beta-carotene and neurosporene to beta-zeacarotene.

-:- ENZYME REGULATION: INHIBITED BY THE BLEACHING HERBICIDE 2-(4-METHYLPHENOXY) TRIBITED BY THE BLEACHING HERBICIDE 2-(4-METHYLPHENOXY) TRIBITED BY THE PURPOSEDE (MPTA).
                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       436 ERKRORSFF-LFGLALILQLDIEGIRSFFRAFFRVPKWMWQGFLGSSLSSAD 486
                                                                                                                                                                                                               92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2)
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
(VBI_TaxID=1140;
                                                                                                                                                               Length 526;
                                                                                                                                                          7.5%; Score 152; DB 1; Length 52
21.1%; Pred. No. 5.1e-05;
Live 66; Mismatches 167; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: Carotenoid biosynthesis.
                                                                                                          37357C3869DBDCAF CRC64;
                                                     LYCOPENE EPSILON CYCLASE. NAD (POTENTIAL).
                                 CHLOROPLAST (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411 AA
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                            ? CH
526 LY
136 NA
5886 MW;
                                                                                                                                                                                      Local Similarity 21.1:
les 87; Conservative
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108 1
526 A.A.;
Transit peptide.
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NP BIND
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 IRKHYIYQFGLEKL---MRFSEAQLMHHP---QTFFGLPKEQWYGFLTWTLSLPELIQAM 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 DKANLQAERARQNIRDYAARQGWPLQTLIREBQGALPITLTGDNRQFWQQQPQACSGLRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 ACPAIPYDRIKQRIYQRLATRGVTVQVIQHEBYCLFPMNLPLPD----LTQSVVGFGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 -----QQGFFRMINRMLFLAGPABSRWRVMQRFYGLPEDLIARFYAGKLTVTD----R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 -----VSAV----HAESVQLADGRIIHASTVIDGRGYTPDSALR-----VGFQAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplanta, Erreptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamids; Solanales; Solanaceae; Capsicum.
                                                                                                                                                                                                                                                                                                                                                                                                                             5 YDLILVGAGLANGLIALRLOQOHPDWRIILLIBAGPEAGGNHTWSFHBEDLTLNQHRWIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 FDALVIGSGPAGLALARABLAQ----RGLKVQGLSPVDPFHPWE------NTYGIWGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 ELDSLGLEHLFGHRWSNCVSYF-----GEAPVOHOYNYGLFDRAQLQQH-WIRQCE
                                                                                                                                                                                                                                                                                                                                                                 109; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Yolo Wonder;
MEDLINE=94197697; PubMed=8147854;
Medline=94197697; PubMed=8147854;
Medicar J., Bouvier F., Steppuhn J., Klein A., Camara B., Kuntz M.;
"Structure and expression of two plant genes encoding chromoplast-
specific proteins: occurrence of partially spliced transcripts.";
Biochem. Biophys. Res. Commun. 199:1144-1150(1994).
                                                                                                                                                                                                                                                                                                  DB 1; Length 411;
                                                                                                                                                                                                                                                                                           7.3%; Score 148.5; DB 1; Length 4
22.7%; Pred. No. 7.2e-05;
tive 54; Mismatches 168; Indels
                                                                                                                                                                                                                                   C46CC5B2E85E7AC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCS CAPAN STANDARD; PRT; 498 AA. Q42435; Q39470; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 28-PER-2003 (Rel. 41, Last annotation update) Capsanthin/capsorubin synthase, chloroplast precursor.
                                                                                                  Pfam, PF05834; Lycopene cycl; 1. FRINTS; PR00469; PNDRDFASEII.
Oxidoreductase; MAD; Carotenoid biosynthesis.
                                                                                                                                                                                                    NAD (POTENTIAL
InterPro; IPR008671; Lycopene_cycl.
InterPro; IPR00205; NAD_BS.
InterPro; IPR000103; Pyridine_redox_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Lamuyo;
MEDLINE=95004653; PubMed=7920703;
                                                                                                                                                                                                                                411 AA; 46085 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Capsicum annuum (Bell pepper)
                                                                                                                                                                                                                                                                                                                                  Local Similarity 22.79
tes 97, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 -QHRWIAPLVVHHWPDYQVRFPQR------RRHVNSGYYCVTSR---HFAGILRQ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 QFGQHLWLHTAVSAVHAE---SVQLADGRIIHASTVIDGRGYTP-----DSALRVGFQAF 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 IGQEWQL-SAPHGLSSPIIMD-----ATVDQQNGYRFVYTLPLSATALLIEDTH 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 YDLILVGAGLANGLIALRLOOQ--HPDMRILLIBAGPEA---GGNHTWSFHEEDLTLN-- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHLOROPLAST (POTENTIAL).
CAPSANTHIN/CAPSORUBIN SYNTHASE.
AA -> R (IN RAF. 3).
ARA -> IRP (IN RAF. 3).
PSD -> LRP (IN RAF. 3).
PSD -> RTCCTQFVPFWTC (IN RAF. 3).
                                                                                                           Bouvier F., Huqueney P., d'Harlingue A., Kuntz M., Camara B., "Xanthophyll biosynthesis in chromoplasts: isolation and molecular cloning of an enzyme catalyzing the conversion of 5,6-epoxycarotenoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF05834; Lycopene_Gycl; 1.
Oxidoreductase; NAD; Carotenoid biosynthesis; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.3%; Score 148.5; DB 1; Length 22.2%; Pred. No. 9.2e-05; ve 58; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: Carotenoid biosynthesis.
-!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Chloroplast; chromoplast.
-!- SIMILARITY: Belongs to the lycopene cyclase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4FB25F676A022A98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X77289; CAA54495.1; --
EMBL; X76165; CAA53759.1; --
EMBL; X78030; CAA54961.1; --
PIR; S51511; S51511.
PIR; S71511; S71511.
InterPro; IPR008671; Lycopene_cycl.
InterPro; IPR000805; NAD BS.
Pfam; PP058934; Lycopene_Cycl.
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les 72, Conservative
                                                                                          Plant J. 6:45-54(1994)
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RC STRAINCE-VIOLUMDia,

RA SALGOUBAR M., Lemacke K., Rieger M., Ansorge W., Unseld M.,

RA Salanoubar M., Lemacke K., Rieger M., Ansorge W., Unseld M.,

RA Salanoubar M., Lemacke K., Rieger M., Perez.Alonso M., Obermaier B.,

RA Partmann B., Vaile G., Bloecker H., Perez.Alonso M., Obermaier B.,

RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,

RA Mincker P., Cattolico L., Meissenbach F., Robert C., Brottier P.,

RA Wincker P., Cattolico L., Meissenbach G., Saurin W., Benes V.,

RA Wincker P., Cattolico L., Meissenbach G., Saurin W., Benes V.,

RA Windelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

RA Wedelmann R., Rauer G., Loehnert T.-H., Nordan B.,

R. Cooke R., Landie M., Sehen O., Bargues M., Terol J., Climent J.,

RA Reichelt J., Scharfe M., Schoon O., Bargues M., Terol J., Climent J.,

RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Masuy D.,

RA Reichelt G., Haase D., Schoof H., Rudd S., Zaccaria P.,

RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,

Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P.,

RA Rooney T., Rizzo M., Malts A., Otterback T., Fujii C.Y., Shea T.P.,

RA Rooney T., Rizzo M., Malts A., Diterback T., Fujii C.Y., Shea T.P.,

RA Peruss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,

RA Sasamoto S., Kimura T., Idesawa K., Kawashima X., Kishida Y.,

RA Sasamoto S., Kimura T., Idesawa K., Kawashima X., Nishida Y.,

RA Sasamoto S., Kimura T., Idesawa K., Kawashima X., Nishida Y.,

RA Sasamoto S., Kimura T., Idesawa K., Kawashima X., Nishida Y.,

RA Hatanabe A., Yamada M., Yasuda M., Tabata S.;

RH Tesquence and analysis of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=96434545; PubMed=8837512;
Cunningham F.X. Jr., Pogson B., Sun Z., McDonald K.A., Dellapenna D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional analysis of the beta and epsilon lycopene cyclase enzymes of Arabidopsis reveals a mechanism for control of cyclic carotenoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Giuliano G., Rosati C., Santangelo G.; "Gene structure and regulation of the carotenoid biosynthesis pathway in Arabidopsis thaliana."; Submitted (DEC.1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                      Arabidopais Lhaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Wassilewskija;
Scolnik P.A., Bartley G.E.;
"Nuclectide sequence of lycopene cyclase from Arabidopsis.";
(In) Plant Gene Register POR95-019.
                                                                                                                                                       LCYB. ARATH STANDARD; PRT; 501 AA.
16-0333; 039145;
16-037-2001 [Rel. 40, Created)
16-037-2001 [Rel. 40, Last sequence update)
18-FSB-2003 [Rel. 41, Last annotation update)
18-FSB-2003 [Rel. 41, Last annotation update)
18-FSB peta cyclase, chloroplast precursor (BC 1.14...)
1671 OR LYC OR AT3010230 OR F14P13.17.
Arabidopsis thaliana (Mouse-ear cress)
263 RAGLFHPTTGYSLPLAVALADRLS 286
                             355 TSGIVHPSSGYWVARSMALAPVLA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ant Cell 8:1613-1626(1996).
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                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMES outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 WIHTAVSAVHAE---SVQLADGRIIHASTVIDGRGYTP-----DSALRVGFQAFIGQEWQ 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 LSA-PHGLSSPIIMDATVDQQNGY------RFVYTLPLSATALLIEDTHYIDKAN 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 LOAERARONIRDYAARQGWPLQTLLREEQ-----GALPITLTGDNRQFWQQQPQACSGL 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 LAMEDIQERMAARLKHIGINVKRIBEDERCVIPMGGPLPVL-------PQRVVGI 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              υ
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                       FUNCTION: Catalyzes the double cyclization reaction which converts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLAIVGGGPAG--LAVAQQVSEAGLSVCSIDPSPKLIMPNNYGVWVDEFEAMDLLDCLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 RWIAPLVVHHWPDYQVRFPQRRRHVNSGYYCVTSRHFAGILRQQF------GQHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 DLILVGAGLANGLIALRLOOOHPDWRILLIEAGPE---AGGNHTW--SFHEED-LTLNQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --RAGLFHPTTGYSLPLAVALADRLS----ALDVFTSSSVH--OTIAHFAQQRW----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                          lycopene to beta-carotene and neurosporene to beta-zeacarotene PATHWAY: Carotenoid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.3%; Score 148.5; DB 1; Length 501;
21.0%; Pred. No. 9.3e-05;
ative 66; Mismatches 175; Indels 105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF05834; Lycopene_Gycl; 1.
Oxidoreductase; NAD; Carotenoid biosynthesis; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYCOPENE BETA CYCLASE.

NAD (POTENTIAL).

NAD (N REP. 2).

V - 1 (IN REP. 2).

C3014578D0BDC4E2 CRC64;
                                                                                    -!- SUBCELLULAR LOCATION: Chioroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHLOROPLAST (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro, IPR008671; Lycopene_cycl.
InterPro, IPR000205; NAD_BS.
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                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF117256; AAF82388.1; -. EMBL; AC009400; AAF02819.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56176 MW;
                                                                                                                                                                                                                                                                                                                               EMBL; U50739; AAB53337.1; -.
EMBL; L40176; AAA81880.1; -.
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408:820-822(2000)
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501
113
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243
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85 1
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243 2
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TRANSIT
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CONFLICT
SEQUENCE
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503 AA.

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LCYB NARPS STANDARD; Q40424; 16-OCT-2001 (Rel. 40, Created)

LCYB_NARPS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 YIDKANLQAERARQNIRDYAARQGWPLQTLLREEQ~~~~~GALPITLTGDNRQFWQQQP 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 YGILAEVEEHPPDVDKMVFMDWRDSHLNGKAELNERNAKIPTFLYAMPFSSNRIFLEETS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- FUNCTION: Carealyzes the double cyclization reaction which converts lycopene to beta-carotene and neurosporene to beta-zeacarotene.
-i- PATHYMAY: Carotenoid biosynthesis.
-i- SUBCELLULAR LOCATION: Chloroplast; chromoplast. Exists as an inactive soluble form and an active membrane-bound form
                                                                                                                                                                             Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                     Al-Babili S., Hobelka B., Beyer P.;
"A cDNA encoding lycopene cyclase from Narcissus pseudonarcissus L.";
(In) Plant Gene Register PGR96-107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLILVGAG------LANGLIALRLQQQHPDMRILLIBAGPEAGGNHTWSFHBEDLTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION.
MEDLINE=97433278; PubMed=9288918;
BODK M., Hoffmann B., von Lintig J., Schledz M., Al-Babili S.,
Hobbeika E., Kleinig H., Beyer P.;
"Chloroplast import of four carotenoid biosynthetic enzymes in vitro reveals differential fates prior to membrane binding and oligomeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR008671; Lycopene cycl.
Pfam; PF05834; Lycopene cycl; 1.
Oxidoreductase; NAD; Carotenoid biosynthesis; Chloroplast;
                                                                                         (EC 1.14.-,-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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NAD (POTENTIAL).
3FD1E355EF184D98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHLOROPLAST (POTENTIAL).
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20.4%; Pred. No. 0.00036;
tive 66; Mismatches 150;
16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Lycopene beta cyclase, chloroplast precursor LCY1 OR LYC.
                                                                                                                                                         Narcissus pseudonarcissus (Daffodil)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Biochem, 247:942-950(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transit peptide; Membrane.
TRANSIT 1 85
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90 1
503 AA;
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Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Paracorolla;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 NCBI_TaxID=39639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
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247 VEEHPFDISKAVLMDWRDSHLGNNWELKERNRKVPTFLYAMPFSSNKIFLEETSLVARPG 306
                                                                                                                   209 LOAERARQNIRDYAARQGWPLQTLLREEQ-----GALPITLTGDNRQFWQQQPQAC--S 260
                                                   161 LSA-PHGLSSPIIMD-----ATVDÇÇNGY--RFVYTLPLSATALLIBDTHYIDKAN 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177180CD5745F64F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHLOROPLAST (POTENTIAL)
LYCOPENE BETA CYCLASE.
                                                                                                                                                                                                                                                                                                                                                                                498 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Capsicum annuum (Bell pepper)
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                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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498
112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WCBI_TaxID=4072;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                  ----- 302
                                               352 QRVVGIGGTAGMVHPSTGY-----MVARTLAAAPIVANSIVQYLVSDSGLSGNDLSADV 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 DLAVVGGGPAG--LAVAQQVSBAGLSVVSIDPSPKLIWPNNYGVWVDEPBAMDLLDCLDA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 RWIAPLVVHHWPDYQVRFPQRRRHVNSGYYCVTSRHFAGILRQQFGQHLW-----L 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 TWSGTVV------YIDDNTTKDLDRPYGRVNRKQLKSKMMQKCILNGVKF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 HTA--VSAVHAESVQLA---DGRIIHASTVIDGRGYTP-----DSALRVGFQAFIGQEWQ 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            District Cell 8:1613-1626(1996).
Plant Cell 8:1613-1626(1996).
-!- FUNCTION: Catalyzes the double cyclization reaction which converts lycopene to beta-carotene and neurosporene to beta-zeacarotene.
-!- PATHWAY: Carotenoid biosynthesis.
-!- SUBCELLUIAR LOCATION: Chloroplast.
                                                                                                                                                                                                                                                                                                                Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                        "Functional analysis of the beta and epsilon lycopene cyclase enzymes of Arabidopsis reveals a mechanism for control of cyclic carotenoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLIEVGAGLANGLIALRLOQOHPDWRILLIEAGPB---AGGNHTW--SFHEED-LTLNQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cunningham F.X. Jr., Pogson B., Sun Z., McDonald K.A., Dellapenna D.,
                                                                                303 ----FAQORWOQQGFFRMINRMLFLAGPAESRWRVMQRFYGLPEDLIARFYAGKIT
                OACSGL--RAGLEHPTTGYSLPLAVALADRLSALDVPTSSSVHQTIAH----
                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
LyCopens (Rel. 41, Last annotation update)
LyCopens beta cyclase, chloroplast precursor (EC 1.14.-.-).
LCT1 OR CRIL-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro, IPR008671; Lycopene_cycl.
InterPro, IPR000205; NAD_BS.
Pfam, PF05834; Lycopene_cycl; 1.
Oxidorechictase; NAD; Carotenoid biosynthesis; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the lycopene cyclase family.
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NAD (POTENTIAL)
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                                                                                                                                                                                                        500 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Samsun NN; TISSUE=Leaf;
MEDLINE=96434545; PubMed=8837512;
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500 LY(
114 NA)
56067 MW;
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83; Conservative
                                                                                                                                                                                                       STANDARD:
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TRANSIT
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86
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Q43578;
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SEQUENCE
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                                                                                                  GLRAGLFHPTTGYSLPLAVALADRLSALDVFTSSSVH------QTIAHFAQQRW- 308
                                                                                                                                                                355 GCTAGLVHPSTGY-----MVARTLAAAPVVANAIIHYLGSEXDLLGNELSAAVWKDLWP 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Capsicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Metabolism of cyclic carotenoids: a model for the alteration of this blosynthetic pathway in Capsicum annuum chromoplasts."; Plant J. 8:417-424(1995).
-i- FUNCTION: Catalyzes the double cyclization reaction which converts
307 LEMDDIQERAVARLNHLGIKVKSIEBDEHCVIPMGGSLPVI------PQRVVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lycopene to beta-carotene and neurosporene to beta-zeacarotene. PATHWAY: Carotenoid biosynthesis: SUBCELLULAR LOCATION: Chloroplast; chromoplast. SUBCELLULAR LOCATION: Chloroplast; chromoplast. SIMILARITY: Belongs to the lycopene cyclase family.
                                                                                                                                                                                                                                                                                                 ----QQQGFFRM-LNRMLFLAGPAESRWRVMQRFYGLPEDLIARFYAGKLT 354
                                                                                                                                                                                                                                                                                                                                                                                         409 IBRRROREFFCFGMDILLKLDLPA-----TRAFFDAFFDLEPRYWHGFLS 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CV. Lamuyo, TISSUE-Fruit,
BEDIJNB=96045549, PubMed=7550379;
Hugueney F., Badillo A., Chen H.C., Klein A., Hirschberg J.,
Camara B., Kuntz M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Lycopene beta cyclase, chloroplast precursor (EC 1.14.-.-).
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InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR008671; Lycopene_cycl.
InterPro; IPR00100505; MAD_BS.
InterPro; IPR001100; Pyr_redox.
InterPro; IPR0318; Lycopene_cycl; 1.
Pfam; PF05834; Lycopene_cycl; 1.
PRINTS; PR00346; PADPNR.
PRINTS; PR00411; PNDRINASEI.
Oxidoreductase; MAD; Carotenoid biosynthesis; Chloroplast;
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InterPro; IPR008671; Lycopene_cycl
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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LCYE_ARATH
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Matches
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                                                                                                                                                  83 DLAVVEGGPAG--LAVAQOVSEAGLSVCSIDPNPKLIWPNNYGVWVDEFEAMDL----- 134
                                                                                                                                                                                                               61 WIAPLVVHHWPDYQVRFPQR-RRHVNSGYYCVTSRHFAGILRQQP---GQHLWLHTAVSA 116
                                                                                                                                                                                                                                                                                                                                 117 VHAESVQLA---DGRIIHASTVIDGRGYTP-----DSALRVGFQAFIGQEWQLSA-PHGL 167
                                                                                                                                                                                                                                                                                                                                                                                              193 IHEESKSMLICHDGITIQATVVLDATGFSRSLVQYDKPYNPGYQVAYGILAEVEHPFDV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 SSPIIMD-----ATVDQQNGY--RFVYTLPLSATALLIEDTHYIDKANLQAERARQ 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 NKMVFMDWRDSHLKNNVELKERNSRIPTFLYAMPFSSNRIFLEETSLVARPGLGMDDIQE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217 NIRDYAARQGWPLQTLLREEQ-----GALPITLTGDNRQFWQQQQQQQGGL--RAGLFH 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 PSTGYMVARTLAAAPVVANAIIQYLSSERSHSGDELSAAVWKDLWPIERRRQREFFCFGM 420
                                                                                            6 DLILVGAGLANGLIALRLQQQHPDMRILLLIEAGPE---AGGNHTW--SFHEEDLTLNQHR 60
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
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-i- PATHWAY: Carotenoid biosynthesis.
-i- SUBCELIULAR LOCATION: Chloroplast.
-i- SIMILARITY: Belongs to the lycopene cyclase family.
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MEDLINE=96434545; PubMed=8837512;
Cunningham F.X. Jr., Pogson B., Sun Z., McDonald K.A., Dellapenna D.,
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                                      Gaps
                                      16;
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   20.4%; Pred. No. 0.00057;
Live 70; Mismatches 170; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 NRMLFLAGPAESRWRVMQRFYGLPEDLIARFYAGKLT 354
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
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Plant Cell 8:1613-1626(1996)
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                                      81; Conservative
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   Best Local Similarity
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CYB LYCES
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InterPro; IPR001327; FAD_pyr_redox

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 TWS----FHEEDLTENQHRWIAPLVVHHWPDYQVRFPQRRRHVNSGYYCVTSRHFAGILR 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 TWSGAAVYIDDNTAKDLHR------PYGRVNRKQLKSKOMQ--KCIMN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 QOFGQHLWLHTAVSAVHAESVQLA---DGRIIHASTVIDGRGYTP-----DSALRVGFQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 AYGILAEVEEHPFDVNKMVFMDWRDSHLKNNTDLKERNSRIPTFLYAMPFSSNRIFLEET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 FIGQEWQLSA-PHGLSSPIIMD-----ATVDQQWGY--RFVYTLPLSATALLIEDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 POACSGL--RAGLEHPTTGYSLPLAVALADRL-SALDVFTSSSVHQTIAHFAOORW----
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eperatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid eurosids II; Erassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 6.6%; Score 133; DB 1; Length 500; Local Similarity 19.4%; Pred. No. 0.0018; es 80; Conservative 74; Mismatches 152; Indels 106;
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16-OCT-2001 (Rel. 40, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Lycopene epsilon oyclase, chloroplast precursor (EC 1.14.-.-).
ATSG57030 OR MEMIT.16.
InterPro; IPR000205; NAD_BS.
InterPro; IPR001100; Pyr_redox.
Prfam; PF00834; Lycopene_cycl; 1.
PRINTS; PR00368; PADPIR.
PRINTS; PR00401; PMDRDTASEI.
Oxidoreductase; NAD; Carotenoid biosynthesis; Chloroplast;
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STRAIN=cv. Columbia;
MEDLINE=96434545; PubMed=8837512;
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113 AVSAVHAES-----VOLADGRIJHASTVIDGRGYTPDSAL-----RVGFQAFIGQEWQ 160
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                                                                                                                                                                                                                                                                                                                                                                                                  325 ASKDVMPFDLLKTKLMLRLDTLGIRILKTYERBWSYIPVGGSLPN----TEQKNLAFGAA 380
                                                                                                                                                                                                                                                                                                                                                                    264 AGLFHPTTGYSLPLAVALADRLSAL--DVFTSSSVHQTIAHFAQQRW------000G 312
     166 VM-RETIVYLDDDKPITIGRAYGRVSRRLLHEELLRRCVES----GV-----SYLSS 212
                                                                                                        213 KVDSITTEASDGLRLVACDDNNVIPCRLATVASGAASGKLLQYEVGGPRVCVQTAYGVEVE
                                                                                                                                                          161 L-SAPHGESSPIIMDATVDQQNGYR------FVYTLPLSATALLIEDTHY
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MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Schwarzz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Systematic sequencing of the Escherichia coli genome: analysis of the 0-2.4 min region."; Nucleic Acids Res. 20:3305-3308(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
Isono K., Mizobuchi K., Nakata A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FFRMINRMIFIAGPAESRWRVMQRFYGLPEDLIARFYAGKLTVTD 357
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Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002)
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Bichler K., Buchet A., Bourgis F., Kleber H.-P.,
Mandrand-Berthelot M.-A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIXC_ECOLI STANDARD; PRT; 428 AA. P31575; P75626; 01-UUL-1993 (Rel. 26, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterobacteriaceae; Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FixC protein.
FIXC OR B0043 OR C0053.
Escherichia coli, and
Escherichia coli 06.
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12 / MG1655;
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STRAIN=CV. Columbia,
MEDLINE=25954850, PubMed=14593172;
MEDLINE=25954850, PubMed=14593172;
MEDLINE=25954850, PubMed=14593172;
MEDLINE=25954850, PubMed=14593172;
MEDLINE=25954850, PubMed=14593172;
MEDLINE=25954850, PubMed=14593172;
MEDLINE=25954850, PubMed=14595172;
MILLANGER A.M., FULL S.X., Lam B., Sakann H., Wu T., Yu G.,
Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
Hayashizaki Y., Johnson-Hopson C., Hann V.W., Tida K., Karnes M.,
Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
Kaniya A., Meyers C., Nakajina M., Narusaka M., Saki M., Sakurai T.,
Samiya A., Meyers C., Nakajina M., Wallender E.K., Wong C., Yamamura Y.,
Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstainnthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: CATALYZES THE SINGLE CYCLIZATION REACTION WHICH CONVERTS LYCOPENE TO DELTA-CAROTENE AND NEUROSPORENE TO ALPHA-ZEACAROTENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regulation of the carotenoid biosynthesis pathway
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                                                                                             SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE-20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                            "Structural analysis of Arabidopsis thaliana chromosome 5. X. Se features of the regions of 3,076,755 bp covered by sixty Pl and
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Transit peptide. TRANSIT 1 45 CHIODORAGE (SANDARY)
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                                                 Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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4C1F98CC72EDD074 CRC64;
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EMBL; AY079371; AAL85102.1; -.
INTER-PROJ IPRO01327; FAD_DYT_redox.
Inter-Pro; IPR0018671; Lycopene_cycl.
Pfam; PF05834; Lycopene_cycl; 1.
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524 AA; 58491 MW;
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                                                                                                                                                                                                                                                                                    clones.";
DNA Res. 7:31-63(2000)
  structure and
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81;

Query Match Best Loca Matches

NP BIND CONFLICT SEQUENCE

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--- DNPRMFSGYPELAVGVA 387
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                                                                                                                  DEIRA
373
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                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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20.0%; Pred. No. 0.061;
iive 56; Mismatches 167; Indels 129; Gaps
                                          Sasic Microbiol. 35:217-227(1995).
FUNCTION: PROBABLY ACCEPTS ELECTRONS FROM FIXA/FIXB AND REDUCES
The fix Escherichia coli region contains four genes related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the BTF-QO / fixC family.
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                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE010114; AAC73154.1; -. EMBL; AE016755; AAN78549.1; -.
                                                                                                                  (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X71977; CAAS0799.1; -.
PIR; C64725; C64725.
EcoGene; EG11564; fixC.
                                                                                                                                                                                                                                                                                                                                                                             EMBL; D10483; BAB96611.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 VHARSVQLADGRIIHASTVIDGRGYTPDSALRVGFQAFIGQEWQL----SAPHG-LSSP 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 IHAER-----SGAGWIVYGA-----GGERWOTRLVVDASGHGALVSP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 IIMDATVDQQNGY----REVYTLPLSATALL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 VRFPGGAALQTAYGVVARFRRPPVTPGSMVMMDYRTPAPELKRGRATFLYAMHLGGDRYF 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 IEDTHYIDK-ANLQAERARQNIRDYAARQGWPLQTLLREEQGALPITLTGDNRQFWQQQP 256
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                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=RI / ATCC 13939 / DSM 20539 / NCIB 9279;
STRAIN=RI / ATCC 13939 / DSM 20539 / NCIB 9279;
STRAIN=RI / ATCC 13939 / DSM 2053 / NCIB 9279;
White O., Eisen J.B., Heidelberg J.F., Hickey B.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W.C., Richardson D.L., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewskin C., Makarova K.S., Azavind L., Daly M.J., Minton K.W., Fleischmann R.D., McCtchum K.A., Nelson K.B., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Oxidoreductase; NAD; Carotenoid biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.3%; Score 106.5; DB 1; Length 410;
22.8%; Pred. No. 0.22;
tive 44; Mismatches 173; Indels 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                              Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcaceae; Deinococcus. NCBL_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 286:1571-1577(1999).
-1- SIMILARITY: Belongs to the lycopene cyclase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 NAD (POTENTIAL).
43161 MW; ElB3162F10F9E6AF CRC64;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interPro; IPR008671; Lycopene cycl.
InterPro; IPR003042; Rng_mnoxygenase.
Pfam; PP05834; Lycopene cycl; 1.
                                                                                                                                Putative carotenoid cyclase DR0801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001934; AAF10377.1; -.
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Matches 100; Conservative
                                                                                                                                                                                                               Deinococcus radiodurans.
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earch completed: February 29, 2004, 14:45:10 ob time: 10.4382 secs

8 Seconds updates/sec
0.632 ints)
i; Search time 10.6328 Seconds (without alignments) 3455.835 Million cell updates/sec
February 29, 2004, 14:34:14; Search time 10.6328 Seconds (without alignments) 3455.835 Million cell updates/
February 29,
kun on:

US-09-941-947A-30 2021 1 MQPHYDLILVGAGLANGLIA.....SGKPPVPVFAALQAIMTHR 382 itle: erfect score: equence:

283366 segs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 coring table: earched:

283366 otal number of hits satisfying chosen parameters:

inimum D3 seq length: 0 aximum D3 seq length: 2000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:* atabase:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			SUMMERTES	
esult No.	Score	Query Match	Length	DB	ID	Description
-		84.9	382	2	852585	dycopene cyclase
~1	-	83.0	382	N	C37802	rein -
m	1148.5	ģ	386	N	S52981	las
4	152	7.5	526	~	T07082	
ហ	•		498	~	S71511	
φ	147.5	7.3	471	2	S51511	capsanthin/capsoru
7	140	φ,	200	C)	S72506	lycopene beta-cycl
00	139	6.9	200	~	S66349	
σn	$^{\circ}$	9.9	200	N	872505	
10	133		200	7	866350	
11	127.5	. 6.3	399	~ 4	E70888	g] £
12	117.5	ω. Θ	391	~	AD0584	probable monocyde
13	4.	5.7	428	2	F90634	flavoprotein [impo
14	114.5	5.7	428	7	FB5485	flavoprotein, elec
15	114.5	5.7	504	C4	G87532	tryptophan halogen
16	113.5	5.6	428	~	C64725	fixC protein - Esc
7	110.5	5.5	405	C)	T37022	probable lycopene
18	108.5	5.4	3161	N	T30342	protein HMWP1 - Ye
13	106.5	5.3	410	N	D75475	
20	105	5.2	398	N	D83122	probable FAD-depen
21	105	5.2	557	Ŋ	F83181	
22		5.2	402	N	AC2797	2-octaprenyl-6-met
23	104.5	5.2	402	~	C97576	2-octaprenyl-6-met
24	0	5.1	413	7	D86920	probable UDP-qalac
25		5.1	722	~	w	GMC oxidoreductase
26	103.5	5.1	3163	~	T17440	probable polyketid
27		5.1	3163	N	AB0233	yersiniabactin bio
28	102.5	5.1	392	~	9	2-octaprenyl-6-met
29	101.5	0.0	391	τ=1	D64801	probable monooxyge

FixC protein (impo	oxydenase (importe	hypothetical prote	outer membrane ush	probable outer mem	hypothetical prote	DNA polymerase III	DNA polymerase III	glutamine-fructose	exodeoxyribonuclea	hypothetical prote	phage-related port				
AG0511	D90716	G85566	A70645	S75024	AF1314	AF1686	C64785	B90703	E85553	B90652	B85503	T45493	B82091	C83407	A82551
N	N	N	0	N	N	N	æ	~	Ŋ	N	N	~	N	~	0
428	391	391	367	425	421	421	867	869	869	1160	1160	611	1208	466	532
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101	100.5	100.5	99	Q,	98	98				ď	97			96	96

ALIGNMENTS

RESULT

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epsilon cyclase during
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary, translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-526 «MON».
A;Residues: 1-526 «MON».
A;Residues: EMBL:Y14387; NID:e1285211; PIDN:CAA74745.1; PID:e1285212
A;Experimental source: cultivar VF36; leaf
VVHHWPDYQVRFPQRRRHVNSGYYCVTSRHFAGILRQQFGQHLWLHTAVSAVHAESVQLA
                                                                                VAHAWPGYEVOPPDIRRRIARGYYSITSERPAEALHOALGENIWINCSVSEVIPNSVRIA
                                                                                                                                     DGRIIHASTVIDGRGYTPDSALRVGFQAFIGQEWQLSAPHGLSSPIIMDATVDQQNGYRF
                                                                                                                                                                                                                                           VYTLPLSADTLLIEDTRYANVPQRDDNALRQTVTDYAHSKGWQLAQLEREBIGCLPITLA
                                                                                                                                                                                                                                                                                      GDNRQFWQQQPQA-CSGLRAGLFHPTTGYSLPLAVALADRLSALDVFTSSSVHQTIAHFA
                                                                                                                                                                                                                                                                                                                                                                                     #text_change 28-Jul-2003
                                                                                                                                                                                                                                                                                                                                                                QQRWQQQGFFRMLNRWLFLAGPAESRWRVMQRFYGLPEDLIARFYAGKLTVTDRLRILSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -ACIEHVWRDTIVYLDDDEPILIGRAYGRVSRHFLHEELLKRCVBAGV------LYLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 SKVDRIVEATNGQSLVECEGDVVIPCRFVTVASGAASGKFLQYRLGSP-RVSVQTAYGVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 DLVVIGCGPAG--LALAAESAKLGLNVGLV--GPDLPFTNNYGVWEDBFKDLGLQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 526;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, July 1997
A; Description: Regulation of expression of the gene
A; Reference number: 215905
A; Status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
7.5%; Score 152; DB 2;
Best Local Similarity 2.11%; Pred. No. 8.9e-05;
Matches 87; Conservative 66; Mismatches 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lycopene epsilon-cyclase (EC 5.5.1.-) - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Description: converts lycopene to delta-carotene C;Superfamily: tomato lycopene beta-cyclase C;Keywords: intramolecular lyase; isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||: | :| :
| KPPVPLGEAWRAAL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                           KPPVPVFAALQAIM 378
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                                C;Species: Erwinia uredovora
C;Spaces: Brwinia uredovora
C;Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 20-Jun-2000
C;Accession: G37802
C;Accession: G37802
J. Bacteriol. 172, 6704-6712, 1990
J. Bacteriol. 172, 6704-6712, 1990
A;Fitle: Blucidarion of the Erwinia uredovora carotenoid biosynthetic pathway by function A;Reference number: A37802, MUID:91072214; PMID:2254247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lycopene cyclase - Erwinia herbicola
C;Species: Erwinia herbicola
C;Date: SEvot-1996 #sequence_revision 13-Mar-1997 #text_change 10-Dec-1999
C;Accession: SS2981
S;Hundle, B.; Alberti, M.; Nievelstein, V.; Beyer, P.; Kleinig, H.; Armstrong, G.A.; Burk A;Cl. Gene. 245, 406-416, 1994
A;Title: Functional assignment of Erwinia herbicola Eho 10 carotenoid genes expressed in A;Reference number: S52976; MUID:95107236; PMID:7808389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGYRFVYTLPLSATALLIEDTHYIDKANLQAERARQNIRDYAARQGWPLQTLIREEQGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MOPHYDLILVGAGLANGLIALRLQQQHPDMRILLIEAGPEAGGNHTWSFHEEDLTLNQHR
                                                                                                                                                                                                                                                                                                                                                                                                                 1 MOPHYDLILVGAGLANGLIALRLQQQQPDMRILLIDAAPQAGGNHTWSFHHDDLTESQHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: EMBL:M87280; NID:g148404; PIDN:AAA64980.1; PID:g148411
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                                                                                                                                                                                                                                             A;Cross-references: GB:D90087; NID:9216681; PIDN:BAA14126.1; PID:9216684
C;Superfamily: Erwinia dycopene cyclase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53; Mismatches 102;
                                                                                                                                                                                                                                                                                                      83.0%; Score 1678; DB 2;
82.2%; Pred. No. 1.9e-132;
iive 31; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 56.8%; Score 1148.5; DB Best Local Similarity 58.3%; Pred. No. 3.3e-88, Matches 218; Conservative 53; Mismatches 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILSGKPPVPVFAALQAIMTTHR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;Start codon: GTG
7;Superfamily: Erwinia dycopene cyclase
                    crtY protein - Erwinia uredovora
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 82.2%.
Matches 314; Conservative
                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-382 <MIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: DNA
Residues: 1-386 <HUN>
                                                                                                                                                                                         A;Status: preliminary
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DD 299 LVSRPMLSYMEVRRRWVARLRHLGIRVRSVLEBERCVITMGGPLPRI-PQNVMALGG- 354	OY 263 RAGLFHPTTGYSLPLAVALADRIS 286	RESULT 6 S51511 capanthin/capsorubin synthase (EC 5.5.1} - pepper C;Species: Capsicum annuum (pepper) C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 28-Jul-2000	C;Accession: S51511 R;Houlne, G:; Schantz, M.L.; Meyer, B.; Pozueta-Romero, J.; Schantz, R. Curr. Genet. 26, 524-527, 1994 A;Title: A chromoplast-specific protein in Capsicum annuum: characterization and expres A;Reference number: S51511; MUID:95179811; PMID:7874747	A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-471 <hou> A;Cross-references: GB:X78030; NID:g840728; PIDN:CAA54961.1; PID:g840729 C;Superfamily: tomato lycopene beta-cyclase C;Keywords: intramolecular lyase; isomerase</hou>	Query Match Best Local Similarity 22.2%; Pred. No. 0.00018; Matches 71; Conservative 57; Mismatches 123; Indels 69; Gaps 16; Qy S YDLILVGAGLANGLIALRLQQQHPDWRILLIRAGPEAGGNHTWSFHEEDLTLN 57		103 QFGQHLWLHTAVSAVHABSVQLADGRI :	CY 155 IGQEWQL-SAFHGLSSFIIMDATVDQQNGTKFVTILFLSAIALLIDIR 202 :: :: :: ::	Qy 203 YIDKANLQAERARQNIRDYAARQGWPLQTLLREEGGALPITLTGDNRQFWQQQPQACSGL 262 :::	Db 355 TSGIVHPSSGYMVARSWALA 374	<pre>KESULT 7 S72506 S72506 Iycopene beta-cyclase (EC 5.5.1) - common tobacco C;Species: Nicotiana tabacum (common tobacco) C;Date: 17-Feb-1998 #sequence revision 26-Feb-1999 #text_change 28-Jul-2000</pre>	C;Accession: S72506 R;Pecker, I:; Gabbay, R.; Cunningham Jr., P.X.; Hirschberg, J. submitted to the RMBL Data Library, September 1994 A;Description: Cloning and characterization of the lycopene cyclase gene from tomato. A;Reference number: S72506	A;Accession: 572506 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-500 <pec> A;Cross-references: EMBL:X81787; NID:g1006689; PID:g1006690 C;Superfamily: tomato lycopene beta-cyclase C;Keywords: intramolecular lyase; isomerase</pec>
320 CLASKDAMPFDLLKKKLIMLRLNTLGVRIKEIYBEBWSYIPVGGSLPNTEQKTLAFG 375	/ 262 LRAGLPHPTTGYSLPLAVALADRESALDVFTSSSVHQTIAHFAQ 305 : : :: ::: ::	306 QRWQQQGFFRMLNRMLFLAGFAESRWRVWQRFYGLPEDLIARFYAGKITVTD 357	1511 Upsanthin/capsorubin synthase (EC 5.5.1) - pepper Alternate names: chromoplast-specific protein Contains: capsorubin synthase; capssanthin synthase Species: Capsicum annuum (pepper) Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 28-Jul-2000	Accession: S71511; JC2141 Bouvier, F.; Fugueney, P.; d'Harlingue, A.; Kuntz, M.; Camara, B. ant J. 6, 45-54, 1994 Title: Xanthophyll biosynthesis in chromoplasts: isolation and molecular cloning of ar Reference number: S71511; MUID:95004653; PMID:7920703	Molecule type: mRNA Residues: 1-498 <bous Cross-references: BMBL:X76165; NID:g522119; PIDN:CAA53759.1; PID:g522120 Experimental source: cv. Lamuyo; developmental stage ripening fruits Deruere, J.; Bouvier, F.; Steppuhn, J.; Klein, A.; Camara, B.; Kuntz, M. ochem. Biophys. Res. Commun. 199, 1144-1150, 1994</bous 	Title: Structure and expression of two plant genes encoding chromoplast-specific prote Reference number: JC2140; MUID: 94197697; PMID: 8147854 Accession: JC2141 Molecule type: DNA Residues: 1-498 < DER> Cross-references: EMBL: X77289; NID: 9468747; PIDN: CAA54495.1; PID: 9468748	instance i Source: V. 1010 Wonder. re, J.; Bouvier, F.; Steppuhh, J.; Klein, A.; Camara, B.; Kuntz, M Biophys. Res. Commun. 201, 486, 1994 ence number: A55775 ence number: A55775 ence number: A55775	Note: the legends of the nucleotide sequence igures were reversed in publication (see Genetics: Gene: CC Complex: monomer	** ***	Query Match 7.3%; Score 148.5; DB 2; Length 498; Best Local Similarity 22.2%; Pred. No. 0.00016; Matches 72; Conservative 58; Mismatches 125; Indels 69; Gaps 16;	5 YDLILVGAGLANGLIALRLQQQHPDMRILLJEAGPEAGGNHTWSFHEBDLTLN 57 	58 -QHRWIAPLVVHHWPDYQVRFPQRRRHVNSGYYCVTSRHFAGILRQ 102	193 KHERFESSIVCDDGRKISGSLIVDASGYASDFIEYDKPRNAGYQVA 238 155 IGQEWQL-SAPHGLSSPIIMDATVDQQNGYRFVYTLPLSATALLIEDTH 202 159 HGILAEVDNHPFDLDXAMLAMDWRDSHLGNEPYLRVKNTKEPTFLYAMPFDRNLVFLEETS 298 203 YIDXANLQAERARQNIRDYAARQGWPLQTLLREEGGALPITLTGDNRQFWQQQPQACSGL 262

Db 307 IRIDDIGERMVARLMHIGIKVKSIEBDEHCVIPMGGSLPVIPQRVVGT 354 Qy 261 GIRAGLEHPTTGYSLPIANALADARISALDVFTSSSVH	6 DILIVGAGLANGLIALRIQQHPDNRILLIEAGPEA-GGNH	RESULT 10 Sc6550 Sc6550 Iycopene beta-cyclase (EC 5.5.1) - tomato C;Species: Lycopersicon esculentum (tomato) C;Species: Lycopersicon esculentum (tomato) C;Species: Lycopersicon esculentum (tomato) C;Accession: S66350 R;Pecker, I.; Gabbay, R.; Cunningham Jr., F.X.; Hirschberg, J. Plant Mol. Biol. 30, 807-819, 1996 A;Title: Cloning and characterization of the cDNA for lycopene beta-cyclase from tomato A;Reference number: S66349; MUID:96194462; PMID:8624411
Query Match Best Local Similarity 20.2%; Pred. No. 6.00084; Matches 83; Conservative 72; Mismatches 152; Indels 104; Gaps 20; Watches 83; Conservative 72; Mismatches 152; Indels 104; Gaps 20; \$ b bilvoaglanglialricomential conservative 72; Mismatches 152; Indels 104; Gaps 20; \$ c bilvoaglanglialricomential conservative 72; Mismatches 152; Indels 104; Gaps 20; \$ c bilvoaglanglialricomential conservative 72; Mismatches 152; Indels 104; Gaps 20; \$ c c conservative 72; Mismatches 152; Indels 104; Gaps 20; \$ c c conservative 72; Mismatches 152; Indels 104; Gaps 20; \$ c c conservative 72; Mismatches 162; Indels 104; Gaps 20; \$ c c conservative 72; Mismatches 162; Indels 104; Gaps 20; \$ c c conservative 72; Mismatches 162; Indels 104; Gaps 20; \$ c c conservative 72; Mismatches 162; Indels 104; Gaps 20; \$ c c c conservative 72; Mismatches 162; Indels 104; Gaps 20; \$ c c c conservative 72; Mismatches 162; Indels 104; Gaps 20; \$ c c c c c c c c c c c c c c c c c c	ESULT 8 66349 ycopene beta-cyclase (EC 5.5.1) - common tobacco ;Species: Micotiana tabacum (common tobacco) ;Species: Micotiana tabacum (common tobacco) ;Date: 14-Feb-1997 #sequence_revision 13-Mar-1897 #text_change 28-Jul-2000 ;Pecker, I: Gabbay, R.; Cunningham Jr., P.X.; Hirschberg, J. lant Mol. Biol. 30, 807-819, 1996 .;Teference number: 866349; MUID: 96194462; PMID: 8624411 .Accession: 866349 .;Actuals preliminary; mucleic acid sequence not shown .;Molecule type: DNA .;Gatus: preliminary; nucleic acid sequence not shown .;Molecule type: DNA .;Gatus: preliminary; nucleic acid sequence not shown .;Molecule type: DNA .;Gatus: 1-500 < PEC;Cross-references: EMBL:X81787 .;Superfamily: tomato lycopene beta-cyclase .;Reywords: intramolecular lyase; isomerase .;Reywords: intramolecular lyase; isomerase .;Reywords: intramolecular lyase; isomerase .;Reywords: intramolecular lyase; isomerase .;Meywords: intramolecular lyase .;Meywords:	111 HTAVSAVHAESVQLADGRIIHASTVIDGRQYTPDSALRVGFQAFIGQEWQ 1

Db 47AYSEAEPQTGIEVHKYGAHLF-HTSNKRV 74 Qy 118 HABSVQLADGRITHASTVIDGRGYTPDSALRVGPQAFIGQEWQLSAEHGLSSPIIMDATV 177	PRESULT 12 AD0684 PYAD0684 PYAD0684 PYAD0684 PYAD0684 PYAD0684 PYAD06864 PYAD06864 PYAD06864 PYAD068666 PYAD068666 PYAD068666 PYAD0686666 PYAD06866666 PYAD06866666 PYAD068666666 PYAD0686666666 PYAD0686666666 PYAD06866666666 PYAD068666666666 PYAD06866666666666 PYAD06866666666666666666666666666666666666	
### Status: preliminary; nucleic acid sequence not shown ####################################	102 QORGOHLWLATAVSAVHABSVOLADCRIHASTVIDGAGYTPDSALRVGPOA 153 153GOYGHUMLHTAVSAVHABSVOLADCRIHASTVIDGAGYTPDSALRVGPOA 153 154GOYGHUMLHTAVSAVHABSKOLIAIII	

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17;

Gaps

129;

64 23 241 288 293 337

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A;Molecule type: DNA
A;Residues: 1-428 <STD-3.
A;Residues: 1-428 <STD-3.
A;Residues: 1-428 <STD-3.
A;Cross-references: GB:AB005174; NID:g12512733; PIDN:AAG54346.1; GSPDB:GN00145; UWGP:Z01
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: fixC
C;Superfamily: fixC protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338 DD------PSKOKLAEY-----ROHLESGPL----ROMRMYOKLPAFL----- 370
                                                                                                                                                                                                                                                                                                                                                                                                                                             65 LVVHHWPDYQVRFPQRR--RHVNSGY-----YC----VTSRHFAGILRQQFGQH 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 SLEHIIPGFAESAPVERLITHEKLAFWTEKSAMTMDYCNGDETSPSORSYSVLKSKF--D 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --LADGRIIHASTVIDGRGYTPDSALRVG 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ITLIGDNRQFWQQQPQACSGLRAGLFHPTTGYSLPLAVALADRLSALDVFTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 ISATALLIEDTHYIDKANLQAERARQNIRDYAARQGWPL---QTLLREEQGALP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPELVGDGVLIAGD------AAGWCMNLGFTIRGMDLAIAAGEAAAKTVLSAMKS
                                                                                                                                                                                                                     Length 428;
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21.3%; Pred. No. 0.11;
ative 65; Mismatches 188;
                                                                                                                                                                                                                  Query Match
5.7%; Score 114.5; DB 2;
Best Local Similarity 20.0%; Pred. No. 0.091;
Matches 88; Conservative 56; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Gene: CC2288
C,Superfamily: Rhizobium plasmid pNGR234a Y4xG protein
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                                                                                                                                                             C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: F90634
R;Haysahi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. B, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genc
                                                                                                             flavoprotein [imported] - Escherichia coli (strain 0157:H7, substrain RIMD 0509952)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 MAKRVKPTNVAVGVKELIBLPKSVIEDRPQLQGNQG-AACLFAGSPTDGLMGGGFLYTNE 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 NTLSLGLVCGLHHLHDAKKSVPQMLBDFKQHPAVA-.-PLIAGGKLVEYSAHVVPEAGINM 288
                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-428 «HAY»
A;Cross-references: GB:BA000007; PIDN:BAB33469.1; PID:g13359502; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVVHHWPDYQVRFPQRR--RHVNSGY-----YC----VTSRHFAGILRQQFGQH 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 SLEHIIPGFABSAPVERLITHEKLAFWTEKSAMTMDYCNGDETSPSORSYSVLRSKF--D 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----LADGRIIHASTVIDGRGYTPDSALRVG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---QAFIGQEWQLSAPHGLSSPIIMDATVDQQNGYRFVYTLP 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289 LPELVGDGVLIAGD-----AAGMCMNLGPTIRGMDLAIAAGEAAAKTVLSAMKS 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DD------FSKQKLAEY-----RQHLESGPL----RDMRMYQKLPAFL------ 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 SSVHQTIAHFAQQRWQQQFFRMLNRMLFLAGPAESRWRVMQRFYGLPEDLIARFYAGKL 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53
                                                                                                                                        Species: Bscherichia coli
Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 YDLILVGAGLANGLIALRLQQQHPDMRILLIEAGPEAGGNHTWSFHEEDLTLNQHRWIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 428;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 5.7%; Score 114.5; DB 2; Similarity 20.0%; Pred. No. 0.091; 88; Conservative 56; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- DNPRMFSGYPELAVGVA 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: Ecsuoro
C,Superfamily: fixC protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---E
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Matches

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Unique part of the probable [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Accession: G87532

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, J.C.; Shapiro, L.; Wenter, J.C.; Fraser, C.M

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Reference number: Ag7249; MUID:21173698; PMID:11229647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                      A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-504 <STO>
A,Cross-references: GB:AB005673; NID:g13423805; PIDN:AAK24259.1; GSPDB:GN00148
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46
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A;Accession: F85485 A;Status: preliminary

March completed: February 29, 2004, 14:52:50 time : 15.6328 secs

377 IMT 379 ::| 462 WYT 464

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Pebruary 29, 2004, 14:51:24 ; Search time 25.3626 Seconds
{without alignments}
3180.293 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                         I MOPHYDLILVGAGLANGLIA.....SGKPPVPVFAALQAIMTTHR 382
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/PCT TWW PUB.pep:*

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7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/USO9_NEW PUB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           4 protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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2021
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			Description	Sequence 30, Appl	Sequence 6, Appli	Sequence 7, Appli	Sequence 5. Appli	Sequence 20, Appl				Sequence 61, Appl	59,	.09	57,			
SCHWARIES			QI.	US-09-941-947A-30	US-10-218-118-6	US-09-547-267-7	US-09-920-923-5	US-10-128-713A-20	US-09-323-998D-53	US-09-323-998D-55	US-09-323-998D-56	US-09-323-998D-61	US-09-323-998D-59	US-09-323-998D-60	US-09-323-998D-57	US-10-335-846-6	US-09-323-998D-54	US-09-323-998D-58
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			Match Length DB	382	382	382	382	376	526	201	502	503	500	511	498	530	516	200
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			Score	2021	2021	783.5	783.5	154.5	152	148.5	142.5	141.5	140	139.5	139	139	334.5	133
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Sequence 20, Appl			Sequence 23, Appl					Sequence 12232, A	Sequence 2, Appli			Sequence 8560, Ap	Sequence 12003, A	Sequence 52, Appl		Sequence 25, Appl	48	Sequence 13043, A	Sequence 8840, Ap	Sequence 27, Appl	Sequence 4489, Ap	Sequence 14057, A	Sequence 8419, Ap	Sequence 7248, Ap	Sequence 4784, Ap	Sequence 7544, Ap	Sequence 60, Appl	1236	2181
US-09-323-		5 US-10-335-846-		US-09-323	us-		SD S				US-09-323-998D-49				u)	US-09-323-998D-25		.5 US-10-369-493-13043	5 US-10-369-493-8840	US-09-323-998D-27	US-10-369-493-4	US-10-369	US-10-156	US-10-369-493-724	5 US-10-369-493-4784	US-10-369-493-7	US-10-001		
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32.	130.5	30.	29.	129.5	N	127	125.5	122.5	122.5	122.5	122.5	119.5	115	115	115	113.5	113.5	113	112	109.5	108.5	107	106.5	106.5	103.5	103.5	102.5	101	100
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5

ALIGNMENTS

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61 WIAPLVVIHWPDYQVRFPQRRRHVNSGYYCVTSRHFAGILRQQFGQHLWLHTAVSAVHAE 120
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                                                                                                        APPLICANT: Cherg, Qiong
APPLICANT: Cherg, Qiong
APPLICANT: Diocosimo, Deana J.
APPLICANT: Diocosimo, Deana J.
APPLICANT: Diocosimo, Deana J.
APPLICANT: Miller, Edward S. Jr.
APPLICANT: Miller, Edward S. Jr.
APPLICANT: Odon, J. Martin.
APPLICANT: Odon, J. Martin.
APPLICANT: Picataggio, Steve
TILE OF INVENTIVE OF INVENTIVE CLI993 US NA
CURRANT PRINGE DATE: 2001-09-01
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR PILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Microsoft Office 97
LENGTH: 382
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Sequence 30, Application US/09941947A Publication No. US20030003528A1 GENERAL INFORMATION:
                                                                                 APPLICANT: Brzostowicz, Patricia C. APPLICANT: Cheng, Qiong APPLICANT: DiCosimo, Deana J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Pantoea stewartii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 382; Conservative
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301 AHFAQQRWQQQGFFRMINRMLFLAGPAESRWRVWQRFYGLFEDLIARFYAGKLTVTDRLR 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 GYRFVYTLPLSATALLIEDTHYIDKANLQAERARQNIRDYAARQGWPLQTLLREEQGALP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 VQLADGRIIHASTVIDGRGYTPDSALRVGFQAFIGQEWQLSAPHGLSSPIIMDATVDQQN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 LSPIRRGEWIDQEVARPDHSRRLITGYGSIRAGALIGLLQ---GVDLKWNIHVATLDDIG
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                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Hohmann, Hans-Peter
APPLICANT: Tessier, Michel
APPLICANT: Tessier, Michel
APPLICANT: van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.8%; Score 783.5; DB 9;
43.7%; Pred. No. 7.6e-72;
Live 64; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                 Hoffmann-La Roche Inc
                                            361 ILSGKPPVPVFAALQAIMTTHR 382
                                                                                   361 ILSCKPPVPVPAALQAIMTTHR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: POKTAS, Bruce A.
REGISTRATION NUMBER: 32,748
RESTERENCE/DOCKET NUMBER: RAN 60
TELECOMMUNICATION INPORMATION:
TELEPHONE: (201) 235-5801
TELEPAX: (201) 235-263
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 382 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
                                                                                                                                                                                      Sequence 7, Application US/09547267; Patent No. US20020147371A1
                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
ZUNTRY: USA
ZUP: 07110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 38.8%
Best Local Similarity 43.7%
Matches 165; Conservative
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STRANDEDNESS: sir
TOPOLOGY: linear
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APPLICANT: Chouse Dietre
APPLICANT: Cheago, Stephen
APPLICANT: Cheago, Stephen
APPLICANT: Cheago, Oiong
TITLE OF INVENTION: Genes Encoding Carotenoid Compounds
FILE REFERENCE: CL1876 US NA
CURRENT FILING DATE: 2002-08-13
FRICR FILING DATE: 2002-08-13
FRICR APPLICATION NUMBER: 60/312,646
FRICR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                   361 ILSGKPPVPVFAALQAIMTTHR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                  361 ILSGKPPVPVFAALQAIMTTHR 382
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Publication No. US20030148319A1
GENERAL INFORMATION:
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ITLTGDNRQFWQQQPQAC--SGLRAGLFHPTTGYSLPLAVALADRLSALDVFTSSSVHQT 299
                                              300 IAHFAQQRWQQQGFFRMLNRMLFLAGPAESRWRVMQRFYGLPEDLIARFYAGKLTVTDRL 359
                                                             --PLVVHHWPDYQVRPPQRRRHVNSGYYCVTSRHFAGILRQQFGQHLWLHTAVSAVHAES 121
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HDL1IAGAGLSGALIALAVRDRRPDARIVMLDARSGPSDQHTWSCHDTDLS---PEWLAR
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15-10-128-713A-20
Sequence 20, Application US/10128713A
Publication No. US20030170847A1
GENERAL INFORMATION:
APPLICANT: Bramucci, Michael G
                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Flavobacterium sp. R1534
US-09-920-923-5
                                                                                              RILSGKPPVPVPAALQAI 377
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RIVTGRPPIPLSOAVRCL 372
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355 RIVTGRPPIPLSQAVRCL 372
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Matches 165; Conserv
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 242
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APPLICANT: SUN, ZAIREN
TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND
TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 108172-09919
CURRENT APPLICATION NUMBER: U$/09/323,998D
CURRENT FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: 09/088,724
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1997-09-25
PRIOR FILING DATE: 1997-09-25
PRIOR FILING DATE: 1996-03-29
PRIOR FILING DATE: 1996-03-29
PRIOR FILING DATE: 1998-03-29
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TITLE OF INVENTION: Genes Involved in Isoprenoid Compound Production FILE REPERENCE: CL-1788
CURRENT APPLICATION NUMBER: US/10/128,713A
CURRENT FILING DATE: 2002-04-22
NUMBER OF SEQ ID NOS: 36
SOFTWARE MICROSOFT Office 97
ENGINENT: 376
                                                                                                                                                                                                                                                                                                                            7.6%; Score 154.5; DB 14; Length 376; 23.8%; Pred. No. 4.3e-07; tive 46; Mismatches 119; Indels 75;
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llarity 21.1%; Pred. No. 1.3e-06;
Conservative 66; Mismatches 167;
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                                                                                                                                                                                                                                            ORGANISM: Rhodococcus erythropolis
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SEQ ID NO 53
LENGTH: 526
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Best Local Similarity
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Best Eccal Similarity
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6 DLILVGAGLANGLIALRIQQQHPDMRILLIEAGP2AGGNFTWSFHESDLTLNQHRWI 62	& q ₀	161 LSA-PHGLSSPIIMDATVDQQNGYRFVYTLPLSATALLIBDTHYIDKAN 208 161
63 APLVVHHWPDYQVRFPQRRRHVNSGYYCVTSRHFAGILRQQFGQHLWLH 111 :	ව ර	209 LQAERARQNIRDYAARQGWPLQTLIREEQGALPITLTGDNRQFWQQPQACSGL 262
112 TAVSAVHAESVQLADGRIIHASTVIDGRGYTPDSALRVGFQAFIGQB 158 :	S da	263RAGLFHPTTGYSLPLAVALADRLSALDVFTSSSVHQTIAHFAQQRW 308
159 WQL-SAPHGLSSPIIMDATVDQQNGXR	\$ g	309 QQQGFFRMINRMLFLAGPAESRWRVWQRFYGLPEDLIARFYAGKLTV 355
202 HYIDKANLQABRARQNIRDYAARQGWPLGTLLREEGGALPITLTGDNRQFWQQQPQACSG 261	& A	356TDRLRILSGRPPVPV 370
262 LRAGLFHPTTGYSLPLAVALADRESALDVFTSSSWHQTIAHFAQ 305	RESULT 8 US-09-323-0 ; Sequence ; Patent No	RESULT 8 WS-09-313-998D-56 S. Application US/09323998D Patent No. US20020102631A1
436 ERRORSFF-LFGLALILQLDIEGIRSFFRAFFRVPRWWWQGFLGSSLSSAD 486 SULT 7 -09-323-99BD-55 Sequence 55, Application US/0932399BD Serient No. US20020102631A1 GENERAL INFORMATION:	APPLIC APPLIC TITLE TITLE FILE R CORREN PRIOR	ANT: CUNNING ANT: SUN, ZZ OF INVENTION, OF INVENTION, OF INVENTION, T APPLICATION T FILING DATE
APPLICANT: CUNN, MAGRAM OR., FRANCIS X. APPLICANT: SUNN, CAIREN TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND TITLE OF INVENTION: METABOS OF USE THEREOF FILE REFERENCE: 108172-09019 CURRANT APPLICATION NUMBER: US/09/323,998D PRIOR APPLICATION NUMBER: 09/088,724 PRIOR APPLICATION NUMBER: 09/088,724	PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR	OR APPLICATION NUMBER: 09/088,725 OR FILING DATE: 1998-06-02 OR FILING DATE: 1997-09-25 OR FILING DATE: 1997-09-25 OR PILING DATE: 1996-03-29 OR PLING DATE: 1996-03-29 SET OF SEQ ID NOS: 61
FILING DATE: 1998-06-02 APPLICATION NUMBER: 09/088,725 FILING DATE: 1998-06-02 APPLICATION NUMBER: 08/937,155 APPLICATION NUMBER: 08/937,155 APPLICATION NUMBER: 08/624,125	SOF SEQ LEI TYI OR US-09-	EST FEE
IOR FILING DATE: 1996-03-29 MERR OF SEQ ID NOS: 61 ID NO 55	Query Ma Best Loc Matches	<pre>y Match 1.0cal Similarity 21.9%; Pred. No. 1.1e-05; heb 70; Conservative 49; Mismatches 131; Indels 69; Gaps 15;</pre>
LENGTH: 501 TYPE: PF: ORCANISM: A-abidopsis thaliana 09-323-998D-55	& g	6 DLILVGAGLANGLIALRLQQQHPDMRILLIBAGPEAGGNHTWSFHEED-LTLNQH 59
th 7.3%; Score 148.5; DB 9; Length 501; Similarity 21.0%; Pred. No. 2.7e-06; Scorservative 66; Mismatches 175; Indels 105; Gaps 20;	& 8	60 RWIAPLVVEHWPDYQVRFPQRRRHVNSGYYCVTSRHPAGILRQQFGQHLWLH 111
6 DLILVGAGLANGLIALRLQQQHPDWRILLIEAGPEAGGNHTWSFHEED-LTLNQH 59	දු පු	112 TAVSAVHABSVQLADGRIIHASTVIDGRGYTPDSALRVGFQAFIGQEWQLSA 163 192 KVIKVIHEESKSLLICNDGITINATVVLDATGFSRCLVQYDKPYNPGYQVAYGINAEVBE 251
60 RWIAPLVVHHWPDYQVRFPQRRRHVNSGYYCVTSRHFAGILRQQFGQHL 108 1 142 TWSGAVVYUDBGVKKDLSRPYGRVNRKQLKSKOLLQKCITNGVKF 185	ov.	164 - PHGLSSPIIMDATVDQQNGYRPVYTLPLSATALLIEDTHYIDKANLQA 211
109 WIHTAVSAVEAESVQLADGRIIHASTVIDGRGYTPDSALRVGFQAFIGQEWQ 160 186 HQSKVTNVVHEEANSTVVCSDGVKIQASVVLDATGFSRCLVQYDKPYNPGYQVAYGIVAE 245	& qa	212 ERARQNIRDYAARQGWPLQTILIREEQGALPITLIGDNRQFWQQQPQACSGLR 263
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IITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND TITLE OF INVENTION: METHODS OF USE THEREOF
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ORGANISM: Nicotiana sp
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CURRENT APPLICATION NUMBER: 09/088,724

PRIOR PELING DATE: 1986-06-02

PRIOR PELING DATE: 1986-06-02

PRIOR APPLICATION NUMBER: 09/088,725

PRIOR APPLICATION NUMBER: 08/937,155

PRIOR PELING DATE: 1996-03-25

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APPLICANT: SUN, ZAIREN
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Patent No. US20020102631A1
GENERAL INFORMATION:
                                  360 AGMVHPSTGYMVARTLAAA 378
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Matches 85; Conservative
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ORGANISM: Narcissus sp
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Sequence 59, Application US/09323998D Patent No. US2002010263.1A1 GENERAL INFORMATION: APPLICANT: CUNNINGHAM UR., FRANCIS X.

-09-323-998D-59

SUN, ZAIREN

APPLICANT:

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APPLICANT: CUNMINGHAM JR., FRANCIS X.
APPLICANT: CUNMINGHAM JR., FRANCIS X.
TITLE OF INVENTION: GENES OF CARCIENOID BIOSYNTHESIS AND METABOLISM AND
TITLE OF INVENTION: METBODS OF CARCIENOID BIOSYNTHESIS AND METABOLISM AND
TITLE OF INVENTION: METBODS OF CARCIENOID BIOSYNTHESIS AND METABOLISM AND
TITLE OF INVENTION: METBODS OF CARCIENOID
FILE REFERENCE: 108172-09019
CURRENT APPLICATION NUMBER: 1999-06-02
PRIOR APPLICATION NUMBER: 09/088,724
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: 08/037,155
PRIOR APPLICATION NUMBER: 08/624,125
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THIE REPERENCE: 108172-09019
CURRENT APPLICATION NUMBER: US/09/323,998D
CURRENT FILING DATE: 1999-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 09/088,725
PRIOR APPLICATION NUMBER: 09/088,725
PRIOR APPLICATION NUMBER: 08/337,155
PRIOR PILING DATE: 1997-09-25
PRIOR PILING DATE: 1997-09-25
PRIOR PILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PATENTIN VOY: 2.1
SEQ ID NO 59
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APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: CUNNINGHAM JR., FRANCIS X.
TITLE OF INVENTION: GENES OF CAROTENOLD BIOSYNTHESIS AND METABOLISM AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 108172-09019
CURRENT PELLON NUMBER: US/09/323,998D
CURRENT FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: 09/088,724
PRIOR PILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 09/088,725
PRIOR APPLICATION NUMBER: 09/0837,155
PRIOR APPLICATION NUMBER: 09/925
PRIOR APPLICATION NUMBER: 08/937,155
PRIOR PILING DATE: 1996-03-29
PRIOR PILING DATE: 1996-03-29
                                                                                                                                                                                                                                                                                                                          61 WIAPLVVHHWPDYQVRFPQR-RRHVNSGYYCVTSRHF-AGILRQQFGQHLWLHTA--VSA 116
                                                                                                                                                                                                                                                                                                                                                                                                                        144 --LDCLDTTWSSAVVYIDEKSTKSLNRPYARVNRKQLKTKMLQKCIANGVKFHQAKVIKV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 SSPIIM---DATVDQQNGYR-----FVYTLPLSATALLIEDTHYIDKANLQAERARQ 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 DKMLFMDWRDSHLDQNLEIKARNSRIPTELYAMPFSSTRIFLEETSLVARPGINGMEDIGE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 NIRDYAARQGWPLQTLLREEQ-----GALPITLTGDNRQFWQQQPQACSGL--RAGLFH 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 RMAYRLKHLGIKVKSIEEDERCVIPMGGPLPVL-------PORVLGIGGTÄGNYH 369
                                                                                                                                                                                                                                                                                             6 DLILVGAGLANGLIALRLQQQHDDMRILLIEAGPB···-AGGNHTW--SFHEEDLTLNQHR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 DLILVGAGLANGLIALRLQQQHPDWRILLIEAGPE---AGGNHTW--SFHEEDLTLNQHR 60
                                                                                                                                                                                              Query Match 6.9%; Score 139.5; DB 9; Length 511; Best Local Similarity 21.0%; Pred. No. 2.4e-05; Matches 66; Conservative 57; Mismatches 132; Indels 59; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 VHAESVQLA---DGRIIHASTVIDGRGYTP----DSALRVGFQAFIGQEWQLSA-PHGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cuery Match 6.9%; Score 139; DB 9; Length 498; Best Local Similarity 20.4%; Pred. No. 2.6e-05; Matches 81; Conservative 70; Mismatches 170; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 57, Application US/09323998D Patent No. US20020102631A1 GENERAL INFORMATION:
PRIOR FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 PTTGYSLPLAVALA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370 PSTGYMVARTLAAA 383
                                                                                                                             ORGANISM: Tagetes erecta
IS-09-323-998D-60
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SOFTWARE: Patentin Ver. 3
SEQ ID NO 57
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ORGANISM: Capsicum sp.
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                                                              SEQ ID NO 60
LENGTH: 511
                                                                                                               TYPE: PRT
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117 VHARSVQLA---DGRIIHASTVIDGRGYTP-----DSALRVGFQAFIGQEWQLSA-PHGL 167
                                                                                                                                                                                                                          193 IHEESKSMIICNDGITIQATVVIDATGFSRSIVQYDKPYNPGYQVAYGILAEVEEHPFDV 252
                                                                                                                                                                                                                                                                                                          168 SSPIIMD-----ATVDQQNGY--RFVYTLPLSATALLIEDTHYIDKANLQAERARQ 216
                                                                                                                                                                                                                                                                                                                                                             253 NKWYPNDWRDSHLKNNVELKERNSRIPTFLYAMPFSSNRIFLERTSLVARPGLGMDDIQE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 RWYARLSHLGIKVKSIEEDEHCVIPMGGPLPVL------PQRVVGIGGTAGWVH 360
61 WIAPLVVHHWPDYQVRPPQR-RRHVNSGYYCVTSRHFAGILRQQP----GQHLWLHTAVSA 116
                                                                       135 --LDCLDATWSGAAVYIDDKTTKDLNRPYGRVNRKQLKSKMMOKCILNGVKFHQAKVIKV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 NIRDYAARQGWPLQTLLREEQ-----GALPITLTGDNRQFWQQQPQACSGL--RAGLFH 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 PTTGYSLPLAVALADRL-SALDVFTSSVHQTIAHFÄQQRW-------QQQGFPRM-L 317
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TITLE OF INVENTION: GENES ENCODING EPSILON LYCOPENE CYCLASE AND METHOD FOR TITLE OF INVENTION: GENES ENCODING EPSILON LYCOPENE CYCLASE AND METHOD FOR TITLE OF INVENTION: GENES ENCODING ENCYLLC EPSILON CAROTENE CURRENT PAPLICATION NUMBER: US/10/335,846
CURRENT APPLICATION NUMBER: US/10/335,846
CURRENT APPLICATION NUMBER: US/90/904,222
PRIOR APPLICATION NUMBER: US/90/904,222
PRIOR APPLICATION NUMBER: US/90/904,222
PRIOR FILING DATE: 1998-05-26
PRIOR FILING DATE: 1997-09-25
PRIOR FILING DATE: 1997-09-25
PRIOR FILING DATE: 1997-09-25
PRIOR FILING DATE: 1997-09-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 --CIEHAWKOTIVYLDNDAPVLIGRAYGRVSRH---LLHEBLLKRC-VBSGVSYLDSKVE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 QLADGRIIHASTVIDGRGYTPDSALRVGFQAFIGQ--EWQLSAP-----HGL----S 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 SP-----IIMD-----ATVDQQNGYRFVYTLPLSATALLIEDTHYIDKANLQAERA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 RQNIRDYAARQGWPLQTLLRREQGALPITLTGDNRQFWQQQPQACSGLRAGLFHPTTGYS 274
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Best Local Similarity 19.6%; Pred. No. 2.8e-05;
Matches 79; Conservative 72; Mismatches 179; Indels 74; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318 NRMLFLAGPAESRWRVMQRFYGLPEDLIARFYAGKLT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 6, Application US/10335846; Publication No. US20030220405A1
; ENERAL INFORMATION: APPLICANT: CUNNINGHAM JR., FRANCIS X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Adonis palaestina
US-10-335-846-6
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| : | | | 479 IFAFYMFIIAPH 490
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SEQ ID NO 58
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APPLICANT: SUN, ZAIREN
TITLE OF INVENTION: GENES OF CARCTENDID BIOSYNTHESIS AND METABOLISM AND
TITLE OF INVENTION: GENES OF CARCTENDID BIOSYNTHESIS AND METABOLISM AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 108172-09019
CURRENT APPLICATION NUMBER: US/09/323,998D
CURRENT APPLICATION NUMBER: 09/088,724
PRIOR FILING DATE: 1999-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR PILING DATE: 1996-03-29
FILOR APPLICATION NUMBER: 08/624,125
PRIOR PILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 61
SEQ ID NO 54
335 KRKLMSRLKTLGIQVIKVYBEEWSYIPVGGSLPN----TEQRALAFGAAASMVHPATGYS 390
                                                                               275 LPLAVALADRL-----CALDVFTSSVHQTIAHFAQQRW-----CQQQGF 313
                                                                                                                                 391 VVRSLSEAPKYASVIAKILKODNSAYVVSGOSSA----VNISMOAMSSLWPKBRKRORAF 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 WHHWPDYOVRFPORRRHVNSGYYCVTSRHFAGILROOFGOHLWLHTAVSAVHAESVOL- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 RITEAPNGLSLIECEGNITIPCRLATVASGAASGKILQYELGGPRVCVQTAYGIEVEVES 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 APHGLSSPIIMDATVDQQNGYR------FVYTLPLSATALLIRDTHYIDK 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 IEHVWRDTVV-----YLDDNDPILIGRAYGRVSRDLLHEELLTRCMESGVSYLSSKVE 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ADGRI---IHASTVIDG--RGYTPDSAL---RVGFQAFIGQEWQL-S 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 FHPTTGYSLPLAVALADRLSAL--DVFTSSSVHQTIAH-----FAQQRWQ----- 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 VHPATGYSVVRSLSEAPNYAAVIAKILGKGNSKÖMLDHGRYTTHISKQAWETLWPLERKR 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QRAFF-LFGLALIVQMDIEGTRTFFRIPTMWWQFLGSSLSSTDLI------478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.7%; Score 134.5; DB 9; Length 516; Best Local Similarity 19.9%; Pred. No. 7.9e-05; Matches 86; Conservative 65; Mismatches 188; Indels 93;
                                                                                                                                                                                      314 FRMINRMIPLAGPAESRWRVMQRFYGLPEDLIARFYAGKLITVTD 357
                                                                                                                                                                                                                                        447 FILEGLELIVOLDIZATRIFFRIPTRIPTRAMWGFLGSSLSSFD 490
                                                                                                                                                                                                                                                                                                                                                                          Sequence 54, Application US/09323998D Patent No. US20020102631A1 GENERAL INFORMATION:
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S-09-323-998D-54
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Query Match 6.6%; Score 133; DB 9; Length 500;
Best Local Similarity 19.4%; Pred. No. 0.00011;
Matches 80; Conservative 74; Mismatches 152; Indels 106; Gaps 19;
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APPLICANT: SUN, ZAREN
APPLICANT: SUN, ZAREN
TITLE OF INVENTION: GENES OF CARCTENOID BIOSYNTHESIS AND METABOLISM AND
TITLE OF INVENTION: METHODS OF USE THEREOF
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CURRENT APPLICATION NUMBER: US/09/323,998D
CURRENT FILING DATE: 1999-06-02
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PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-07,155
PRIOR APPLICATION NUMBER: 08/937,155
PRIOR APPLICATION NUMBER: 08/937,155
PRIOR APPLICATION NUMBER: 08/624,125
PRIOR FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 61
US-09-323-998D-58
Sequence 58, Application US/09323998D
Patent No. US20022102631A1
GENERAL INFORMATION:
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6479, Ap 52, Appl 25, Appl

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COMPUTER READABLE FORM:

MEDULUM TYPE: Diskette, 3.50 inch, 720Kb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/783,705A
FILING DATE: 19911023
CLASSIFICATION NUMBER: US /07/783,705A
FILING DATE: 19811023
FILING DATE: 19811023
APPLICATION NUMBER: US 07/519,011
FILING DATE: 05-MAR-1990
APPLICATION NUMBER: US 07/519,011
FILING DATE: 19-ARR-1990
APPLICATION NUMBER: US 07/519,011
FILING DATE: 19-ARR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Schwadron, Janet I.
REGISTRATION NUMBER: 212-708-1935
TELEPOMNUMICATION INFORMATION:
TELEPOMNUMICATION NUMBER: 212-708-1935
TELEPOMNUMICATION NUMBER: 212-708-1935
TELEPOMNUMICATION NUMBER: 212-708-1935
TELEPOMNUMICATION NUMBER: 212-708-1935
TELEPOMNUMICATION SEQ ID NO: 3:
SEQUENCE CHARACTERIFICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/07783705A
Patent NO. 5422939
GENERAL INFORMATION:
APPLICANT: Misawa. No. 542939ihiko
APPLICANT: Misawa. No. 542939ihiko
APPLICANT: Nakamura, Katsumi
APPLICANT: Nakamura, Katsumi
APPLICANT: Nakamura, Katsumi
APPLICANT: Nakamura, Katsumi
APPLICANT: Nakamura, Katsumi
APPLICANT: Nakamura, Katsumi
APPLICANT: Nakamura, Katsumi
APPLICANT: Nakamura, Katsumi
APPLICANT: Nakamura, Katsumi
APPLICANT: SEQUENCES:
CORRESPONDENCS:
ADDRESSEE: Ladas & Parry
STREET: 26 West 61 Street
CITY: New York
STATE: NY
                      US-08-624-125-20

US-09-321-998E-51

US-09-323-998E-51

US-09-323-998E-47

US-09-323-998E-47

US-09-323-998E-47

US-09-323-998E-26

US-08-624-125-21

US-08-937-155-21

US-08-937-155-21

US-08-937-155-21

US-09-323-998E-21

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US-07-783-705A-3
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     Sequence 14, Appl
Sequence 17, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 19, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 61, Appl
                                                                                                                                                                 February 29, 2004, 14:35:44 ; Search time 11.6083 Seconds (without alignments) 1698.885 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                            1 MQPHYDLILVGAGLANGLIA.....SGKPPVPFAALQAIMTTHR 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                         GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-06-623A-14

US-08-660-645A-7

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US-09-546-96-7

US-09-546-96-7

US-09-20-921-9

US-09-134-607A-19

US-09-134-998E-5

US-09-323-998E-5

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                      4 protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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SOFIMARS: FACERLIN RELEASE #1.0, VET CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,623A FILING DATE: 22-UUL-1993
CLASSIPICATION A35
PRICA APPLICATION NUMBER: US 07/805,061
FILING DATE: 09-DEC-1991
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 07/662,921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS CONTWARE: PatentIn Policy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-08-096-623A-14
; Sequence 14, Application US/08096623A
; Patent No. 5684238
    TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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          ; TYPE: amin
; TOPOLOGY:
; MOLECULE TYPE
US-08-095-726-14
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                                                                                                                                                         61 WIAPLVVHHWPDYQVRFFTRRRKINSGYFCITSQRFAEVLQRQFGPHLWMDTAVAEVNAE 120
                                                                                                                                                                                                            121 SVQLADGRIIHASTVIDGRGYTPDSALRVGFQAFIGQEWQLSAPHGLSSPIIMDATVDQQ 180
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                                                                              1 MQPHYDLILVGAGLANGLIALRLQQQQPDMRILLIDAAPQAGGNHTWSFHHDDLTESQHR 60
                                                            1 MQPHYDLILVGAGLANGLIALRLQQQHPDMRILLIEAGPEAGGNHTWSFHEEDLTLNQHR
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                      Indels
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APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Brinkhaus; Friedhelm L
APPLICANT: Brinkhaus; Indrant
APPLICANT: Proffitt, John H
APPLICANT: Yarger, James G
APPLICANT: Yarger, James G
APPLICANT: Yen, Huei-Che B
TITLE OF INVENTION: Beta-Carotene Biosynthesis in
TITLE OF INVENTION: Genetically Engineered Hosts
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Amoco Corp., Patents and Licensing Dept 200 E Randolph St
    82.2%; Pred. No. 1.2e-159;
:ive 31; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,726
FILING DATE: 21.-ULL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,566
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Galloway, No. 5530188val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128567180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILSGKPPVPAALQAIMTTHR 382
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Patent No. 5530188
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INFORMATION FOR SEQ ID NO: 14:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 374 amino ació
                        Conservative
Best Local Similarity
Matches 314; Conserv
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CITY: Chicago
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GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L.
APPLICANT: Ausich, Rodney L.
APPLICANT: Mukharji, Indrani
APPLICANT: Wicharji, Indrani
APPLICANT: Yarger, James G.
APPLICANT: Yen, Huei-Che B.
TITLE OF INVENTION: Biosynthesis of Zeaxanthin and
TITLE OF INVENTION: Glycosylated Zeaxanthin in Genetically Engineered Hosts
NUMBER OF SEQUENCES: 104
CORRESPONDENCES: 104
                                                                                                                                                                                                                              63 VAHAWPGYEVQFPDLRRRIARGYYSITSERFAEALHQALGENIWLNCSVSEVLPNSVRLA 122
                                                                                                                                                                                                                                                                                          66 VVHHWPDYQVRPPQRRRHVNSGYYCVTSRHPAGILRQQPGQHLWLHTAVSAVHAESVQLA 125
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                                                                                                                             186 VYTLPLSATALLIEDTHYIDKANLQAERARQNIRDYAARQGWPLQTLLREEQGALPITLT
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  Length 374;
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Query Match
55.8%; Score 1127; DB 1;
Best Local Similarity 58.4%; Pred. No. 1.7e-104;
Matches 213; Conservative 53; Mismatches 99;
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STREET: 120 S. Riverside Plaza, 22nd Floor
CITY: Chicago
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Nutley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 QRWQQQGFFRMLNRMLFLAGPABSRWRVMQRFYGLPBDLIARFYAGKLTVTDRLRILSGK 365
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APPLICANT: Pasamontes, Luis
APPLICANT: Pasamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: Tessier, Michel
APPLICANT: Van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE HOFFmann-La Roche Inc.
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 55.8%; Score 1127; DB 1; Best Local Similarity 58.4%; Pred. No. 1.7e-104; Matches 213; Conservative 53; Mismatches 99;
Sequence 7, Application US/08660645A Patent No. 6087152 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          LENGTH: 374 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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3 HDLLIAGAGLSGALIALAVEDRRPDARIVWLDARSGPSDQHTWSCHDTDLS---PEWLAR
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38.8%; Score 783.5; DB 3; Length 3
Best Local Similarity 43.7%; Pred. No. 4.4e-70;
Matches 165; Conservative 64; Mismatches 136; Indels
                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDION TYPE: RIOPY disk

COMPUTER: IBM PC compatible

FILING DATE: 07-UN-1996

CLASSIFICATION NUMBER: EP 9510888.9

FILING DATE: 09-UN-1995

ATTORNEY AGENT INFORMATION:

NAME: POATE: 09-UN-1995

ATTORNEY AGENT INFORMATION:

NAME: COMPUTER: 327-48

REGISTRATION NUMBER: RAN 6002/170

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION NUMBER: RAN 6002/170

TELEBRONE: (201) 235-2801

TELEBRONE: (201) 235-2801

TELEBRONE: CLANACTER: STATICS:

SEQUENCE CHARACTER: STATICS:

LEWSTONE CHARACTER: STATICS:

LEW
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Patent No. 6124113
GENERAL INFORMATION:
APPLICANT: Hohmann, Hans-Peter
APPLICANT: Pasamontes, Luis
APPLICANT: Tessier, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||::||:||::
355 RIVTGRPPIPLSQAVRCL 372
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
USA
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60 LSPIRRGEWTDQEVARPDHSRRLTTGYGSIEAGALIGLIQ---GVDLRWNTHVATLDDTG 116
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3 HDLLIAGAGLSGALIALAVRDRRPDARIVALDARSGPSDQHTWSCHDTDLS---PEWLAR 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.8%; Score 783.5; DB 3; Length 382; 43.7%; Pred. No. 4.4e-70;
APPLICANT: van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/09/298,718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Pokras, Bruce A.
REGISTRATION NUMBER: 32,748
REPERENCE DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INPORMATION:
TELEPHONE: (201) 235-5801
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 382 amino acids
                                                                                        ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
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RIVTGRPPIPLSQAVRCL 372
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 382 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Matches 165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                    07110
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RESULT 6 US-09-546-969-7

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ITLTGDNRQFWQQQPQAC--SGLRAGLFHPTTGYSLPLAVALADRLSALDVFTSSSVHQT 299
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                                                                               APPLICANT: Passamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: Tessier, Michel
APPLICANT: van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEGUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,969
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POFKTEN, BILLOE A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 125-5801
                                                                                                                                                                                                             Hoffmann-La Roche Inc
Sequence 7, Application US/09546969
                                                                                                                                                                                                                        STREET: 340 Kingsland Street
CITY: Mutley
STATE: NJ
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 RILSGKPPVPVFAALQAI 377
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TELEPAX: (201) 235-2263
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 382 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-09-546-969-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                 Patent No. 6207409
GENERAL INFORMATION:
APPLICANT: Hohman
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                                                                                                                                                                                                                                                                                                            07110
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TYPE: amino acid
STRANDEDNESS: siz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 LSPIRRGEWTDQEVAFPDHSRRLTTGYGSIEAGALIGLLQ---GVDLRWNTHVATLDDTG 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 -- PLVVHHWPDYQVRFPQRRRHVNSGYYCVTSRHFAGILRQQFGQHLWLHTAVSAVHAES 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :||:: ||||: ||||| :: : || ||::::|
3 HDLLIAGAGLSGALIALAVRDRRPDARIVMLDARSGPSDQHTWSCHDTDLS---PEWLAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.8%; Score 783.5; DB 3; Length 382; 43.7%; Pred. No. 4.4e-70; tive 64; Mismatches 136; Indels 13;
                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Pasamontes, Luis
APPLICANT: Pasamontes, Luis
APPLICANT: Tsygankov, Turus
TITLE OF INVENTION: Improved Fermentative Carotenoid
FILE REFERENCE: Improved Fermentive Carotenoid
CURRENT APPLICATION NUMBER: US/08/980,832B
CURRENT FILING DATE: 1997-12-01
NUMBER: OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Hohmann, Hans-Peter
APPLICANT: Pasamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: van Loon, Adolphus
APPLICANT: van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
                                                                                                             S-08-980-832-5
Sequence 5, Application US/08980832B
Patent No. 6291204
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Flavobacterium sp. R1534 S-08-980-832-5
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Patent No. 6613543
355 RIVTGRPPIPLSQAVRCL 372
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RIVTGRPPIPLSQAVRCL 372
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                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 382
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STATE: NJ
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Best Local S
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242 ITLIGDNRQFWQQQPQAC--SGLRAGLFHPTTGYSLPLAVALADRLSALDVPTSSSVHQT 299
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Patent No. 6677134
CENREAL INFORMATION:
PAPLICANT: Pasamontes, Luis
APPLICANT: Tsygankov, Yuri
TITLE OF INVENTION: Fermentative Carotemoid Production
FILE REFERENCE: 15464 US (C384315/125944)
CURRENT APPLICATION NUMBER: US/09/920,923B
CURRENT FILING DATE: 2001-08-02
                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,267 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                     RAN 6002/170
                  MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    355 RIVTGRPPIPLSQAVRCL 372
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                                                                                                                                                                                                                                                                                                                   NAME: Pokras, Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAI
                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pokras, Bruce A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 382 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICATION NUMBER:
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US-09-006-491-6
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.8%; Score 783.5; DB 4; Length 382;
Best Local Similarity 43.7%; Pred. No. 4.4e-70;
Matches 165; Conservative 64; Mismatches 136; Indels 13; Gaps
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APPLICANT: MISAWA, NO. 5811273ihiko
APPLICANT: KONDO, Keiji
APPLICANT: KONDO, Keiji
APPLICANT: KONDO, Keiji
APPLICANT: YOKOYAWA, Akihiro
TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
TITLE OF INVENTION: XANTHORHYLLS
NUMBER OP SEQUENCES: 12
CORRESPONDENCE ADDRESS: 2
ADDRESSE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppd disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,310
FILING DATE: 23-5EP-1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/980,832
PRIOR FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
IENGTH: 382
                                                                                                                                                                                                                                                                                    ORGANISM: Flavobacterium sp. R1534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 RIVIGRPPIPLSQAVRCL 372
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63 A---PLVVHHWPDYQVRFPQRRRHVNSGYYCVTSRHFAGILRQQFGQHLWLHTAVSAVHA 119
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Patent No. 5972690

Patent No. 59726901

APPLICANT: MISHAW, No. 59726901hiko

APPLICANT: KONDO, Keiji

APPLICANT: KONDO, Keiji

APPLICANT: KONDO, Keiji

TITLE OF INVENTION: ANITHOPHYLLS AND THE PROCESS FOR PRODUCING THE TITLE OF INVENTION: XANTHOPHYLLS

NUMBER OF SEQUENCES: 12

CORRESPONDRUE ADDRESS: 12

CORRESPONDRUE ADDRESS: 12

CORRESPONDRUE ADDRESS: 12

SANDRESSES: FOLEY & Lardner

STREET: 3000 K Street, N.W., Suite 500
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43.0%; Pred. No. 1.1e-67;
tive 65; Mismatches 137;
JMBER: WO PCT/JP94/02220
26-DEC-1994
                                    PRICING DATE: 26-DEC-1994
PRICING DATE: 26-DEC-1994
PRICATION NUMBER: JP 6-235917
FILING DATE: 05-SEP-1994
PRICATION NUMBER: JP 5-348737
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOTH STEPHEN BOT
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DQLRIVTGKPPIPLGTAIRCL 376
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TELEPHONE: (202)07-5399
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Best Local Similarity 43.0%
Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 386 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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TELEX: 904136
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179

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JS-09-335-919-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ONGYRFVYTLPLSATALLIEDTHYIDKANLQAERARQNIRDYAARQGWPLQTLLREEQGA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 A---PLVVHHWPDYQVRFPQRRRHVNSGYYCVTSRHFAGILRQQFGQHLWLHTAVSAVHA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESVQLADGRIIHASTVIDGRGYTPDSALRVGFQAFIGQEWQLSAPHGLSSPIIMDATVDQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPITLIGDNROFWQQQP--QACSGLRAGLFHPTTGYSLPLAVALADRLSALD-VFTSSSV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 HOTIAHPAOORWOOOGFFRMINRMIFIAGPAESRWRVMORFYGIPEDLIARPYAGKLTVT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 RGAIRDYAIDRARRDRFLRILNRMLFRGCAPDRRYTLLQRFYRMPHGLIBRFYAGRLSVA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 HDVLLAGAGLANGLIALALRAARPDIRVLLLDHAAGPSDG--HTWSCHDPDLSPD---WL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.6%; Score 759.5; DB 2; Length 36
43.0%; Pred. No. 1.1e-67;
tive 65; Mismatches 137; Indels
                                                COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: IBM PC comparible

COMPUTER: IBM PC comparible

COMPUTER: Patent PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/006,491
                                                                                                                                                                                                                                                       PRIOR ADDITION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/663,310
FILING DATE: 23-SEP-1996
APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
FILING DATE: 26-DEC-1994
APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 05-SEP-1994
FILING DATE: 07-DEC-1993
ATTORNARY ACTION NUMBER: UP 5-348737
FILING DATE: 27-DEC-1993
ATTORNARY ACTION NUMBER: 29-768
REGISTRATION NUMBER: 29-768
REGISTRATION NUMBER: 29-768
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29,768
8R: 49441/109
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DQLRIVTGKPPIPLGTAIRCL 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (202) 672-5300
(202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 904136
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 386 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 43.0
Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
S-09-006-491-6
Washington
D.C.
Y: USA
                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                        COUNTRY:
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58 ARLXPLRRANWPDQEVRPPRHARRLATGYGSLDGAALADAVVRSGABIRW-DSDIALLDA 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 YDLILVGAGLANGLIALRLQQQHPDMRILLIE--AGPEAGGNHTWSFHEEDLTLNQHRWI
                                              GENERAL INFORMATION:
APPLICANT: MISAWA, No. 61501301hiko
APPLICANT: KONDO, Katji
APPLICANT: KONDO, Katji
APPLICANT: KONDO, Katji
APPLICANT: YOKOYAMA, Akihiro
TITLE OF INVENTION: DNA STRADBS USEFUL FOR THE SYNTHESIS OF
TITLE OF INVENTION: XANTHOPHYLLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.6%; Score 759.5; DB 3; Length 386; 43.0%; Pred. No. 1.1e-67; tive 65; Mismatches 137; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/335,919
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/663,310
FILING DATE: 22-296
APPLICATION NUMBER: WO PCT/JP94/0220
FILING DATE: 26-DEC-1994
FILING DATE: 26-DEC-1994
FILING DATE: 05-SEP-1996
FILING DATE: 05-SEP-1996
FILING DATE: 05-SEP-1994
FILING DATE: 05-SEP-1994
FILING DATE: 05-SEP-1994
FRICK APPLICATION NUMBER: UP 5-348737
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: UP 5-348737
FILING DATE: 17-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29-768
REFERENCE (202) 672-5300
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 2000'-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 6, Application US/09335919
Patent No. 6150130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 164; Conservative
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187 AKVW-----KVEHEEFESSIVCDDGKKİRGSLÄVVDASĞPASDFIEYDKPRAHĞYQIAHĞV 241
                                                                                                                                           158 EWQL-SAPHGLSSPIIMD-----ATVDQQNGYRFVYTLPLSATALLIEDTHYID 205
                                                                                                                                                                          242 IVEVDNHPPPLDKAVLADWRDSHLGNEPYLRVANAKEPTFLYAMPFDRNLVFLEBTSLVS 301
                                                                                                                                                                                                                                      206 KANLOABRARONIRDYAAROGWPLOTLLREEGGALPITLIGDNROFWQQOPQACSGLRAG 265
                                                                                                                                                                                                                                                                     302 RPVLSYMEVRRWVARLRHLGIKVRSVIEBEKCVIPM---GGPLPRIPQNVMAIGG-NSG 357
138 LDHKW--PMTCVHINDNKTKYLGRPYGRVSRKKLKLKLLNS---CVENR-----VKFYK 186
                                                106 QHLWLHTAVSAVHAB---SVQLADGRIIHASTVIDGRGYTP-----DSALRVGFQAFIGQ 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 YDLILVGAGLANGLIALRLOOQ--HPDMRILLIEAGPEA---GGNHTWSFHEEDLTLN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Joseph Hirschberg et al.
APPLICANT: Joseph Hirschberg et al.
TITLE OF INVENTION: POLYNUCLEDTIDES CONTROLLING THE EXPRESSION
TITLE OF INVENTION: OF AND CODING FOR GENE B IN TOWATO AND USE
TITLE OF INVENTION: OF SAWE FOR ALTERING CAROTENOID
TITLE OF INVENTION: BIOSYNTHESIS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS: Ask M. Friedman c/o Anthony Castorina
ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 20001 Jefferson Davis Highway, Suite 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 498;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk COMPUTER: Twinhead, Slimnote 890TX OPERATING SYSTEM: MS DOS version 6.2, OPERATING SYSTEM: Windows version 5.2, OPERATING SYSTEM: Windows version 2.0, CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/09/134,607A FILING DATE: CLASSIFICATION: 800 PRIOR APPLICATION NUMBER: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virginia
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/09134607A; Patent No. 6252141; GENERAL INFORMATION:
APPLICANT: Joseph Hirschberg et al
                                                                                                                                                                                                                                                                                                                                       266 LFHPTTGYSLPLAVALADRLS 286
                                                                                                                                                                                                                                                                                                                                                                   358 IVHPSTGYMVARSMALAPVLA 378
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REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET UNDBER: 32:
TELECOMMUNICATION:
TELEPHONE: 972-3-562553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 972-3-5625554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 1.44 me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Arlington
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
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  240 LPITLIGDNROFWQQQP--QACSGLRAGLFHPTTGYSLPLAVALADRLSALD-VFTSSSV 296
                                                                                                        236 LPIALAHDAAGFWADHAAGPVPVGLRAGFFHPVTGYSLPYAAQVADVVAGLSGPPGTDAL 295
                                                                                                                                                                       297 HQTIAHFAQQRWQQQGFFRMLNRMLFLAGPAESRWRVMQRFYGLPEDLIARFYAGKLTVT 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: JOSEPH HITSCHDERG et al.
TITLE OF INVENTION: POLYNUCLEOOTIDES CONTROLLING THE EXPRESSION
TITLE OF INVENTION: OF AND CODING FOR GENE B IN TOMATO AND USE
TITLE OF INVENTION: OF SAME FOR ALTERING CAROTENOID
TITLE OF INVENTION: BLOSYNTHESIS
CORRESPONDENCE: 25
CORRESPONDENCE: 25
CORRESPONDENCE: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
STREET: 20001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
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MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead, Slimnote 890TX
COMPUTER: Twinhead, Slimnote 890TX
COMPUTER: MS DOS version 6.2,
OPERATING SYSTEM: Windows version 3.11
SOFTWARE: Word for Windows version 2.0,
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/134,607A
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: United States of America
                                                                                                                                                                                                                                                                                                   356 DQLRIVTGKPPIPLGTAIRCL 376
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                                                                                                                                                                                                                                                                       357 DRIRILSGKPPVPVFAALQAI 377
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REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 32E
TELECOMMUNICATION: TELEPHONE: 972-3-562553
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PRIOR APPLICATION DATA:
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S-09-134-607A-18
Sequence 18, Application US/09134607A
Sequence 18, Application US/09134607A
Patent No. 6252141
GENERAL INFORMATION:
APPLICANT: Joseph Hirschberg et al.
TITLE OF INVENTION: POLYNUCLEGOTEDES CONTROLLING THE EXPRESSION
TITLE OF INVENTION: OF SAME FOR ALTERING CAROTENOLD
TITLE OF INVENTION: BIOSYNTHESIS
NUMBER OF SEQUENCES: 25
CORRESPONDANCE ADDRESS:
ADDRESSER: Mark M. Friedman c/o Anthony Castorina
STREET: 20001 Jefferson Davis Highway, Suite 207
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22.1%; Pred. No. 1e-06;
tive 59; Mismatches 128;
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ZIP: 22202
COMPUTER READABLE FORM: WEBJUM TYPE: 1.44 megabyte, 3.5" microdisk COMPUTER: Twinhead, Slimnote 890TX OPERATING SYSTEM: Windows version 6.2, OPERATING SYSTEM: Windows version 3.11 SOFTWARE: Word for Windows version 2.0, CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/09/134,607A FILING DATE: ATTORNEY/AGBYT INFORMATION: NAME: FILENG DATE: ATTORNEY/AGBYT INFORMATION: NAME: FILEGRAM NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 325/12
TELECOMMUNICATION INFORMATION: TELECOMMUNICATION: TELECOMMUNICATION: TELECOMMUNICATION: TELECOMMUNICATION: TELECOMMUNICATION: TELECOMMUNICATION: TELEFONE: 972-3-5625553
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Best Local Similarity
Matches 71; Conserva
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5 YDLILVGAGLANGLIALRLQQQ--HPDMRILLIEAGPEA---GGNHTWSFHEEDLTLN-- 57
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The invention relates to a method for producing carotenoid compounds. The method comprises a transformed metabolising host cell, comprising suitable levels of isopentenyl pyrophosphate and a nucleic acid molecule encoding an enzyme in the carotenoid biosynthetic pathway, under the control of regulatory sequences, and contacting the host cell with carbon substrate to produce a carotenoid compound. The method is useful for producing carotenoid compounds such as antheraxanthin and astexanthin, by using microorganism having a nucleic acid molecule encoding enzymes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing carotenoid compounds e.g. antheraxanthin and astaxanthin, by using microorganisms having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolize single carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carotenoid, isopentenyl pyrophosphate, antheraxanthin, astaxanthin, d:
anti-oxidant; steroid; flavour; fragrance; electro-optic application;
aquaculture; enzyme; lycopene cyclase; CrtY.
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Rouviere PE;
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the carotenoid biosynthetic pathway and which metabolise single carbon substrates. The carotenoids have potent anti-oxidant properties useful in diet, and aquaculture elements. The carotenoids are also useful as intermediates in the synthesis of steroids flavours and fragrances and compounds for potential electro-optic applications. The present sequence is Pantoea stewartii lycopene cyclase (CrtX) enzyme used in the invention
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Pred. No. 8.1e-192;
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04-MAY-2001; 2001US-0288984P
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                                                The invention comprises the amino acid and coding sequence of a number o carotenoid (crt)-related proteins. The crt-related DNA and protein sequences of the invention are useful for engineering cells which are able to produce carotenoids. The present amino acid sequence represents crt-related protein of the invention
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                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pantoea stewartii; carotenoid biosynthetic enzyme; crtE; crtX; crtY; crtI; crtB; crtZ; lycopene cyclase; enzyme; phytoene; carotenoid.
                                                                                                                                                                                                  ö
                                                                                                                                                                        Length 382;
                                                                                                                                                                                                  Indels
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                                                                                                                                                                     Query Match 100.0%; Score 2021; DB 6; Best Local Similarity 100.0%; Pred. No. 8.1e-192; Matches 382; Conservative 0; Mismatches 0;
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-free systems to make particular carotenoids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pantoea stewartii lycopene cyclase SEQ
                          Claim 14; Page 60-61; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILSGKPPVPVFAALQAIMTTHR 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cheng Q,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pantoea stewartii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brzostowicz PC,
                                                                                                                                             Sequence 382 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003016503-A2
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EP393690-A.
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                                                                                                                                                                The present invention describes Pantoea stewartii carotenoid biosynthetic enzymes (I). More specifically described are the geranylgeranyl pyrophosphate synthase (crtE), zeaxanthin glucosyl transferase (crtX), lycopene cyclase (crtE), phytoene desauturase (crtI), phytoene synthase (crtI) and beta-carotene hydroxylase (crtZ) enzymes (see ABP96685 to carotenoid biosynthesis in an organism, by over-expressing (I) in an organism, such that the carotenoid biosynthesis is altered in the organism. (I) and the genes encoding (I) are useful for converting phytoene to the carotenoids, for creating recombinant organism that have the ability to produce various carotenoid compounds, and also for enhancing or manipulating carotenoid compounds, (I) can also be used for producing gene products having enhanced or altered activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 WIAPLVVHHWPDYQVRFPQRRRHVNSGYYCVTSRHFAGILRQQFGQHLWLHTAVSAVHAE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 SVQLADGRIIHASTVIDGRGYTPDSALRVGFQAFIGGEWQLSAPHGLSSPIIMDATVDQQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 AHFAQQRWQQQGFFRMINRWIFIAGPASSRWRVWQRFYGLFBDLIARFYAGKITVTDRLR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptide with enzymatic activity for the conversion of lycopene into beta-carotene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MOPHYDLIIVGAGLANGLIALRIQQQHPDWRILLIEAGPEAGGNHTWSFHEEDLTLNQHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MQPHYDLILVGAGLANGLIALRLQQQHPDMRILLIEAGFEAGGNHTWSFHEEDLTLNQHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WIAPLVVHHWPDYQVRFPQRRRHVNSGYYCVTSRHFAGILRQQFGQHLWLHTAVSAVHAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                     Novel nucleic acid molecule isolated from Pantoea stewartii encoc carotenoid biosynthetic enzyme, useful for regulating carotenoid biosynthesis in an organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 2021; DB 6; Length 382; 100.0%; Pred. No. 8.1e-192; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carotenoid biosynthesis; vitamin A; cancer; food coloring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 ILSGKPPVPVFAALQAIMTTHR 382
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                                                                                                                                     Claim 4; Page 61-62; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR07465 standard; protein; 382 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 382; Conservative
  2003-268323/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                      N-PSDB; ACC44761
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 382 AA;
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61 WIAPLVVHHWPDYQVRFPQRRRHVNSGYYCVTSRHFAGILRQQFGQHLWLHTAVSAVHAE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PITLIGDNRQFWQQQPQACSGLRAGLFHPTTGYSLPLAVALADRLSALDVFTSSSVHQTI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 PITLSGNADAFWQQRPLACSGLRAGLFHFTTGYSLFLAVAVADRLSALDVFTSASIHHAI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 AHFAQQRWQQQGFFRMINRMLFLAGPAESRWRVMQRFYGLPEDLIARFYAGKLTVTDRLR 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MOPHYDLILVGAGLANGLIALRLQQQHPDMRILLIEAGPEAGGNHTWSFHEBDLTLNQHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 NGYRFVYTLPLSATALLIEDTHYIDKANLQAERARQNIRDYAARQGWPLQTLLREEQGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene products are useful for the synthesis of carotenoids, useful as coloring, vitamin A precursor, and possibly in prevention of cancer. also AAQ06293-9. (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HMG-CoA; 3-hydroxy-3-methylglutaryl coenzyme A reductase; crtY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 382;
                                                                                                                                                                                                                                                                                                                               DNA sequences encoding enzymes for carotenoid biosynthesis of carotenoid cpds. e.g. beta-carotene, lycopene, phytoene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.0%; Score 1678; DB 2;
82.2%; Pred. No. 1e-157;
ive 31; Mismatches 37;
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                                                                                                                                                                                                                 Nakamura
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                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Fig 3; 40pp; English.
                                                                                         89JP-00103078.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 82.2
Matches 314; Conservative
                                                                                                                                                                                                            Kobayashi K,

 utilis crtY protein.

                                                                                                                                                                 (KIRI ) KIRIN BEER KK
                                                                                                                                                                                                                                                             WPI; 1990-322212/43.
                                                                                                                                                                                                                                                                                      N-PSDB; AAQ06295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 382 AA;
                                                                                            21-APR-1989;
05-MAR-1990;
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16-JUL-1999
                                              20-APR-1990;
24-OCT-1990
                                                                                                                                                                                                                 Misawa N,
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                                                                                                                                                                                                                               This invention describes a novel method for the preparation of carotenoids using genes and proteins isolated from Candida utilis. The invention specifically describes the isolation of a 3-hydroxy-3 methylglutaryl coenzyme A (HWG-COA) reductase protein. This sequence represents the Candida utilis crty protein which is used in the method of the invention. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVQLADGRIIHASTVIDGRGYTPDSALRVGFQAFIGQEWQLSAPHGLSSPIIMDATVDQQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
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                                                                                                                                                                                                                                                                                                                                                                                                                  WIAPLVVHHWPDYQVRFPQRRRHVNSGYYCVTSRHFAGIIRQQFGQHLWLHTAVSAVHAB 120
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                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                             useful for increase in carotenoid production - and preparation of
                                                                                                                                                                                                                                                                                                                                                                                   1 MQPHYDLILVGAGLANGLIALRLQQQQPDYRILLIDAAAQAGGNFFWSFHHDDLTESQHR
                                                                                                                                                                                                                                                                                                                                                                                                                            NGYRFVYSLPLSPTRLLIBDTHYIDNATLDPECARQNICDYAAQQGWQLQTLLREEQGAL
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                                                                                                                                                                                                                                                                                                                           83.0%; Score 1678; DB 2; Length 382;
82.2%; Pred. No. 1e-157;
tive 31; Mismatches 37; Indels
                                                                                                                                                                                                              Example 2; Fig 15-17; 54pp; Japanese
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                                                                                 97JP-00058012
                                                                                                       97JP-00058012
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                           (KIRI ) KIRIN BREWERY
                                                                                                                                                WPI; 1998-560727/48
                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 314; Conserv
                                                                                                                                                          N-PSDB; AAV73182
                                                                                                                                                                                                                                                                                                           Sequence 382 AA;
                    Pichia jadinii.
                                        JP10248575-A
                                                                                 12-MAR-1997;
                                                                                                       12-MAR-1997;
                                                              22-SEP-1998
carotenoid.
                                                                                                                                                                                         carotenoid
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 SVQLADGRIIHASTVIDGRGYTPDSALRVGFQAFIGQEWQLSAPHGLSSPIIMDATVDQQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THEARERWQQQGFFRMIANRLFLAGPADSRWRVWQRFYGLPBDLIARFYAGKLTLTDRLR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                    gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 WIAPLVVHHWPDYQYRPQRRRHVNSGYYCVTSRHFAGILRQQ>QQHLWLHTAVSAVHAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MOPHYDLILVGAGLANGLIALRLQQQHPDMRILLIBAGPEAGGNHTWSFHBEDL71LNQHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MOPHYDLILVGAGIANGLIALRLQQQQPDWRILLIDAAPQAGGNHTWSPHHDDLTESQHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 PITLTGDRRQFWQQQPQACSGLRAGLFHPTTGYSLPLAVALADRLSALDVPTSSSVHQTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carotenoid biosynthesis, astaxanthin diglucoside, crtE gene; crtB crtI gene; adonixanthin-3'-glucoside; astaxanthin monoglucoside; carotenoid glycoside; crtY gene; crtZ gene; crtX gene; crtM gene; food additive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.0%; Score 1678; DB 2; Length 382;
82.2%; Pred. No. 1e-157;
Live 31; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                           New carotenoid glucoside(s) - used as food additives
Protein encoded by the carotenoid biosynthesis gene
                                                                                                                                                                                                                                                                                     (KIRI ) KIRIN BREWERY KK.
(KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 22-23; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILSGKPPVPVPAALQAIMTTHR 382
                                                                                                                                                                                                                        97JP-00140460
                                                                                                                                                                                                                                                         97JP-00140460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 82.24
Matches 314; Conservative
                                                                                                                                                                                                                                                                                                                                          WPI; 1999-099030/09.
                                                                                                                       Pantoea anamatis
                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAV84083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 382 AA;
                                                                                                                                                       JP10327865-A
                                                                                                                                                                                                                                                         29-MAY-1997;
                                                                                                                                                                                                                        29-MAY-1997;
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(revised)
(first entry)

17-OCT-2003 10-MAR-1999

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AAW01125 standard; protein; 374 AA
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                      AAW01125
          RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes beta-carotin hydroxylase. Beta-carotene can be used in the preparation of xanthophylls and their metabolites. The present sequence represents an Erwinia uredovora crtY protein sequence from the present invention. (Updated on 17-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 WIAPLVVHHWPDYQVRFPTRRRKINSGYFCITSQRFAEVLQRQFGPHLWMDTAVAEVNAE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MQPHYDLILVGAGLANGLIALRLQQQQPDMAIILIDAAPQAGGNHTWSFHHDDLTBSQHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WIAPLVVHHWPDYQVRFPQRRRHVNSGYYCVTSRHPAGILRQOFGQHLWLHTAVSAVHAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVOLADGRIIHASTVIDGRGYTPDSALRVGFQAFIGQEWQLSAPHGLSSPIIMDATVDQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AHFAQQRWQQQGFFRMINRMLF1AGPABSRWRVMQRFYG1PED1JARFYAGKITVTDRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGYRFVYSLPLSPTRLLIEDTHYIDNATLDPECARQNICDYAAQOGWQLQTLLREEQGAL

    useful for preparation of xanthophylls and

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                        Beta-carotene hydroxylase; crtY; crtB; crtI; xanthophyll;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.0%; Score 1678; DB 2; Length 382; 82.2%; Pred. No. 1e-157; ive 31; Mismatches 37; Indels (
                                                                                                Erwinia uredovora crtY protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 15-17; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILSGKPPVPVFAALQAIMTTHR 382
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            AAW99100 standarā; protein; 382
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                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                     Beta-carotin hydroxylase
their metabolites.
                                                                                                                                                                                                                                                                                        (KIRI ) KIRIN BREWERY KK
                                                            (revised)
                                                                                                                                                                                                                                                                                                                  WPI; 1999-208113/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                              Pantoea ananatis.
                                                                                                                                                                                                                                                                                                                               N-PSDB; AAX19120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 382 AA;
                                                                                                                                                                                      JP11046770-A
                                                                                                                                                                                                                                        07-AUG-1997;
                                                                                                                                                                                                                                                                07-AUG-1997;
                                                           17-0CT-2003
14-MAY-1999
                                                                                                                                                                                                              23-FEB-1999
                                                                                                                                       metabolite.
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                                    AAW99100;
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AW99100
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66 VVHHWPDYQVRFPORRRHVNSGYYCVTSRHFAGILRQQFGQHLWLHTAVSAVHAESVQLA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Manipulation of the DNA encoding the present sequence, lycopene cyclase, by in frame linkage to the chloroplast transit peptide (AAW01124) of the tobacco ribulose bis-phosphate carboxylase-oxygenase gene can lead to increased production of total carotemoids in the chloroplast of transformed plants as compared to native, non-transformed plants of the same type. Beta-carotene is an effective and apparently harmless food colourant and is also in the pathway for biological synthesis of further of carotemoids such as zeaxanthin and zeaxanthin diglucoside. Other enzymes involved in the carotemoid biosynthesis pathway include geranylgearnyl pyrophosphate (AAW01119), phytoene synthase (W01121) and phytoene dehydrogenase-4H (AAW01123). (Updated on 25-MAR-2003 to correct pp field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Increasing prodn. of total carotenoid(s) in a higher plant - by transforming with vector encoding chloroplast transit peptide operably linked to the Erwinia herbicola lycopene cyclase structural gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGPP synthase; lycopene cyclase; phytoene synthase; beta-carotene; phytoene dehydrogenase-4H; carotenoid; C40; zeaxanthin; diglucoside; pigment; food colourant; chloroplast transit peptide; increase yield; tobacco ribulose bis-phosphate carboxylase-oxygenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLILVGAGLANGLIALRLQQQHPDMRILLIEAGPEAGGNHTWSFHEEDLTLNQHRWIAPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yarger J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.4%; Pred. welve 53, Mismatches
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90US-00525551.
90US-00562674.
91US-00662921.
91US-00785566.
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                                                    (revised)
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(first entry)
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Matches 213; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-308823/31.
                                                                                                                                                                                                                                                                                                                                                                           Pantoea agglomerans
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Best Local Similarity
                                                                                                                                                                         Lycopene cyclase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (STAD ) AMOCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-0CT-1991;
                                                    16-OCT-2003
25-MAR-2003
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AAW01125;
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AAR13987 standard; protein; 374 AA.
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90US-00525551.
90US-00562674.
91US-00662921.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           - variant
                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                         Query Match
Best Local Similarity 58.4<sup>†</sup>
Matches 213; Conservative
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PPVPL 367
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                                                                        Sequence 374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (STAD ) AMOCO
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18-MAY-1990;
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25-MAR-2003
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28-FEB-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A novel DNA molecule has been isolated which encodes an Brwinia herbicola lycopene cyclase enzyme that converts lycopene to beta- carotene. The DNA
                                                                                                                                                                                                                                                                                       Geranylgeranyl pyrophosphate synthase; Erwinia herbicola; GGPP;
lycopene cyclase; recombinant enzyme; transgenic organism; beta-carotene;
yeast; plant; vitamin A; cancer.
                                                 246 GDNRQFWQQQPQACSGLRAGLFHPTTGYSLPLAVALADRLSALDVFTSSSVHQTIAHFAQ 305
                                                                                    DGRIIHASTVIDGRGYTPDSALRVGFQAFIGQBWQLSAPHGLSSPIIMDATVDQQNGYRF 185
                  VYTLPLSATALLIEDTHYIDKANLQAERARQNIRDYAARQGWPLQTLLREEQGALPITLT 245
                                                                                                           QRWQQQGFFRMLNRMLFLAGPAESRWRVMQRFYGLPEDLIARFYAGKUTVTDRLRILSGK 365
                                                                                                                    /note= "Encoded by GTG in wild-type, but by ATG in the genetically engineered form"
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                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 17; Fig 19; 102pp; English.
                                                                                                                                                                                                       AAW32474 standard; protein; 374 AA.
                                                                                                                                                                                                                                                                        Erwinia herbicola lycopene cyclase
                                                                                                                                                                                                                                                                                                                                                                                                                                   90US-00487613.
90US-00525551.
90US-00562674.
91US-00662921.
93US-00095726.
                                                                                                                                                                                                                                                                                                                                                                                                                      95US-00473512
                                                                                                                                                                                                                                        (revised)
(revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proffitt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-414592/38.
N-PSDB; AAT91547.
                                                                                                                                                                                                                                                                                                                            Pantoea agglomerans
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                                                                                                                                              PPVPV 370
                                                                                                                                                             PPVPL 367
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03-AUG-1990;
28-FEB-1991;
21-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mukharji I,
Brinkhaus FL;
                                                                                                                                                                                                                                        17-OCT-2003
25-MAR-2003
15-JAN-1998
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Active-sîte
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                                                                                                                                                                                                                         AAW32474;
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molecule comprises at least 1125 bp and is present in the plasmids pARC147, pARC1509, pARC1510 and pARC1520. The present sequence represents lycopene cyclase. The new DNA molecule can be used to produce the recombinant enzyme and transgenic organisms, e.g. yeasts or plants, with increased beta-carotene levels. Beta-carotene is used as a colourant in margarine and butter and as an intermediate for vitamin A, and may prevent cancer. (Updated on 22-MAR-2003 to correct PP field.) (Updated on 17-0CT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 VYTLPLSADTLLIBDÍRYANVPORDDNALRÓTVTDYAHSKGWQLAQLEREFTGCLPITWR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 GDNRQFWQQQPQACSGLRAGLFHPTTGYSLPLAVALADRLSALDVFTSSSVHQTIAHFAQ 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VYTLPLSATALLIBDTHYIDKANLQAERARQNIRDYAARQGWPLQTLLREEQGALPITLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 VISRLCGPMRRRAASGARAGLFHPTTGYSLPLAVALADALADSPRLGSVPLYQLTRQFAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QRWQQQGPFRMLINRMLFLAGPABSRWRVMQRFYGLPEDLIARFYAGKLTVTDRLRILSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLILVGGGLANGLIAWRLRQRYPQLNLLLIERGEQPGGNHTWSFHEDDLTPGQHAWLAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVHHWPDYQVRFPQRRRHVNSGYYCVTSRHFAGILRQQFGQHLWLHTAVSAVHABSVQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 DGRIIHASTVIDGRGYTPDSALRVGFQAFIGQEWQLSAPHGLSSPIIMDATVDQQNGYRF
                                                                                                                                                                                                                                                                                                                                                                                                             6 DLILVGAGLANGLIALRLQQQHPDMRILLIEAGPEAGGNHTWSFHEEDLTLNQHRWIAPL
                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                            Length 374;
                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                         55.8%; Score 1127; DB 2;
58.4%; Pred. No. 5.6e-103;
ive 53; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGPP; carotenoid; phytoene; zeaxanthin; lycopene
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1 17:23:13

Mon Mar

genetic analysis;

Danchin A;

Kunst F,

Frangeul L,

Glaser P,

Tacurit S,

Duchand B, Buchrieser MPI; 2003-148459/14.

(INSP) INST PASTEUR. (CNRS) CNRS CENT NAT RECH SCI

07-FEB-2002; 2002WO-IB003040. 17-PEB-2001; 2001FR-00001659.

detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;

Photorhabdus luminescens.

W0200294867-A2.

whooping cough.

Antibacterial; fungicide; insecticide; polymorphism; Photorhabdus luminescens protein sequence #3219.

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There are a total of six relevant genes in a 7900 bp region that cause E. coli cells to produce GGPP and the carotemoids phytoene through zeaxanthin diglucoside, which is the final prod. identified in the carotemoid pathway contd. in plasmid pakc176 (contg. a ca. 13 kb chromosomal DNA fragment isolated by Perry et al., J. Bacteriol., 168:607 (1986). The genes for geranylgeranyl pyrophosphate (GGPP) synthase, phytoene synthase, phytoene debydrogenase-44! Jycopene cyclase, beta-caroteme hydroxylase, and caexanthin glycosylase are represented in AAQ13716, AAQ13718, AAQ13729, AAQ13724 and AAQ13726 crespectively. The native sequence (AAQ13722 and AAQ13724 and AAQ13726 the genetically engineered for use in expression in yeast. At the 5' end of the gene, the native initiation GTG codon has been changed to an ATG codon. The second anno acid residue, Arg, was originally encoded by an AGG codon that was changed to a CGG codon, while retaining its coding for the Arg amino acid residue. Recombinant expression plasmids can be used to produce large amis. Of the enzymes and hence large amis. of the carotemoids which they synthesise. (Updated on 25-MAR-2003 to correct PP field.) (Updated on 23-MAR-2003 to correct PP field.) (Updated on 24-OCT-
                                                                                                                                                                                                                                                                                                                    Biosynthesis of carotenoid(s) in genetically engineered hosts - using DNA encoding enzymes from Brwinia herbicola.
     Mukharji I, Proffitt JH, Yarger JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 19(1-3); 313pp; English.
Ausich RL, Brinkhaus FL,
Yen HC;
                                                                                                                                                                        WPI; 1991-281410/38
                                                                                                                                                                                                                          N-PSDB; AAQ13723
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Sequence 374 AA;

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                                                                                                                                                                                                                                                                                                                                                                                             66 VVHHWPDYQVRFPQRRRHVNSGYYCVTSRHFAGILRQOFGQHLWIATTAVSAVHAESVQLA 125
                                                                                                                                           126 DGRIIHASTVIDGRGYTPDSALRVGFQAFIGQEWQLSAPHGLSSPIIMDATVDQQNGYR? 185
                                                                                                                                                                                                      186 VYTLPLSATALLIEDTHYIDKANLQAERARQNIRDYAAROGWPLOTILLREEQGALPITLT 245
                                                                                                                                                                                                                                                                       246 GDNRQFWQQQPQACSGLRAGLFHPTTGYSLPLAVALADRLSALDVFTSSSVHQTIAHPAQ 305
                                                                                                                                                                                                                                                                                                                                  306 QRWQQQGFFRMINRMLFLAGPAESRWRVMQRFYGLPEDLIARFYAGKLTVTDRLRILSGK 365
                                                                                   6 DLILVGAGLANGLIALRLQQQHPDMRILLIEAGPEAGGNHTWSFHEBDLTLNQHRWIAPL 65
                               0; Gaps
55.7%; Score 1126; DB 2; Length 374; S8.4%; Pred. No. 7e-103; Live 53; Mismatches 99; Indels (
                                  Matches 213; Conservative
 Query Match
Best Local Similarity
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ABM70122 standard; protein; 392 AA.

ABM70122

20-NOV-2003 ABM70122;

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The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detection, the genome of P. Luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypepiides encoded by the genes are used for detection/identification of P. Luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. croombinant production of the proteins, particularly toxins and carticularly toxins and sensitive to P. luminescens enalthe proteins or antibiotics) and as the sensitive to P. luminescens and the proteins are as virulence factors and for identifying targets of human diseases for which P. C. luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 WIAPLITYRASGYDVIFPAPQRTLPHSYFSITSQHFASILHAYLGBRIQTRLLVQBLTPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGYRFVYTLPLSATALLIEDTHYIDKANLQAERARQNIRDYAARQGWPLGTLREEGGAL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 WIAPLVVHHWPDYQVRPPQRRRHVNSGYYCVTSRHFAGILRQQFGQHLWLHTAVSAVHAE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 SVOLADGRIIHASTVIDGRGYTPDSALRVGFQAFIGQEWQLSAPHGLSSPIIMDATVDQQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MQPHYDLILVGAGLANGLIALRLQQQHPDMRILLIBAGPEAGGNHTWSPHBEDLTLNQHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MMYDWDLILVGGGLANGLIAMRFQQCKPHLRVLLIENTETIGGNHTWSFHQHDLTEAEHB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6; Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.5%; Score 1040.5; DB 6; Length
52.5%; Pred. No. 2.4e-94;
tive 51; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; SEQ ID NO 3219; 1205pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similaries
nes 201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 392 AA;
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The invention describes the preparation of carotenoid pigments e.g. canthaxanthins using a cell transformed by a vector having DNA sequences (a) to or substantially homologous sequences (a) a DNA sequence (crEB) coding GSPP synthase of Flavobacterium sp. R1534; (b) a DNA sequence (crEB) coding prephytoene synthase of Flavobacterium sp. R1534; (c) a DNA sequence (crII) coding phytoene describes of Flavobacterium sp. R1534; (d) a DNA sequence (crIY) coding lycopene cyclase of Flavobacterium sp. R1534, and (e) a DNA sequence (crIY) coding lycopene cyclase of Flavobacterium sp. R1534, and (e) a DNA sequence (crIX) coding lycopene cyclase of Earoteners beca-oxygense of a microbe E-196 (FERM BP-4283). The carotenoid or a caroteme of a miscobe used in preparation of food products. The method is an improved method of fermentation for carotenoid
                                                                                                                                                                                                         242 ITLICONROFWQQQQQQC--SGLRAGLFHPTTGYSLPLAVALADRLSALDVFTSSSVHQT 299
                                                                                                                                                                                                                                                                                        IAHPAQQRWQQQGFFRMLNRMLFLAGPAESRWRVMQRFYGLPEDLIARFYAGKLTVTDRL 359
60 LSPIRRGEWIDQEVAFPDHSRRLTIGYGSIEAGALIGLLQ---GVDLRWNTHVATLDDTG 116
                                                                          Preparation of carotenoid - comprises fermentation with transformed cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carotenoid; pigment; canthaxanthin; R1534; crtB; prephytoene synthase; crtI; phytoene desaturase; crtY; lycopene cyclase; GGPP synthase; crtB; crtW2396; beta-carotene beta-oxygenase; food product; fermentation.
                                                                                                                                                                                                                                 VQLADGRIIHASTVIDGRGYTPDSALRVGFQAFIGQEWQLSAPHGLSSPIIMDATVDQQN
                                                                                                                          GYRFVYTLPLSATALLIEDTHYIDKANLQABRARQNIRDYAARQGWPLQTLLRBEQGALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Flavobacterium sp. R1534 crtY gene product lycopene cyclase.
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No. 7.9e-69;
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Pred. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW69533 standard; protein; 382
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||XIVTGRPPIPLSQAVRCL 372
                                                                                                                                                                                                                                                                                                                                                                              RILSGKPPVPVFAALQAI 377
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV40146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- PLVVHHWPDYQVRPPQRRRHVNSGYYCVTSRHFAGILRQQFGQHLWLHTAVSAVHABS 121
                                                                                                                                                           TGYRFIYVLPFSSTRLLIEDTHYVDRGPPDKALSQATIABYAKKHGWKLGKLIREESGCL 240
                                                                                       241 PITLIGDETSFWAQLAGQPTCGLRAALFHPTTGYSLPHAIRLADRIVALPECFDTSLFIT 300
                                                                                                                                   IAHPAQQRWQQQGFFRMLNRMLFLAGPAESRWRVMQRFYGLPEDLIARFYAGKLTVTDRL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flavobacterium gene sequences encoding carotenoid biosynthesis enzymes for the production of carotenoid(s), useful in foods and animal feeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 HDLLIAGAGLSGALIALAVRDRRPDARIVMLDARSGPSDQHTWSCHDTDLS---PEWLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 YDLILVGAGLANGLIALRLQQQHPDMRILLIEAGPEAGGNHTWSFHEEDLTLNQHRWIA-
                                                      PITLIGDNRQFWQQ-QPQACSGLRAGLFHPTTCYSLPLAVALADRLSALDVFTSSSVHQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     echinenone; canthaxanthin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adonixanthin; astaxanthin; crtY; lycopene synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.8%; Score 783.5; DB 2; Length 382; 43.7%; Pred. No. 7.9e-69; Live 64; Mismatches 136; Indels 13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Flavobacterium sp. ATCC 21588; WT (ATCC 21588)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         beta-carotene;
                                                                                                                                                                                                                       RIESGKPPVPVFAALOAIMTTHR 382
                                                                                                                                                                                                                                               ||| |||||||
RILIGKPPVPIKGALKAMFKQHK 383
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                                                                                                                                                                                                                                                                                                                                                                   AAW06517 standard; protein; 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Flavobacterium lycopene cyclase.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lycopene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-023160/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT45143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 382 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carotenoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-DEC-1996
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08-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             zeaxanthin;
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Query Match

Best Local

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WPI; 1999-099030/09.
N-PSDB; AAV87884.
                                                                                                                                                                                                   Similarity
                                                                                                                        Sequence 386 AA;
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                                                                                                                                                                             Query Match
                                                                                                                                                                                                        Local
                                                                                                                                                                                                        Best Loca
Matches
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AAW87884
8888888
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                                                                                                                                                                                                                                                                                                                                                                                                           235
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                                                                                                                                                                                                                                                       122 VQLADGRIIHASTVIDGRGYTPDSALRVGFQAFIGQEWQLSAPHGLSSPIIMDATVDQQN 181
                                                                                                                                                                                                                                                                                  GYRFVYTLPLSATALLIEDTHYIDKANLQAERARQNIRDYAARQGWPLQTLLREEQGALP 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --PLVVHHWPDYQVRFPQRRRHVNSGYYCVTSRHFAGILRQQFGQHLWLHTAVSAVHAES 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 IALAHDAIGFWRDHAQGAVPVGLGAGIFHPVTGYSLPYAAQVADAIAARDL-TTASARRA 294
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                                                 YDLILVGAGLANGLIALRLQQQHPDMRILLIEAGPEAGGNHTWSFHEEDLTLNQHRWIA- 63
                                                                                  ITLIGDNRQFWQQQPQAC--SGLRAGLFHPTTGYSLPLAVALADRLSALDVFTSSSVHQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide.
  Gaps
  13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xanthophyli; astaxanthine; methylene; keto group; conversion; 3-hydroxy-beta-ionone ring.
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64; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ą.
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(MARI-) MARINE BIOTECHNOLOGY INST CO LTD.
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RIVTGRPPIPESQAVRCL 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR79062 standard; peptide; 386
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94JP-00235917.
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(first entry)
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  165; Conservative
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N-PSDB; AAQ99489.
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28-FEB-1996
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Matches
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                                                                                                                                                                                                                                                                                              DNA sequences may be used in the production of astaxanthine and other keto gp. contg. xanthophylls, the sequences may also be used to transicertain yeasts and other microorganisms. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                    5 YDLILVGAGLANGLIALRLQQQHPDWRILLIB--AGPEAGGNHTWSFHEEDLTLNQHRWI
                                                                                                                                                                                                                                                                                                                                                             A---PLVVHHWPDYQVRFPQRRRHVNSGYYCVTSRHFAGILRQQFGQHLWLHTAVSAVHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPITLIGDNRQFWQQQP--QACSGLRAGLFHPTIGYSLPLAVALADRLSALD-VFTSSSV
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carotenoid biosynthesis; astaxanthin diglucoside; crtE gene; crtE crtI gene; adonixanthin-3'-glucoside; astaxanthin monoglucoside; carotenoid glycoside; crtY gene; crtZ gene; crtX gene; crtW gene;
                                                                                                                                                                                                                      15;
                                                                                                                                                                           Length 386;
                                                                                                                                                                                                                        137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein encoded by the carotenoid biosynthesis gene crtY
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                                                                                                                                                                               DB 2;
                                                                                                                                                                           37.6%; Score 759.5; DB
43.0%; Pred. No. 2e-66;
tive 65; Mismatches 1
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(KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO
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|DQLRIVTGKPPIPLGTAIRCL 376
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                                                                                                                                                                                                                        164; Conservative
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Sequence 386 AA;

Query Match 37.6%; Score 759.5; DB 2; Length 386;
Best Local Similarity 43.0%; Pred. No. 2e-66;
Matches 164; Conservative 65; Mismatches 137; Indels 15; Gaps 8;
Matches 5 YollivGAGLARGLAACHOMMRILLE--AGPEAGGNHTWSPHEEDLTLANGHRM 62

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Search completed: February 29, 2004, 14:44:00 Job time : 48.265 secs

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Q47843 pantoea agg
Q8vuj 7 pantoea agg
P72650 synechocyst
Q8a1v2 streptomyce
Q825u1 streptomyce
Q8x61 streptomyce
Q8x61 streptomyce
Q8x61 streptomyce
Q8x61 streptomyce
Q8x61 streptomyce
Q81x94 bacillus an
Q8dsh9 streptomyce
Q8dsh3 streptomyce
Q8dsh3 streptomyce
Q8dsh3 streptomyce
Q6341 streptomyce
Q6841 streptomyce
Q6841 streptomyce
                                                            February 29, 2004, 14:33:49; Search time 35.4397 Seconds (without alignments) 3837.172 Million cell updates/sec
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1 MSHFAVIAPPFSHVRALQN.......EQAMRTCQPVLSGQDYATAL 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                        1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                        otal number of hits satisfying chosen parameters:
                                                                                                                                                                                  1017041 segs, 315518202 residues
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                                                                                                                                                                                                                                                            ost-processing: Minimum Match 0%
    Maximum Match 100%
    Listing first 45 summaries
                                       - protein search, using sw model
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1: sp_archeai.*

2: sp_bacteria.*

3: sp_lungi.*

5: sp_lunman.*

6: sp_mammal.*

7: sp_mic.*

7: sp_phage.*

8: p_lorganelle.*

8: p_lorganelle.*

1: sp_lorganelle.*

1: sp_lorganelle.*

2: sp_virus.*

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Q9S25U1
Q9XC67
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Q8vif8 cavia porce	QBVIF8	Ξ	529	7.3	163	45
_	049841	16	392	7.4	164	44
	Q91W57	11	541	7.4	164.5	43
Q93mw2 nocardia br	Q93MW2	Ŋ	406	7.4	164.5	42
	Q9RPA1	~	388	7.4	164.5	41
070023 streptomyce	070023	Ŋ	422	7.5	167	40
Q81cw9 bacillus ce	081CW9	9	333		169.5	39
Q8knc3 micromonosp	Q8KNC3	N	401		170.5	38
ų,	Q9F2F9	N	382		171	37
N	033282	19	420	7.7	172	36
Q7ty01 mycobacteri	Q7TY01	9	388	٠	172	35
Q9r110 cavia porce	Q9R110	11	530	•	172.5	34
Q8pjg6 xanthomonas	Q8PJG6	16	418	7.8	175	33
Q97fm0 clostridium	Q97FM0	16	407	•	175	32
	098595	0	414	7.9	175.5	31
v	016243	S	594		177	30
Q9sbll sorghum bic	Q9SBL1	10	492	8.0	178.5	29
Φ	Q8KUHS	7	402		178.5	28
	Q9VCL3	ß	540	e-1 60	181.5	27
	Q8KHE4	N	421	٠,	187.5	26
m	031853	16	287	٠,	195.5	25
	Q89RS0	16	450	8.8	197	24
	09ADH3	16	418	8.9	197.5	23
Q9ryi3 deinococcus	Q9RYI3	76	418		σ'n	22
H	Q8KNE0	۲3	397		201	21
σ	034539	16	392	9.1	204	20
	097TQ3	16	406	•	207	19
Q81cg5 bacillus ce	081065	19	397		207	18
Q98el9 rhizobium 1	098819	16	427	Q,	210.5	17

ALIGNMENTS

DDT. 431 AN	Created)	Last	15, Last annotation update)	terase.		Gammaproteobacteria; Enterobacteriales;	жа.			•	R., Schroeder W.A.;	(WO 02/079395 A2).";		rase activity, transferring hexosyl; IEA.		ism; IEA.	1 M61.	gluco_trans.		. MW; A9BC082567039732 CRC64;	0%; Score 2231; DB 2; Length 431;	ö	1 MSHFAVIAPPFFSHVRALQNIAQELVARGHRVTFFQQHDCKALVTGSDIGFQTVGLQTHP 60	MSHFAVIAPPFPSHVRALQNLAQBLVARGHRVTFFQQHDCKALVTGSDIGFQTVGLQTHP 60	PGSLSHLLHLAAHPLGPSMLRLINEMARTSDMLCRELPAAFHALQIEGVIVDOMEPAGAV 120
SULT 1 3CSS CORPES DESTINITIND DET.	; -2003 (TTEMBLTE) 23	(TrEMBLrel. 23, Last		Zeaxanthin glucosyl transferase. CRTX.	Pantoea stewartii.		Enterobacteriaceae; Pantoea.	[1]	SEQUENCE FROM N.A.	STRAIN=ATCC 8200;	deSouza M.L., Kollmann S.R., Schroeder W.A.;	"Carotenoid Biosynthesis (WO 02/079	EMBL: AY166713: AAN85597.1;	GO; GO: 0016758; F:transferase activity,	GO:0016740;	GO; GO:0008152; P:metabolism; IEA.		<pre>InterPro; IPR002213; UDP_gluco_trans. Pfam; PF00201; UDPGT; 1.</pre>	TIGREAMS; TIGR01426; MGT; 1.	Transferase. SBQUENCE 431 AA; 46611 MW; A9BC	100.08;	Jest Local Similarity 100.0%; Fred. Matches 431; Conservative 0; Mis	1 MSHFAVIAPPFSHVRALQNLAQELV	1 MSHFAVIAPPFFSHVRALQNIAQBIV	61 PGSLSHLLHLAAHPLGPSMLRLINEW

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Query Match
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W NEDLINE=94236237; PubMed=8180698;

W MEDLINE=94236237; PubMed=8180698;

A TO K.Y., Lai E.M., Lee L.Y., Lin T.P., Hung C.H., Chen C.L.,

A TO K.Y., Lai E.M., Lee L.Y., Lin T.P., Hung C.H., Chen C.L.,

A To K.Y., Lai E.M., Lee L.Y., Lin T.P., Hung C.H., Chen C.L.,

R Tanalysis of the gene cluster encoding carotenoid biosynthesis in

R To Revisia bershocla Bhol3.*;

Microbiclosy 140:331-339[1994].

B Microbiclosy 140:331-339[1994].

B Microbiclosy 155268; Paransferase activity, transferring hexosyl . .; IEA.

BR GO; GO:0016758; F:transferase activity, transferring hexosyl . .; IEA.

BR GO; GO:0016758; P:transferase activity, transferring hexosyl . .; IEA.

BR GO; GO:0016758; P:transferase activity, transferring hexosyl . .; IEA.

BR GO; GO:0016759; UDPGT; 1.

BR FROSITE; PS00375; UDPGT; 1.
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181 IAHHACRMGLAPREKLHHCFSPLAQISQLIPELDFPRKALPDCFHAVGPLRQPQGTPGSS 240
                                                                                                                 181 IAHHACRMGLAPREXLHACFSPLAQISQLIPELDFPRKALPDCFHAVGPLRQPGTPGSS 240
                                                                                                                                                      241 TSYFPSFDKFRIFASLGTLQGHRYGLFRTIAKACEEVDAQLLLAHCGGLSATQAGELARG 300
                                                                                                                                                                     241 TSYPSPSPXPRIFASLGTLQGHRYGLFRTIAKACEBVDAQLLLAHCGGLSATQAGBLARG 300
                                                                                                                                                                                                           301 GDIQVVDFADQSAALSQAQLTITHGGMNTVLDAIASRTPLLALPLAFDQPGVASRIVYHG 360
                                                                                                                                                                                                                                301 GDIQVVDFADQSAALSQAQLTITHGGMYTVLDAIASRTPLLALPLALPLAFDQPGVASRIVYHG 360
                                                                                                                                                                                                                                                                                   361 IGKRASRFTISHALARQIRSLITWIDYPQRWTKIQAALRLAGGTPAAADIVEQAMRTCQP 420
                                          121 VAEASGLPFVSVACALPLAREPGLPLAVMPFBYGTSDAARBRYTTSEKIYDWLMRRHDRV 180
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Enterobacteriaceae, Pantoea.
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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301 RHIQVVDFADQSAALSQAQLAITHGGANITVLDAINYRTPLLALPLAFDQPGVASRIVSHG 360
                                        241 TSYFPSPDKPRIFASLGTLQGHRYGLFRTIAKACEEVDAQLLLAHCGGLSATQAGELARG 300
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70.8%; Score 1579.5; DB 2; Length 431;
Best Local Similarity 70.9%; Pred. No. 3e-110;
Matches 304; Conservative 53; Mismatches 71; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pantoea agglomerans pv. milletiae Wist 801.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
ENBL, AB076662; BAB79501.1;
GO; GO:0016758; F:transferase activity, transferring hexosyl
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR002213; UDP_gluco_trans.
Pfam; PF00201; UDPgT; 1.
SEQUENCE 431 AA; 47439 MW; F7B124F2632A8EF7 CRC64;
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                301 ASHVQVVDFADQAAALAQADLVITHGGANTVLDGINHLTPLLITIPLAFDQPGVAARVVWH 360
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EMBL, D90899; BAA16652.1; ...
PIR, S74500; S74500.

GO, GO:0016739; F:transferase activity, transferring hexosyl . . .; IBA. (G): GO:0008152; P:metabolism; IBA.
                                                                                                                                                                                                                                                                                                                                                                                                                        Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.;
300 GGDIQVVDFADQSAALSQAQLTITHGGWNTVLDAIASRTPLLALPLAFDQPGVASRIVYH
                                                           GIGKRASRFITSHALARQIRSLLIMIDYPQRMTKIQAALRLAGGIPAAADIVEQAMRICQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
25.0%; Score 558.5; DB 16; Length 419;
Best Local Similarity 31.7%; Pred. No. 1.1e-33;
Matches 132; Conservative 81; Mismatches 196; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAE7DFFDE2592CB3 CRC64;
                                                                                                                                                                                                                                                                                                                                              Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                            01-FEB-1997 (TrEMBLrel. 02, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR006326; UDPGT_MGT.
InterPro; IPR002213; UDP_gluco_trans.
                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                        Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=97061201; PubMed=8905231;
                                                                                                                                                                                                                                                                                                       Zeaxanthin glucosyl transferase.
CRIX OR SLR1125.
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45330 MW; 1
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                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                      PVLSGQDYA 428
                                                                                                                                                    PVLTRRHYA 429
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18;
300 GGDIQVVDFADQSAALSQAQLTITHGGMNTVLDALASRTPLLALPLAFDQPGVASRIVYH 359
                           Redembach M., Kieser H.M., Denapaite D., Bichner A., Cullum J., Kinashi H., Hopwood D.A.;
*A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicalor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                       412
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                                                                                                                                       360 GIGK--RASRFTTSHALARQIRSLLTNTDYPQRMTKIQAALRLAGGTPAADIVEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STTAIN=A3(2);
Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A. Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saunders D.C., Harris D.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 407 AA; 43498 MW; A61E94CF6088B4A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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11.7%; Score 262; DB 16;
Best Local Similarity 26.8%; Pred. No. 1.8e-11;
Matches 123; Conservative 59; Mismatches 165;
                                                                                                                                                                                                                                                                                         407
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STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Putative glycosyl transferase
SCO0040 OR SCJ4 21
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                                                                                                                                                                                                                                                                                            PRELIMINARY;
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371 AAGGSESAADRLE 383
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AVEBI OR SAV945.
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                                                                                                                                                                 54 YPGGD-----QPLPDPPAPITLMEALARTSLDL---LPAVLADLRDDRPDLIVHDS 101
                                                                                                                                                                                                                                              114 MEPAGAVVAEASGLPFVSVACALPLNREPGLPLAVMPFEYGTSDAARERYTTSEKIYDWL 173
                                                                                                                                                                                                                                                                                                        102 ACFWGALAARVLGLPAVSSFTTFAYNRHVPSF-----TRASRE------139
                                                                                                                                                                                                                                                                                                                                                                       174 MRRHDRVIAHHACRMSLAPRBKLHHCFSPLAQISQL----IPBLDFPRKALPDCFHAVGP 229
                                                                                                                                                                                                                                                                                                                                                                                                                             140 -----LLAGAAAR----PRNLAGYVGARLALRRRFAATGVPLVD-----LAD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 IRQPENLVYTSRAFQPAVEEFDRSYRFVGPSIGARPDDPSFPVNRLRDPVLYASLGTVFN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 HRYGLFRTIAKACEEVDAQLLLAHCGGLSATQAGELARGGDIQVVDFADQSAALSQAQLT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 ADPLILERTFATALSPL-AGTVVVSTGQTDPAALGBLP--GNVLARRSVPQLEVLDRAALF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITHGGMNTVLDAIASRTPLLALPLAFDQPGVASRIVYHGIGK--RASRFT--TSHALARQ 377
MSHFAVIAPPFFSHVRALQNLAQELVARGHRVTF--FQQHDCXALVTGSDIGFQTVGLQT 58
                                                     1 MSTLAFLNIGMHGHINPTLPVAAELVRRGHTVTYHTFPAFREEIAATGANV-----RL 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=MA-4680 / ALCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948;
Gmura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitiils: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces avermitilis.

Bacteria, Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycineae; Streptomycineae; NCB1_TaxID=33903;
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MEDLINE=22608306; PubMed=12692562;
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SEGUENCE 397 AA: 40868 MW: 77065B1CC04D6FE7 CRC64;
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01-07N-2003 (TrEMBirel. 24, Last sequence update)
01-0CT-2003 (TrEMBirel. 25, Last annotation update)
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Nat. Biotechnol. 21:226-331(2003).
EMBL; APO05505 BAC75069.1; -.
GO: GO:0016740; F:transferase activity; IEA.
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TIGRPAMS; TIGR01426; MGT; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 AVVAEASGLPFVSVACALPLNREPGLPLAVMPFEYGTSDAARERYTTSBKIYDWLMRRHD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 RVIAHHACRM----GLA-PREKLHHCFSPLAQISQLIPELDFPRKALPDCFHAVGP--LR 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 GLIGELRRRITGGAGAADPR-----FSPHGVLAYTTRALIGEVE-LPDRVMLVGPSVAA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 QPQGTPGSSTSYFPSPDKPRIFASLGTLQGHRYGLFRTIAKACEEVDAQLLLAHCGGLS- 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291 ATQAGELARGGDIQ-----VVDFADQSAALSQAQLTITHGGWWTVLDAIASRTPLLA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 RVRAVLVDPGGVVEHPVPDTVLVRRYVPQLALLERLDAVVCHAGHNTVCEALWHGVPLVV 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 LPLAFDQPGVASRIVYHGIGKRASRFTTSHA--LARQIRSLLTNTDYPQRMTK-IQAALR 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 RPAGPDDFPWEWLEASALPTVLVSLGTANNDAGARFLNAA-----AEAL----GGIAD 251
                                                                                                                                                                                                                                                                                               1 MGRFLFVVPPLVGHVNPAVGTAAALAARGHDIAWAGHPELVRGLAGADAVVFPCAL---P 57
                                                                                                                                                                                                        1 MSHPAVIAPPPFSHVRALQNLAQELVARGHRVTFFQQHDCKALVTGSDIGFQTVGLQTHP
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STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MRDLINE-22608306; PubMed=12692562;
Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
                                                                                                       71; Gaps
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Query Match 11.3%; Score 251.5; DB 16; Length 397; Best Local Similarity 26.6%; Pred. No. 1.1e-10; Matches 115; Conservative 61; Mismatches 186; Indels 71;
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SEQUENCE FROM N.A.
STRAIN=WA-4680 / ATC. 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE-147403; PubMed=11572948;
Omura S. Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
Rénome sequence of an industrial microorganism Streptomyces avermitlis: deducing the ability of producing secondary
metabolites.";
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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MEDLINE=99380548; PubMed=10449723;
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50 ---GFQTVGLQTHPPGSLSHLLHLAAHPLGPSMLRLINEMA--RTSDMLCRELPAAFHAL 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 TSEKIYDWIAMRRHDRVIAHHACRMGLAPREKLHHCPS---PLAQISQLIPEL----- 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence and comparative analysis of the industrial microcognatus Streptowayoes avermitilis.";

Nat. Biotechnol. 21:226-531(2003).

EMBL; AB0032523; BAA84592.1;

EMBL; AB003252; BAC68655.1;

GO; GO:0016740; Fitransferase activity, transferring hexosyl . . .; IEA.

GO; GO:0016740; Fitransferase activity; IEA.

GO; GO:005959; Fitransferase activity; IEA.

GO; GO:005959; P:1ipid glycosylation; IEA.

InterPro; IPR004276; Glycosylation; IEA.

InterPro; IPR004276; Glycosylation; IEA.

InterPro; IPR004276; Glycosylation; IEA.

InterPro; IPR004276; Glycosylation; IEA.

InterPro; IPR004276; Glycosylation; IEA.

Fram; PF03033; Glyco transferase.

Pfam; PF03033; Glyco transferase.

Rem: PF03033; Glyco transferase.

Rem: PF03033; Glycosylation; IEA.

Rem: PF03033; Glycosylation; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transferase; Complete proteome.
SEQUENCE 412 AA; 45379 MW; FECD619FD6F88A54 CRC64;
Sakaki Y., Hattori M., Omura S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS; TIGRO1426; MGT; 1.
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Best Local Similarity
Matches 102; Conserv
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STRAIN=7434AN4;
Mochizuki S., Hiratsu K., Suwa M., Ishii T., Sugino F., Yamada K.,
                                                                                                                                                                                   Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative glycosyltransferase.
                                                                                                                                                                                                    Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                 Streptomyces rochei (Streptomyces parvullus).
                                                    389 AA
                                                  PRT;
                                                PRELIMINARY;
                                                                                                                                                                                                                    NCBI_TaxID=1928;
                                                                                                                                                                lasmid pSLA2-L
                                                  QB3X61
                                                                    283X61,
                   RESULT 8
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63 SLSHLIHLAAHPLGPSMLRLINEMARTSDMLCR--ELPAAFHALQIEGVIVDQMEPAGAV 120
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Kinashi H., Fulii S., Hatani A., Kurokawa T., Shinkawa H.;
Kinashi H., Fulii S., Hatani A., Kurokawa T., Shinkawa H.;
Physical mapping of the linear plasmid pSLA2-L and localization of
the eryAl and actI homologus.";
Biosci. Biotechnol. Biochem. 62:1892-1897(1998).
BMBL; AB08024; BAC7601.1;
GO; GO:00464821; C:extrachronsomal DNA; IEA.
GO; GO:00466821; C:extrachronsomal DNA; IEA.
GO; GO:0016769; F:transferase activity, transferring hexosyl . .; IEA.
GO; GO:001676; F:transferase activity; IEA.
InterPro; IPR005325; UDPGT MGT.
InterPro; IPR005213; UDPGT MGT.
InterPro; IPR004213; UDPGT MGT.
INTERPAMS; TIGR01426; MGT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Numl O., Kinasni H.;
"Identification of two polyketide synthase gene clusters on the linear
plasmid pSLA2-L in Streptomyces rochei.";
Gene 246:123-131(2000).
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                                                                                                                                                                                                                                          STRAIN=7434AN4;
MEDLINE=20408175; PubMed=10954087;
MEDLINE=20408175; Mochizuki S., Kinashi H.;
"Cloning and analysis of the replication origin and the telomeres of the large linear plasmid pSLAD-L in Streptomyces rochei.";
Mol. Gen. Genet. 263:1015-1021(2000).
                                "The large linear plasmid pSLA2-L of Streptomyces rochei has an unusually condensed gene organization for secondary metabolism."; Mol. Microbiol. 0.0-0(12003).
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MEDLINE=20231737; PubMed=10767533;
Suwa M., Sugino H., Sasaoka A., Mori E., Fujii S., Shinkawa H.,
Nimi O., Kinashi H.;
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Matches 116; Conservative
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SEQUENCE 389 AA; 4:
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 ----EKLHHCFSPLAQISQLIPELDFPRKALPDCFHAVGPLRQPQGTPGSSTSYFPSPDK 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 PLGDVLPHTDLLVNHGGTSTAMEALAHGVPIVAMPEMPERPRATARRIAELDLGDWLLPGE 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 MAHIAFFILFAAGHVNPTLGVAEELAARGHRVTYALPEDMADRAVRVGA------ 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 ------RAVTYPLDRERFR-----ADMVPKEBSDEYTDEGEFLKVLEWLLDTT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 ---LPAAFHALQIEGVIVDQMEPA----GAVVAEASGLPFVSVACALPLNREPGLPLAVM 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 PPEYGTSD---AARERYTTSEKIYDWLMRRH----DRVIAHHACRMG----LAPR---- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 PPEPGAAQVDPALIELTARAEK---LLKEHGTTSDPVARAATVQSGPGLFYMPRYFQYA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 GETFDDRHHFVGPCA-----PRAS----PH------GTWQRPEDGR 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 PRIFASLGTLOGHRYGLFRTIAKACEEVDAQLLLAHCGGLSATQAGELARGGDIQVVDFA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 PLVMVSLGTIYNERPGIFRACVRAPRDRPWNILLVLGGGLGAGDLGPLPE--NVLVRDFV 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310 DQSAALSQAQLTITHGGMNTVLDAIASRTPLLALPLAFDQPGVASRIVYHGIGK-RASRF 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSHFAVIAPPFFSHVRALQNLAQELVARGHRVTFFQQHDC--KALVTGSDIGFQTVGLQT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 HPPGSLSHLLHLAAHPLGPSMLRLINEMARTSDMLCRE------96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF14704; AAD41824.]; -..

GO; GO: 0016758; P: transferase activity, transferring hexosyl . . ; IEA.
GO; GO: 001679; P: transferase activity, iEA.
GO; GO: 0016575; P: carbohydrate metabolism; IEA.
GO; GO: 0030259; P: lipid glycosylation; IEA.
InterPro; IPR004276; Glyco_trans_28.
InterPro; IPR006326; UD9GT MGT.
Ffam; PF03031; Glyco_transf_28; 1.

TIGRFAMS; TIGR01426; MGT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=T59235;
MEDLINE=20121747; PubMed=10658660;
Bate N., Butler A.R., Smith I.P., Cundliffe E.;
"The mycarose-biosynthetic genes of Streptomyces fradiae, producer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58; Mismatches 179; Indels 119; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.7%; Score 239.5; DB 2; Length 461; 23.3%; Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                               Streptomyces fradiae.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               369 TISHALARQIRSLLTNTDYPQRMTKIQAALRLAGGTPAAADIVE 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       461 AA; 50120 MW; 4A51AFE1F06A2F59 CRC64;
                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Mycarosyl transferase TylCV.
381 -LLTNTDYPORMTKIQAALRLAGGTPAAADIVEQAM 415
                        461 AA
                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tylosin.";
Microbiology 146:139-146(2000).
EMBL; AF147704; AAD41824.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 23.3%
es 108; Conservative
                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase.
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                                                                                                                                         09XC67
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61 PGSLSHILIHLAAHPLGPSMIRLINEMARTSDMLCRELPAAFHALQIEGVIVDQMEPAGAV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 IYDWLMRRHDRVIAHHACRMGLAPREKLHHCPSPLAQISQLIPELDFPRKALPDCFHAVG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 PLRQPQGTPGSSTSYPPSPD---KPRIFASLGTLQGHRYGLFRTIAXACREVDAQLLLAH 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 IVNILQLPSVSSCTTFAVNQYINFHDEQESRQVDEMDPLYQSCLAGMERWNKQYGMKCNS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 MYDIMMHPGDITIVY-----TSKR----YQPRSEV------PDESYKFVG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 PSIATRKEVĠS----FPTEDLKNEKVİPISMGTVFNEQPALYEKCPEAFKDVDĀTVVLVV 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 CGGLSATQAGELARGGDIQVVDPADQSAALSQAQLFITHGGMNTVLDAIASRTPLLALPL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 GKKINISQFENIPK--NFKLYNYVPQLEVLOHADVFVTHGGMVSSSBALYYGVPLVVIPV 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346 AFDOPGVASRIVYHGIGKRASR-FTTSHALARQIRSILTNTDYPORYTKIQAALRIAGGT 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE017004; AAP09035.1; -.
GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR006326; UDPOT MGT.
InterPro; IPR0062213; UDP_GIuco_trans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-22008415; PubMed=12721630; Ivanova N., Candelon B., Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A., Capatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T., Overbeek R., Kyrpides N., Grechkin Y., Ryrpides N., Genowe sequence of Bacillus cereus and comparative analysis with Bacillus anthracis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 10.7%; Score 238.5; DB 16; Length 402; Local Similarity 21.6%; Pred. No. 1e-09; hes 92; Conservative 81; Mismatches 199; Indels 53;
                                                                                                                                                                                                                                                                           Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEGURA PRO0201; UDPGT; 1.
TIGREAMS; TIGR01426; MGT; 1.
GlyCosyltransferase; Transferase; Complete proteome.
SEQUENCE 402 AA; 45743 MW; 75B9D25EBC38D582 CRC64;
                                                                                              01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                         402 AA
                                                                                                                                                                                            Macrolide glycosyltransferase (EC 2.4.1.-).
                                         PRT;
                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 423:87-91(2003)
                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=226900;
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                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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081BB6
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378 RNAGGYKRAVD 388
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                                                                                                        QBDSH9
                                                                   RESULT 1
QBDSH9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 CFHANGPLRQPQGTPGSSTSYFPSPD---KPRIFASLGTLQGHRYGLFRTIAKACEEVDA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 SYKEVGPSIATRKEVGS----PPMEDLKGEKLIFISMGTVFNBQPELYBKCFBAFKGVEA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 TVILAVGKKINISQEENIP--NNPKLYNYVPQLEVLQHADVPVTHGGMNSSSEALYYGVP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PGSLSHILHLAAHPLGPSMLRLINEWARTSDMLCRELPAAFHALQIBGVIVDQMEPAGAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 VAEASGLPFVSVACALPLNR-------EPGLPLAVMPFBYGTSDAARERYTTS- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 IANVIQLESISSCTTFAFNQYITFNDEQESRQVDETNPL----YQSCLAGMEKWNRQY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 ----EKIYDWLMRRHDRVIAHHACRMGLAPREKLHHCPSPLAQISQLIPELDFPRKALPD 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 GMXCNSMYDIMNHPGDITIVYTS-------KEYQPRSD----VFDE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 QLLLAHCGGLSATQAGELARGGDIQVVDFADQSAALSQAQLTITHGGWYTVLDAIASRTP 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: :|: || || || || :| :| || 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54
                                                                                                                                                                                                                                            Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T., Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R., Holtzapple E.K., Okstad O.A., Helgason R., Rilstone J., Mu M., Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M., DeBoy R.T., Madpu R., Daudherty S.C., Durkin A.S., Haft D.H., Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D., Berry K.J., Plaut R.D., Wolf A.M., Warkins K.L., Nierman W.C., Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MANVLVINFPGEGHINPTLAIISELIRRGETVVSYCIEDYRKKIEATGAEFREF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                           "The genome sequence of Bacillus anthracis Ames and comparison closely related bacteria.";
Nature 423:81-86(2003).
EMBL; AR017030; AAP255969.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16; Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transferring hexosyl
IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
10.5%; Score 234.5; DB 16; Length
Best Local Similarity 21.6%; Pred. No. 2.1e-09;
Matches 93; Conservative 76; Mismatches 197; Indels
                             01-JUN-2003 (TrEMBirel. 24, Created)
01-JUN-2003 (TrEMBirel. 24, Last sequence update)
01-GN-2003 (TrEMBirel. 25, Last sequence update)
Glycosyltransferase, MGT family.
BA2083.
BA211Us anthracis (strain Ames).
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI TaxiD=198094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1017D0020E819BEC CRC64;
                        402 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO, GO:0016758, F:transferase activity, GO; GO:0016740; F:transferase activity; GO; GO:0008152; P:metabolism; IEA. InterPro; IPR005213; UDPGT_MGT. InterPro; IPR002213; UDP_GT_MGT. Pfam; PF00201; UDPGT; 1.
                                                                                                                                                                                                                                    MEDLINE=22608414; PubMed=12721629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS; TIGRO1426; MGT; 1.
Transferase; Complete protecme.
SEQUENCE 402 AA; 45803 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLAGGTPAAAD 409
                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Fraser C.M.
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                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 ----FHAVGP-LROPQGTPGSSTSYFPSPDXPRIFASLGTLQGHRYGLFRTIAKACBEVD 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 YSIIISLGNRIKKEQLGTMP--ANVHLYSFVPQLQILERASLELFHGGMNSVNEAIYYGC 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 BPAGAVVABASGLPFVSVACALPLNRBPGLPLAVMPPBYGTSDAARBRYTTSEKIYDWEM 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98
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EMBL; AE015008; AAN59431.1; -

EMBL; AE015008; AAN59431.1; -

GO; GO:0005489; F:electron transporter activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:001618; P:electron transport; IEA.

InterPro; IPR000345; Cytc heme BS.

InterPro; IPR000345; UDPGT MGT.

InterPro; IPR00201; UDPGT; II.

PFam; PF00201; UDPGT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 LRH-------LLSR-KLORTFQLAYDDLAKEISLNTPELNFTYTVREFQIDADTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 DENHYQYVGPSINRPVEPPFDFTPP----KNPIIYISLGTLIARSVSFFKKCIKAFENEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279 AQLLLAHCGGLSATQAGELARGGDIQVVDFADQSAALSQAQLTITHGGMNTVLDAIASRT
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                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=UALSO / ALCC 700610 / Serotype C;
STRAIN=UALSO / ALCC 700610 / Serotype C;
STRAIN=UALSO / ALCC 700610 / Serotype G., Chang J.,
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tlan R., Kenton S., Jia H., Lin S., Qian Y.,
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.;
Genome sequence of Streptococcus mutans UALSO, a cariogenic dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 SHPAVIAP--PFFSHVRALQNIAQELVARGHRVTFFQQHDCXALVTGSDIGFQTVGLQTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ROKKVKSWSAAYQTVLRMGKDYDCLIYEML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                   Streptococcus mutans.
Bacteria, Firmicutes, Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               389 AA; 44560 MW; 055BA3B779090CCD CRC64;
                                                                               01-WAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
389
                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00190; CYTOCHROWE_C; 1.
PROSITE; PS00375; UDPGT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase, Complete proteome.
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                                                                                                                                                 Putative glycosyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 23.49
Matches 103; Conservative
PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 -----PSPHGVLAYTTRALLGPVE-LPDRVMLVGPSVAARPAGPDDFPWEWLRASALPTV 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 FASLGTLQGHRYGLFRTIAKACEEVDAQLLLAHCGGLS-ATQAGELARGGDIQ----- 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 IVSLGTANNDAGARFLNAA-----ABAL----GGIADRVRAVIVDPGGVVEHPVPDTV 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 -VVDFADQSAALSQAQLTITHGGMNTVLDAIASRTPLLALPLAPDQPGVASRIVYHGIGK 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 LVRRYVPQLALLERLDAVVCHAGHNTVCBALWHGVPLVVAPIRDDQPIVAAQVVDAGAGV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metabolites.", with Maded Sci. U.S.A. 98:12215-1220(2001).

EMBL, ABO70941; BAB69204.1;
GO, GO:0016758; F:transferase activity, transferring hexosyl . . ; IEA.
GO, GO:0016759; F:transferase activity, IEA.
InterPro; IPR006325; UDPGT MGT.
InterPro; IPR006326; UDPGT MGT.
InterPro; IPR0063213; UDPGT MGT.
INTERPRO; IPR0063213; UDP_Gluco_trans.
Pfam; PF00201; UDPGT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 AAALAARGHDIAWAGHPELVRGLAGADAVVFPCAL---PEDGLSRPAGIK----GPAAFQ 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE FROM N.A.
MEDINE-21187403; PubMed-11572948;
MEDINE-21187403; PubMed-11572948;
Omnra S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
fikuchi H., Shiba T., Sakaki Y., Hattori M.,
Genome sequence of an industrial microorganism Streptomyces
avermitilis: Deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.8%; Score 219.5; DB 2; Length 379; 26.5%; Pred. No. 2.6e-08; tive 60; Mismatches 172; Indels 71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Putative glycosyl transferase.
Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     379 AA; 38968 MW; BSFED865CB111DSC CRC64;
                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=33903;
                                                368 AQTAGGNTLIAQTIKDLQT 387
398 LRLAGGTPAADIVEQAMRT 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 109; Conservative
                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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RESULT 14

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Query Match
9.8%; Score 219; DB 2; Length 417;
Best Local Similarity 24.8%; Pred. No. 3.2e-08;
Matches 111; Conservative 68; Mismatches 185; Indels 84; Gaps 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 QTHPPGSLSHLLHLALAAHP--LGPSMLRLINEMARTSDMLCRELPAAFHALQIEGVIVDQM 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 SYPARVLAHRWGVPAVSLSPNLVAWEGYEEEVGRPTWEEPLKTERGRAYDARFRGWLKEN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 ----PGP------DADPDAWGTTPLDNVEPFLDDAIQALPQLIAAYEGDEPDLVLHDIT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 EPAGAVVARASGLPFVSVACAL----PLNREPGLPLAVMPP--BYGTSDAARERYTTSE- 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 ---KIYDWLMRRHDR------VIAHHACRMGLAPREKLHHCFSPLAQISQLIPELDFPR 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 KALPDCFHAVGPLROPOGTPGSSTSYPPSPOKPRIFASLGTLOGHRYGLFRTIAKACEEV 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278 DAQLLLAHCG-GLSATQAGELARGGDIQVVDFADQSAALSQAQLTITHGGMNTVLDAIAS 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337 RTPLLALPLAEDQPGVASRIVYHGIGKRASRFTTSHALARQIR----SLLTNTDYPQRMT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 AHIAMPSIAAHGHYNPSLBVIRELVARGHRVTYAIPPLFAE---KVAETGAEPKLMNSTL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pernodet J.L., Gournelen A., Blondelet-Rouault M.H., Cundliffe E.;
"Dispensable ribosomal resistance tp spiramycin conferred by srmA in
the spiramycin producer Streptomyces ambofactens.";

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EMBL, AJ223970; CAA11707.1; -
GO; GO:0016758; Fitransferase activity, transferring hexosyl . .; II
GO; GO:0016758; Fitransferase activity, IEA.
GO; GO:0016740; Fitransferase activity; IEA.
GO; GO:0016729; Fitransferase activity.

InterPro; IPR006325; UDPOT MGT.
InterPro; IPR006326; UDPOT MGT.
INTERPANS; TIGR01426; MGT.
ITGRFAMS; TIGR01426; MGT.
PROSITE; PS00375; UDPGT; 1.
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                                                                                                                                                                                                                                                                        Streptomyces ambofaciens.
streptomyces Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomycineae;
NCBL_TaxID=1889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           417 AA; 45427 MW; B693EF18F6FCASFD CRC64;
                                                                    01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
417 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 BIOAGMAREGGTRRAADLIEAELAAART 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC23877;
MEDLINE=99445176; PubMed=10517588;
                                                                                                                                                                                           Macrolide glycosyl transferase.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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SEQUENCE FROM N.A.
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159 ARBRYTTSSKIYDWIMRRHDRVIA----HH-----ACRMGLAPREKIJHHCFSPLAQISQLI 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 ------ILPREFNPERLLAEDQGSRWACSLAEAFRVLPQLRTATPTTGRDLIVY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 DOMEPAGAVVAEASGLPEV----SVACA-----LPLNREPGLPL---AVMPFEYGTSDA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 --BEGARAE---DGLVRFFTRLSAFLEEHGVDTPATEFLIAPNRCIVGCRAP----SQIK 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 PELDEPRKALPDCFHAVGPL---ROPOGT---PGSSTSYPPSPDKPRIFASLGTLQGHRY 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 HFAVIAPPFFSHVRALQNLAQELVARGHRVTFFQQHDCKALV----TGSDIGFQTVGLQ 57
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STRAIN=ATCC [1891;
Aguirrezabalaga I., Olano C., Mendez C., Salas J.A.;
L Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
R MBL; AF055579; AAC12648.1; -.
RMBL; AF055579; AAC12648.1; -.
R MBL; AF055579; AAC12648.1; -.
R GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; II
R GO; GO:0016758; F:transferase activity, IEA.
R GO; GO:0016758; F:transferase activity, IEA.
R GO; GO:0016752; P:metabolism; IEA.
R THCETPC; IPR062213; UDP_Gluco_trans.
R DIAPPC; IPR062213; UDP_Gluco_trans.
R Pfan; PF00201; UDPGT; 1.
R PROSITE; PS00375; UDPGT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 11891;
MIRDLINE=28943801. PubMed=9680207;
Quiros L.M., Aguirrezabalaga I., Olano C., Mendez C., Salas J.A.;
Quiros L.M., Aguirrezabalaga II., Olano C., Mendez C., Salas J.A.;
"Two glycosyltransferases and a glycosidase are involved in
"Two glycosyltransferases and a glycosidase are involved in
andibioticus.",
Mol. Microbiol. 28:1177-1185(1998).
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4.
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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earch completed: February 29, 2004, 14:50:54

Job time : 40.4397 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

101.07 PIFF TFF CO 01

Pebruary 29, 2004, 14:27:18; Search time 7.26404 Seconds (without alignments) 3089.496 Million cell updates/sec M protein - protein search, using sw model uo un

US-09-941-947A-28 2231 1 MSHFAVIAPPPFSHVRALQN.......BQANRTCQPVLSGQDYATAL 431

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141681 seqs, 52070155 residues earched:

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ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* atabase : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	PANAN P21686 pa	ERWHE Q01330	STRAT 053685		Q54387	Q16880 .	D14726	CGT MOUSE Q64676 mus musculu		RAT Q64550	MYCTU	RAT	HUMAN 09y4x1	CAREL Q18081	HUMAN	MACFA Q9xt55	MOUSE P70691	MAIZE P16165 zea m	HUMAN Q9haw8	MAIZE P16167 zea m	HUMAN P36509	MAIZE P16166 zea m	HUMAN Q9by64 homo	Obhaw7 homo		RAT	UDBF HUMAN P54855 homo sapien	RAT P20720	HUMAN	RAT Q64637	88	
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Q9haw9 homo sapien Q7vep8 mycobacteri Q91280 pleuronecte Q63886 mus musculu Q77649 macaca fasc P36537 homo sapien Q19103 cryctolagus Q64634 rattus norv Q6224 mycobacteri P36513 oryctolagus Q8p2b2 methanosarc P09875 rattus norv
UD18 HUMAN MURG MYCEO UGT3 PLEBL UD11 MOUSE UDBA HUMAN UDBA RABIT UD18 RABIT UD18 RABIT UDBE RABIT YS 82 METWA UDBI RABIT
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ALIGNMENTS

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1 MSHFAIVAPPLYSHAVALHALALEMAQRGHRVTF-----LTGNVASLARQETERVA 51
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                                                                              301 GDIQVVDFADQSAALSQAQLTITHGGMNTVLDAIASRTPLLALPLAFDQPGVASRIVYHG 360
                                                                                                                                                                                                801 RHTQVVDFADQSAALSQAQLAITHGGMNTVLDAINYRTPLLALPLAFDQPGVASRIVYHG 360
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                        IAHHACRMGLAPREKLHHCFSPLAQISQLIPELDFPRKALPDCFHAVGPLRQPQGTPGSS 240
                                                                                                                    241 TSYFPSPDKPRIFASLGTLQGHRYGLFRTIAKACEKVDAQLLLAHCGGLSATQAGELARG 300
       VAEASGI PEVSVACALPINREPGLPLAVMPFEYGTSDAARERYTTSEKIYDWLMRRHDRV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=EHO10;
MEDIATE=9028456; PubMed=1409639;
MEDIATE=903028456; PubMed=1409639;
MEDIATE=903028456; PubMed=1409639;
"Functional expression of zeaxanthin glucosyltransferase from Erwinia herbicola and a proposed uridine diphosphate binding site.";
Proc. Nacl. Acad. Sci. U.S.A. 89:9321-9325(1992).
-i. FUNCTION: CATALYZES THE GLYCOSYLATION REACTION WHICH CONVERTS
-ZEAXANTHIN TO ZERNANTHIN PERA-DIGLUCOSIDE.
-i. PATHWAY: Carclemoid biosynthesis.
-i. PATHWAY: Carclemoid biosynthesis.
                                                                                                                                                                                                                                   IGKRASRFTTSHALARQIRSLLTWIDYPQRMTKIQAALRLAGGTPAADIVEQAMRTCQP
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002213; UDP_gluco_trans.
Pfam; PF00201; UDPGT; 1.
PR0021TB; PS00315; UDPGT; 1.
Transferase; Carotenoid biosynthesis.
SEQUENCE 413 AA; 44852 MW; 353406A12B27D2E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Zeaxanthin glucosyl transferase (BC 2.4.1.-)
                                                                                                                                                                                                                                                                                                                                                                                               413 AA
                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Q01330;
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Matches 211;
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MSHFAVIAPPFFSHVRALQNLAQELVARGHRVTFFQQHDCKALVTGSDIGF---QTVGLQ 57

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                                                                                             PGVASRIVYHGIGKRASRFTTSHALARQIRSILTNTDYPQRMTKIQAALRLAGGTPAAAD 409
                    117 AGAVVAEASGLPFVSVACALPINREPGLFLAVMPPEYGTSDAARERYTTSEKIYDWLMRR
                                                                                                                                                  177 HDRVIAHHACRMGLAPREKLHHCPSPLAQISQLIPBLDPPRKALPDCFHAVGPLRQPQGT
                                                                                                                                                                                                                            237 PGSSTSYFPSP-----DKPRIPASLGTLQGHRYGLFRTIAKACEEVDAQLLLAHCGGL
                                                                                                                                                                                                                                                                  ----YOPPPOVERSPRSTPRIFASIGTLOGHRIRLFOKIARACASVGABVTIAHCDGL
                                                                                                                                                                                                                                                                                                       290 SATQAGELARGGDIQVVDFADQSAALSQAQLTITHGGMNTVLDALASRTPLLALPLAFDQ
58 THP-PGSLSHLLHLAAHPLGPSMLRLINEMARTSDMLCRELPAAFHALQIEGVIVDQMEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
STRAIN=ATCC 11891;
MEDININE=ATCC 11891;
Hernandez C., Olano C., Mendez C., Salas J.A.;
Hernandez C., Olano C., Mendez C., Salas J.A.;
"Characterization of a Streptomyces antibioticus gene cluster encoding a glycosyltransferase involved in oleandomycin inactivation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 134:139-140(1993)
-1- FUNCTION: SPECIFICALLY INACTIVATES OLEANDOMYCIN VIA 2'-0-GLYCOSYLATION USING UDP-GLUCOSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces antibioticus.
Bacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase, Glycosyltransferase, Antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-Bandomycin glycosyltransferase (EC 2.4.1.-)
0LED OR UGT102A2.
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PIR, S33184; S33184.
Interpro; IPR002213; UDP_gluco_trans.
Interpro; IPR006326; UDPGT_MGT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR006326; UDPGT_MC
Pfam; PF00201; UDPGT; 1.
TIGRFAMS; TIGR01426; MGT; 1.
PROSITE; PS00375; UDPGT; 1.
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MGT_STRLI
Q54387;
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TRANSMEM
CARBOHYD
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MGT_STRLI
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SEQUENCE FROM N.A.

STRAINNEW Zealand white; TISSUB-liver;

MEDLINE-93315511; PubMed-8325897;

Tukey R.H., Pendurthi U.R., Nguyen N.T., Green M.D., Tephly T.R.;

Tukey R.H., Pendurthi U.R., Nguyen N.T., Green M.D., Tephly T.R.;

Toloning and characterization of rabbit liver UDP-

Tylouronosyltransferase cDNAs. Developmental and inducible expression of 4-hydroxybiphenyl UGT2B13.";

J. Biol. Chem. 268:1526-15266(1993).

- FUNCTION: UDPGT is of major importance in the conjugation and subsequent elimination of potentially toxic xenobiotics and endogenous compounds.

- CAPALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor beta-D-glucuronoside.

- CAPALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor

- SIMILARITY: Belongs to the UDP-glycosyltransferase family.

- SIMILARITY: Belongs to the UDP-1.

- This SWISS-PROT entry is copyright. It is produced through a collaboration contains the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Characterion the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euch on the Euc
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                                                                                                                                                                                        2 SHFAVIAPPFFSHVRALQNLAQELVARGHRVTF----PQQHDCKALVTGSDIGFQTVGL
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UGT2C1 OR UGT2A2.
UGT2C1 OR UGT2A2.
Oryctolagus cuniculus (Rabbit).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-GCT-2001 (Rel. 40, Last annotation update)
UDP-glucuronosyltransferase 2C1 microsomal (EC 2.4.1.17) (UDPGT)
                                                                                                 85;
                                              Query Match
10.2%; Score 228.5; DB 1; Length 430;
Best Local Similarity 25.3%; Pred. No. 2.6e-10;
Matches 112; Conservative 67; Mismatches 178; Indels 85.
  47136 MW; 320512217B42A0B7 CRC64;
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LRRIQAEMAQEGGTRRAADLIB 395
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     430 AA;
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     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 RIFASLGTLOGHRYGLFRTIAKACEEVDAQLLLAHCGGLSATQAGELARGGDIQVVDFAD 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 LIRSYW------DFEPPRPFLPN-FEYVGGLHCKPAKPLPEBLEEFVQSSGNDGV
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MEDLINE-92104506; PubMed=1761231;
Jenkins G., Cundliffe B.;
"Cloning and characterization of two genes from Streptomyces lividans that confer inducible resistance to lincomycin and macrolide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 FSHVRALQNLAQELVARGHRVTFFQQHDCKALVTGSDIGPQTVGLQTHPP-----GSLSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 GVIVDQMEPAGAVVAEASGLPFV-----SVACALPLNREPGLPLAVMPFBY--G
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N-LINKED (GLCNAC. . .) (POTENTIAL)
B6E65670BFAELD35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98;
                                                                                                                                                                                        Přem; Pr00201; UDPGT; 1.
PROSITB; PS00375; UDPGT; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Streptomycineae, Streptomyces, Streptomyces, NCBI_TaxID=1916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.2%; Score 183; DB 1; Length 50
21.7%; Pred. No. 1.1e-06;
tive 75; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MGT OR UGF10231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392 IMTTSSLLKALKDVINNPSYKENAMKL 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368 FITSHALARQIRSLLTNTDYPORMTKI 394
                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                   EMBL; L01083; AAA18023.1; -. InterPro; IPR002213; UDP_gluco_trans
                                                                                                                                                                                                                                                                                                                                                                                                        57449 MW;
                                                                                                                                                                                                                                                                       Multigene family; Microsome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 21.78 Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                               481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces lividans
                                                                                                                                                                                                                                                                                                                                                                                 288 ;
502 AA;
                                                                                                                                                                                                                                                                                                                            466
177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 GSLSHLLHLAAHP--LGPSMLRLINEMARTSDMLCRELPAAFHALQIEGVIVDQMEPAGA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 VVAEASGLPFVSVA-CALP---LNREPGLPLAVMPPEYGTSDAARERYTTSEKIYDWLMR 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 RHDRVIAHHACRMGLAPREKLHHCFSPLAQISQLIPELDFPRKALPDCFHAVGPLRQPQG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 BENGITDHPDPFIGRPDRSLV------LIP-----KAL-----QPHA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 VLGRRWEVPVISLSPCMVAWEGYEQEVGEPMWEEPRKTERGQAYYARF-----HAWL-- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 TPGSSTSYR------PSPDKPRIFASLGTLQGHRYGLFRTIAKACEEVD 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 AQLILLAHCGGLSATQAG---BLARGGD----IQVVDFADQSAALSQAQLTITHGGANTVL 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 -----GWHTVLQVGRHVDPAELGDVPDNVEVRTWVPQLAILQQADLFVTHAGAGGSQ 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 DAIASRTPLLALPLAFDQPGVASRIVYHGIGKRASRFTTSHALARQIR----SLLTNTDY 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 SHFAVIAPPFFSHVRALQNLAQELVARGHRVTFFQQHDCKALVTGSDIGFQTVGLQTHPP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCT HUMAN STANDARD, PRT; 541 AA.

01680; 00196;

01-NOV-1997 [Rel. 35, Created)

10-NOV-1997 [Rel. 35, Last sequence update)

28-FBB-2003 [Rel. 4], Last annotation update)

28-FBB-2003 [Rel. 4], Last annotation update)

28-FBB-2003 [Rel. 4], Last annotation update)

CEC 2.41.45 (UDP-galactose-ceramide galactosyltransferase) (Ceramide UDP-galactosyltransferase) (Cerebroside synthase).

HOMO Sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.1%; Score 181.5; DB 1; Length 418;
22.7%; Pred. No. 1.1e-06;
tive 67; Mismatches 186; Indels 91; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 DRVDETTYTFVGACQGDRTAEGDWARPEGAEKVVLVSLGSAFTKQPAFYRECVRAFGELP
                  Gene 108:55-62(1991).
-!- FUNCTION: SPECIFICALLY INACTIVATES MACROLIDES VIA 2'-0-GLYCOSYLATION USING UDP-GLUCOSE.
-!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase, Glycosyltransferase, Antibiotic resistance.
SEQUENCE 418 AA, 45682 MW, P7349765ECE8D2E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45682 MW; F7349765ECE8D2E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 386 AARLKEIQARMAQEAGTRGPADLIE 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         388 PORMTKIQAALRLAGGIPAAADIVE 412
                                                                                                                                                                                                                                                                                                                                           InterPro, IPR002213; UDP gluco trans.
InterPro, IPR006326; UDPGT MGT.
                                                                                                                                                                                                                                                                                                    EMBL; M74717; AAA26780.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMS; TIGRO1426; MGT; 1.
PROSITE; PS00375; UDPGT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 22.7% Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00201; UDPGT; 1
                                                                                                                                                                                                                                                                                                                           PIR; JS0636; JS0636.
  antibiotics.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0008489; F:UDP-galactose-glucosylceramide beta-1,4-gal. . .; TAS. GO; GO:0007417; P:central nervous system development; TAS. GO; GO:0007422; P:peripheral nervous system development; TAS. InterPro; IPR02213; Pipelipheral nervous system perelopment; TAS. Pfam: PF00211; UDP-gluco_trans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 IIVPPIMFESHWYIPKTLASALHERGHHTVFL-----LSEGADIAPSNHYSLQRYPGI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00375; UDFGT; 1.
Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
                                                                                                                                                                                20.1%; Pred. No. 5.3e-06;
tive 71; Mismatches 173; Indels 137; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 VIAPP--FFSHVRALQNLAQBLVARGHRVTFFQQHDCKALVTGSDIG-FQTVGLQTHP--
                                                                MEDINE-96299661; PubMed-8661025; Bosio A., Binczek E., Lebeau M.M., Fernald A.A., Stoffel W.; The human gene CGT encoding the UDP-galactose ceramide galactosyl transferase (cerebroside synthase): cloning, characterization, and assignment to human chromosome 4, band q26."; Genomics 34:69-75(1996).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
T -> P (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.8%; Score 174.5; DB 1; Length 541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2-HYDROXYACYLSPHINGOSINE 1-BETA-GALACTOSYLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61455 MW; EC532798F7E15834 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T -> P (IN REF. 2).

L -> M (IN REF. 2).

L -> V (IN REF. 2).

L -> V (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U30930; AACS0565.1; -...
EMBL; U31370; AACS0815.1; JUNED.
EMBL; U31461; AACS0815.1; JUNED.
EMBL; U31461; AACS0815.1; JUNED.
EMBL; U31864; AACS0815.1; JUNED.
EMBL; U62899; AACS187.1; JUNED.
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96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGNC:12555; UGT8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           492
442
442
1116
356
                                                SEQUENCE FROM N.A. MEDLINE=9620055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 AA;
                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 601291;
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Matches
 8
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Transferase; Glycosyltransferase. SEQUENCE 455 AA; 47079 MW; FFDBBC2F2103AC9C CRC64;

455 AA;

SEQUENCE

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                                                                                                                                                                           AL-IQGLKKEKFDLLIVDPNDMCGFVIAHLLGVKKAVPSTGLWYPABVGAPAPLAYVP-E 179
                                                                                                                                                                                                                                                                                                   FNSLLTDRMK-----YBRIMGKYN 223
                                                                                                                                                                                                                                                                                                                                                                                                                           274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPRIFASIGTLØGHRYGLFRTIAKACEEVDAQLLLLAHCGGLSATQAGELAR----- 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275 DLQRWVNGANEHGFVLVSFGAGVKYLSEDIANKL------AGALGRLPQKVIWRF 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GGDIQVVDFADQSAALSQAQLT--ITHGGMNTVLDAIASRTPLLALPLAFDQ 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152
                                                                                                                                                                                                                                         153 YGTSDAARERYTTSEKIYDWIARRHDRVIAHHACRMGLA----PREKLHHCFSPLAQISQ 208
                                                                                                                                                                                                                                                                                                                                                                    384 YDJWTRVQAKGMGIILEWKTVTEKELYEALVKVINNPSYRQRAQKLSEIHKDQPGHP 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 PGVASRIVYHGIGKRAS-RFITSHALARQIRSLLINIDYPORMIKIOAALRLAGGIP 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1990 (Rel. 14, Created) . 01-APR-1990 (Rel. 14, Last sequence update) . 28-PEB-2003 (Rel. 14, Last annotation update) . 18-2003 (Rel. 41, Last annotation update) . 18-18-2010 . 29-18-2010 . 20-21ucosyltransferase (BC 2.4.1.91) (UDP-glucosyltransferase) (Bronze-1). . BZ1 OR UGT71A2.
                                                                                                                                                                                                                                                                                                                                                                                                                           LLPEKSMYDLVHGSSLWMLCTDVALEFPRPTLPNVVYVGGILTKPAS-----PLPE
                                                             77 FNSTTSDAFLOSKWRNIFSGRLTAI-----BLFDILDHYTKNCDLM----VGNH
                                                                                                                       ----VIVDOMEPAGAVVAEASGLPFVSVACALPLNREPG--LPLAVMPFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BZI OR UGT71A2.
Hordeum vulgare (Barley).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae, Pooideae,
Triticeae, Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vulgare.";
Plant Mol. Biol. 14:277-279(1990).
Plant Mol. Biol. 14:277-279(1990).
Plant Mol. Biol. 14:277-279(1990).
Plant Mol. Biol. 14:277-279(1990).

plant Mol. Biol. 14:277-279(1990).

pigments.
-:- CATAMYTIC ACTIVITY: UDP-glucose + a flavonol = UDP + flavonol 3-0-D-glucoside.

-:- PATHWAY: Anthocyanin biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wise R.P., Rohde W., Salamini F.; "Nucleotide sequence of the Bronze-1 homologous gene from Hordeum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               455
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MEDLINE-91329682; PubMed-2151660;
Wise R.P., Rohde W., Salamini F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBE; X15694; CAA33729.1; -.
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P14726;
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                                                                                                                              103
                                                                                                                                                                                                                                                                                                                                                                                                                                     224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249
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                                                                                                                                                                                                                                                                                                             180
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InterPro; IPR002213; UDP_gluco_trans. Pfam; PF00201; UDPGT; 1. PROSITE; PS00375; UDPGT; 1.

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302 DIQVVDFADQSAALSQAQL--TITHGGMNTVLDAIASRTPLLALPLAFDQPGVASRIV-Y 358
                                                                                                                  105
                                                                                                                                              111
                                                                                                                                                                           161
                                                                                                                                                                                                        155
                                                                                                                                                                                                                                    RYTTSEKIYDWLMRRHDRVIAHHACRMGLAPRE------KLHHCFSPLA--QISQL-- 209
                                                                                                                                                                                                                                                       330 GL-VVPWAPQVGVLRHAAVGAFVTHAGWASVMEGVSSGVPWACRPFFGDQTMNARSVASV 388
                                                                                  99
                                                       54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  064576; 061634;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
2-hydroxyacylsphingosine 1-beta-galactosyltransferase precursor
(RC 2.41.45) (UDP-galactose-ceramide galactosyltransferase) (Ceramide UDP-galaccosyltransferase) (Cerebroside synthase).
                                                                                                                                             PDGV---PPGETSCLSPPRRMDLFMAAEAGGVRVGL-----EAAC----ASAGGAR
                                                                                                                                                                        106 IEGVIVDQMEPAGAVVAEASGLPFVSV----ACALPLNREPGLPLAVMPFEYGTSDAARE
                                                                                                                                                                                                                                                                                                                          211 AATAVALNTEPGLÜPPDLIAALAABLPNCL-PLGPYHLLPGAEPTADTNEAPADPHGCLA
                                                                                                                                                                                                                                                                                                                                                                                   270 WLDRRPARSVAYVSPGTNATARPDELQELAAGLEASGAPFLWSLRGVVAAAPRGFLERAP
                                                                               7 HIAVVAFPFSSHAAVLFSFARALAAAPACTSLSFLTTADNAAQLRKAGALPGNLRFVEV
                                                                                                                --GLQTHPPGSLSHL------LHLAAHPLGPSMLRLINEMARTSDMLCRELPAAFHALQ
                                                                                                                                                                                                        112 VSCVVGDAFVWT-ADAASAAGAPWVAVWTAASCAL------LAHLRTDALR-
                                                                                                                                                                                                                                                                                                                                                           ----PDKPRIFASLGTLQGERYGLFRTIAKACBEVDAQLLLAHCGGLSATQAGELARGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HFAVIAPPFFSHVRALQNLAQELVA---RGHRVTFFQQHD-----CKALVTGSDIGFQTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coetzee T., Li X., Fujita N., Marcus J., Suzuki K., Francke U.,
7.5%; Score 167; DB 1; Length 455;
24.1%; Pred. No. 1.6e-05;
ive 56; Mismatches 194; Indels 102;
                                                                                                                                                                                                                                                                                                 -----IPELDFP-----RKALPDCFHAVGPLR-OPQGTPGSSTSYFPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389 WGFGTAFDGPMTRGAVANAVATLLRGEDGERMRAKAQELQAMVG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 HGIGKRASRFTTSHALARQIRSLLTNTDYPQRMTKIQAALRLAG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bosio A., Binczek E., Stoffel W.; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                 Local Similarity 24.19
les 112, Conservative
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      Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the ENEMS outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 FNSTISDAFLQSKMRNIFSGRLTAV------ELVDILDHYTKNCDMMVGNQALIQG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ------PGSLSHLIHLAAHPLGPSMLRLINEMARTSDMLC--RELPAA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 FHALQIEGVIVDQMEPAGAVVARASGLPFVSVACALPLAREPG--LPLAVMPPEYGTSDA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 LKKEKFDLILVDPNOMCGPVIAHLLGVKYAVFSTGLMYPABVGAPALAYVP-EFNSLLI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 ARERYTTSEK------IYDWLMRRHDRVLAHHACRMGLAPREKLHHCP--SPLAQ 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 DRANFLERMKNTGVYLISRIGVSFLVLPKYERING----KYNLLPAKSMYDLVHGSSLWM 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 LFRTIAKACEEVDAQLLLAHCGGL-----SATQAGELARGGDIQVVDFADQSAALSQ 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 SFGAGVKYLSEDIANKLAGALPQKVIWRFSGTKPKNL--GNNTKLIEWLPQNDLLGH 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 ISQLIPELDFPRKALPDCFHAVGPLRQPQGTPGSSTSYFPSPDKPRIPASIGTLQGHRYG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 LCTDV-ALEFPRPTLDWVYVGGILTKPAS------PLPEDLORWVSGAQEHGFVLV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 AQLT--ITHGGMNTVLDAIASRTPLLALPLAFDQPGVASRIVYHGIGKRASRFT-TSHAL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350 SNIRAFISHGGINSIFETMYHGVPVVGIPLFGDHYDTMTRVQAKGMGILLEMNTVTEGEL 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 VIAPP--FFSHVRALQNLAQELVARGHRVTFFQQHDCKALVTGSDIG-PQTVGLQTHP-- 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 IIVPPIMFESHLYIFKTLASALHERGH-----HTVLLLSEGRDIAPSNHYSLQRYPGI 76
                                                                                                                                                                                                                                                                                                                                                                                                                      Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
T -> S (IN REF. 2).
K -> E (IN REF. 2).
Y -> E (IN REF. 2).
H -> N (IN REF. 2).
H -> R (IN REF. 2).
H -> R (IN REF. 2).
H -> R (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B76F80A9B5326EE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GALACTOSYLTRANSFERASE.
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                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002213; UDP_gluco_trans.
                                                                                                                                                                         EMBL, X92123, CAA63091.1, EMBL, X92124, CAA63091.1, JOINED. EMBL, X92126, CAA63091.1, JOINED. EMBL, X92176, CAA63091.1, JOINED. EMBL, X92177, CAA63091.1, JOINED. EMBL, U48895, AACS3576.1, JOINED. EMBL, U48893, AACS3576.1, JOINED. EMBL, U48893, AACS3576.1, JOINED. EMBL, U48893, AACS3576.1, JOINED.
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335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94358923; PubMed=7521399;

MEDLINE=94358923; PubMed=7521399;

MEDLINE=94358923; PubMed=7521399;

MEDLINE=94358923; PubMed=7521399;

MEDLINE=94358923; PubMed=7521399;

MEDLINE=94358923; PubMed=7521399;

MEDLINE=94358923; PubMed=7521399;

MEDLINE=94358923; PubMed=7521399;

MEDLINE=94358923; PubMed=184;

MEDLINE=94358923; PubMed=184;

MEDLINE=94358923; PubMed=184;

MEDLINE=943184282; MEDLINE=94;

MEDLINE=943884; MEDLINE=94;

MERVOUS SYSTEM AND PRRIPHERAL NERVOUS SYSTEM

MERVOUS SYSTEM AND PRRIPHERAL NERVOUS SYSTEM

MERVOUS SYSTEM AND PRRIPHERAL NERVOUS SYSTEM

MERVOUS SYSTEM AND PRRIPHERAL NERVOUS SYSTEM

MERVOUS SYSTEM AND PRRIPHERAL DEPOSITION SYSTEM

MEDLINE=943884 SPECIFICITY: BRAIN, RESTRICTED TO THE OLIGODENDROCYTE-

CONTAINING CELL LAYERS OF CEREBRUM AND CEREBELLUM.
                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-REB-2003 (Rel. 41, Last annotation update)
2-hydroxyacylsphingosine 1-bet-galactosyltransferase precursor
(EC 2.4.1.45) (UDP-galactose-ceramide galactosyltransferase) (Ceramide UDP-galactosyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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POTENTIAL.

78 N.LINKED (GLCNAC. ..) (FOTENTIAL).

342 N.LINKED (GLCNAC. ..) (FOTENTIAL).

61126 MW, 260D7603170151BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     Schulte S., Stoffel W.; "Ceramide Uppgalactosyltransferase from myelinating rat brain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 164.5; DB 1; Length 541;
Pred. No. 3.1e-05;
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2-HYDROXYACYLSPHINGOSINE 1-BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                       purification, cloning, and expression.";
Proc. Natl. Acad. Sci. U.S.A. 90:10265-10269(1993).
: :: | | | : : | | 410 YDALVKVINNPSYRQRAÇKLSBIHKDQRGHP 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A48801; A48801.
InterPro; IPR002213; UDP_gluco_trans.
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94052143; PubMed=7694285;
Schulte S., Stoffel W.;
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-Wistar; Tissue-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L21698; AAA16108.1; -.
EMBL; U07683; AAA50212.1; -.
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                                                                                                       STANDARD;
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442
541 AA;
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Best Local Similarity
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SIGNAL
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186 DRMNF-----YERMKNIGVYLISRMGVSFLVLPK----YBRIMOKYNLLPAKS 229
                                                                                                                                                                          ------PGSLSHILHLAAHPLGPSMLRLINEMARTSDMLC--RELPAA 100
                                                                                                                                                                                                            77 FNSTISDAFLQSRÆRNIFSGRLTAV-----BLVDILDHYTKNCDMMYGNQALIQG 126
                                                                                                                                                                                                                                                                                   101 FHALQIEGVIVDQMEPAGAVVARASGLPFVSVACALPLNREPG--LPLAVMPFEYGTSDA 158
                                                                                                                                                                                                                                                                                                                           159 ARBRYTTSEKIYDWLMRRHDRVIAHHACRMGLA----PREKLHHCFSPLAQISQLIP--- 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 ------BLDFPRKALPDCFHAVGPLRQPQGTPGSSTSYFPSPDKPRIFA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 MYDLVHGSSLWMLCTDVALEFPRPTLPNVYYYGGILTKPAS-------PLPEDLQRWY 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 SIGTLOGHRYGLFRTIAKACEEVDAQLLLAHCGGL-----SATQAGELARGGDIQVV 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 DGAQEHGFVLVSFGAGVKYLSEDIANKLAGALGRLPQKVIWRFSGTKPKNL--GNNTKLI 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 DFADQSAALSQAQLT--ITHGGMNTVLDAIASRTPLLALPLAFDQPGVASRIVYHGIGKR 364
                                                                                         24 IIVPPIMFESHLYIFKTLASALHERGHHTVFL-----LSEGRDIDPSNHYSLQRYPGI 76
                                                       6 VIAPP--PFSHVRALQNIAQELVARGHRVTPFQQHDCKALVTGSDIG-PQTVGLQTHP-- 60
   Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
UDP-glucuronosyltransferase 1-1 precursor, microsomal (RC 2.4.1.17)
(UDP-GT) (UGT1*1) (UGT1-01) (UGT1-1) (UGT1A1) (B1).
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MEDLINE-95327065; PubMed=7603447;
Coffman B.L., Green M.D., King C.O., Tephly T.R.;
Cloning and stable expression of a cDNA encoding a rat liver UDP-
glucuronosyltransferase (UDP-glucuronosyltransferase 1.1) that
catalyzes the glucuronidation of opioids and bilirubin.";
Mol. Pharmacol. 47:1101-1105(1995).
      Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                365 ASRFT-TSHALARQIRSLLTNTDYPORMTKIQAALRLAGGTP 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        399 LEWNÍVTEGELYDALVKVINNPSYRORAOKLSEIHKDOPGHP 440
70; Mismatches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta-D-glucuronoside.
-!- SUBCELLULAR LOCATION: Microsomal.
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94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI TaxID=10116;
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Matches
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This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMB: outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensee.besb.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 ENVIAARVELGRSVFDQDPFLLRVVKTYNKVKRDSSMLLSGCSHLLHNAEFMASLEQSHF 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 KKAM--EIAEALGRIPOTVLMRYTG---TRPSNIAK--NTILVKWLPONDLLGHPKARA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 EKIYDWIAMRRHDRVIA---HHACRMGLAPREKLHHCFSPLAQISQLIPEL----- 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 ----DFPRKALPDCFHAVGPLR--QPQGTPGSSTSYF-PSPDKPRIFASLGTLQG---H 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 RYGLFRIIAKACEEVDAQLLLAHCGGLSATQAGELARGGDIQVVDFADQSAALS--QAQL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 TITHGGMNTVLDALASRTPLLALPLAFDQPGVASRIVYHGIGKRASRF-TTSHALARQIR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371 FITHSGSHGIYEGICMGVPMVMMPLFGDQMDNAKRMETRGAGVTLNVLEMTADDLENALK 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U20551; AAC52219.1; -.
EMBL; U3065; BAA07260.1; -.
PIR; 157961; 157961; 157961.
InterPro; IPR002213; UDP_gluco_trans.
Pfam; PF00201; UDFGT; 1.
PR051ER; PS00375; UDFGT; 1.
PR051ER; PS00375; UDFGT; 1.
PR051ER; PS00375; UDFGT; 1.
PR051ER; PS00375; UDFGT; 1.
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PR051ER; PS00375; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDFGT; UDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 EGVIVDQMRPAGAVVAEASGLPFVSVACALPLNREPGLPLAVMPPEYGTSDAARERYTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 DALLTDPFLPCGSIVAQYLSLPAVYFLNALPCSLDLEATOCPAPLSY----VPKSLSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 VIAPPFFSHVRALQNIAQELVARGHRVTFFQQHDCKALVTGSDIGFQTVGLQTHPPGSLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 7.3%; Score 162; DB 1; Length 535; Similarity 20.8%; Pred. No. 4.8e-05; Conservative 87; Mismatches 191; Indels 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                               Bvent=Alternative splicing; Named isoforms=1;
Comment=A number of isoforms are produced. The different
isozymes have adifferent N-terminal domain and a common
C-terminal domain of 245 residues;
                                                                                                                                                                                     Isoid=064550-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A -> D (IN REF. 2).
26B642FCA7DD4082 CRC64;
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493 509 P2O
89 N-1
297 297 N-1
435 435 N-1
253 AA, 59662 MM, 2
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-!- ALTERNATIVE PRODUCTS:
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RESULT 11 YF24 MYCTU 24 BLVARGHRVTFFQQHDCKALVTGSDIGF-QTVGLQTHPPGSL-----SHLLHLAAHPL 75

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Matches 108; Conservative 56; Mismatches 173; Indels 108; Gaps

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                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

KEDINE=98295937, PubMed=9634230,
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Cole S.T., Brosch R., Barkhill J., Garnier T., Churcher C., Harris D.,
A Gordon S.V. Elglmeier K., Gas S., Barry C.B. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Geniles S., Hamlin N., Holroyd S.,
A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Seeger K., Skelton S., Squares S.,
Rutter S., Seeger K., Skelton S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
T. Gocziphering the biology of Mycobacterium tuberculosis from the
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SPECIES=M. Dovis; STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=12788972;
MEDLINE=2709107; PubMed=12788972;
MEDLINE=2709107; PubMed=12788972;
Marris B., Altin R., Doggett J., Mayes R., Keating C., Simon S., Harris B., Altin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Colle S.T., Gordon S.V., Hewinson R.G.;
The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
:- SIMILARITY: STRONG, TO M.LEPRAE ML2348 AND M.TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=M tuberculosis, STRAIN=CDC 1551 / Oshkosh,
MEDELNB=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Bishai W., Jacobs W.R., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs N.R., Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tuberculist, Rvi524; -.
Tuberculist, Rvi524; -.
InterPro, IPR04276; Glyco trans 28.
Pfam, PR0303; Glyco transf 28, I.
Hypothetical protein; Complete proteome.
SEQUENCE 414 AA, 44361 MW; 5D3534G5173E2544 CRC64;
                                                                                                                                                                                                      Corynebacterineae, Mycobacteriaceae, Mycobacterium
                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein Rv1524/MY1575/MD1551.
RV1524 OR MT1575 OR MTCY19G3, 04C OR MB1551.
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             laboratory strains.";
J. Bacteriol. 184:5479-5490(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, Z77826, CAB01393.1, -.
EMBL, AE067024, AAK45842.1, -.
EMBL, BX248339, CAD96218.1; -.
    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BX248557,
PIR; D70723; D70723.
                                                                                                                                                                        Mycobacterium bovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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YP24 MYCTU
Q50583;
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7.1%; Score 158; DB 1; Length 414; 24.3%; Pred. No. 7.1e-05;

Query Match Best Local Similarity

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                                                       76 GPSMLRLINE-----MARTSDMLCRELPAAFHA-LQIEGVIVDQMEPAGAVVAEASG 126
                                                                                                                                              127 LPFVSV-ACALPLNREPGLPLAVMPFBYGTSDAARERYTTSEKIYDWLMRRHDRVIAHHA 185
                                                                                                                                                                                       127 IPLAALHFYPVRANGBIAPP-ARLP----APLVRSTITAIDWLY-WRWTK------- 170
                                                                                                  75 NP--IKLLRBAMAPVTBGWAELSAML---TPVAAGÄDLLLTGOIYQEVV---ANVAEHHG 126
                                                                                                                                                                                                                                    186 CRMGLAPREKLHHCFSPLAQISQLIPBLDFPRKALPD--------------------FFHA- 226
                                                                                                                                                                                                                                                                             171 ---GVEDAQR------RBIGLPKASTPAPRRMAVRGSLEIQAYDALCFPGL 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 -----VGPLRQPQGTPG-SSTSYPPSPDKPRIFASLGTLQ-GHRYGLFRTIAKAC 274
                                                                                                                                                                                                                                                                                                                                                                  213 AAEWGGRRPFVGALTMESATDADDEVASWIAADTPPIYPGFGSMPIGSLADRVAMISAAC 272
                                                                                                                                                                                                                                                                                                                                                                                                             275 BEVDAQLILLAHCGGLSATQAGELARGGDIQVVDFADQSAALSQAQLTITHGGMNTVLDAI 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                        273 AELGERALI--CSGPS--DATGIPOFDHVKVVRVVSHAAVFPTCRAVVHHGGAGTTAAGL 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    335 ASRIPLLALPLAFDQPGVASRIVYHGIGKRASRFT--TSHALARQIRSLLINIDYPQRMI 392
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
UDP-glucuronosyltransferase 2B8 precursor, microsomal (EC 2.4.1.17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor beta-D-glucuronoside.
-i- SUBCELLULAR LOCATION: Microsomal.
-i- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H4IIEC3 hepatoma cells.";
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: UDPGT is of major importance in the conjugation and subsequent elimination of potentially toxic xenobiotics and endogenous compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cohen H., Trus M., Benvenisty N., Reshef L.; A novel member of the UDPGT family is abundantly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       387 BIASRMIKPAASVTATADLLEDAAR 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 KIQAAL-RLAGGTPAAADIVEQAMR 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U27518; AAA86833.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
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Q62789;
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UGTF_CAEEL
ID UGTF_CAE
AC Q18081;
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                                                                                                                                                                                                                                                                                                                                                                                               104 LQIEGVIVDQMEPAGAVVAEASGLPFVSVACALPLNREPGL------PLAVM 149
                                                                                                                                                                                                                                                                                                                                                                                                                       144 SQFDVVLSDAVGPCGELIAEILQLPFV---YSLRPATAPGIBKYSAGQPFPPSYVPIILS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 GFSSONTFMERVENMICLLYFDSWFRSPPAKDWDPFFSBILGRPTTMVDTWKKAEIWLIR 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 -----PLPKEMEDFAQSSGEHGVWVFSLGSMIRNITQERANTIASALAQIPQKVFW 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284 AHCGGLSATQAGELARGGDIQVVDFADQSAALS--QAQLTITHGGMNTVLDAI-ASRTPL 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPEGKKPDT-----LGPNTRVFKWIPQNDLLGHPKTKAFVTHGGANGIYESIHYGIPPM 392
                                                                                                                                                                                                                                                                                                                            66 HLLHLAAHPLG-----BDALRLINEMARTSDMLCR-----BLPAAFHA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----EYGTSDAARE------RYTTSEKIYDWLMR 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 REDRVIAHERACRMGLAPREXLHHCFSPLAQISQLIPELDFPRKALPDCFHAVGPLRQPQG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 TPGSSTSYFPSPDKPRIFA-----SLGT-LQGHRYGLFRTIAKACEEVDAQLLL 283
                                                                                                                                                                                                                                                           6 VIAPPPFSHVRALQNLAQELVARGHRVTFPQQHDCKALVTGSDIGFQTVGLQTHPPGSLS 65
                                                                                                                                                                                                                                                                                          27 LVWPLEYSHWMNLKIILDELVORGHEVTVLRPSSSVSLDPKKASG---LVVETSPTTSNN 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               393 VGIPLFAEQRDNVAHRVAKGAAVSIDFHTMSSSDLINALKAVINNPSYKGKVMWLSA 449
                                                  Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal; Multigene family; Microsome.

SIGNAL

17

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341 LALPLAFDQPGVASRIVYHGIGKRASRFTTSHA-LARQIRSLLTNTDYPQRMTKIQA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Olfactory organ;
MEDLINE-99289328; PubMed=10359671;
MEDLINE-99289328; PubMed=10359671;
Medlineshky G.A., Casaidy A.J., Sales M., Pratt N., Burchell B.,
"Cloning and characterization of a novel human olfactory UDP-
glucuronosyltransferase.";
Biochem. J. 340:837-843(1999).
-: FUNCTION: UDPGT is of major importance in the conjugation and
subsequent elimination of potentially toxic xenobictics and
endogenous compounds. This isoform is active on odorants and
seems to be involved in olfaction; it could help clear libophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
UDP-Glucuronosyltransferase 2Al precursor, microsomal (BC 2.4.1.17)
UGP-2Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                    316 N-LINKED (GECNAC, . .) (POTENTIAL) 60089 MW; 532519950C6CAEDE CRC64;
                                                                                                                                                                                        7.0%; Score 156; DB 1; Length 530;
19.7%; Pred. No. 0.00014;
tive 72; Mismatches 171; Indels 140;
                                                                                                       UDP-GLUCURONOSYLTRANSFERASE 2B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., CHARACTERIZATION, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                527 AA
                                                                                                                       POTENTIAL.
InterPro, IPR002213; UDP_gluco_trans.
Pfam; PF00201; UDPGT; 1.
PROSITE; PS00375; UDPGT; FALSE_NEG.
                                                                                                                                                                                                        Local Similarity 19.7
Les 94; Conservative
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                                                                                                       530
516
316
                                                                                                                       496 5
316 3
530 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 SY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 PF-
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                                                                                                     CHAIN
TRANSMEM
CARBOHYD
                                                                                                                                                        SEQUENCE
                                                                                                                                                                                          Query Match
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Q9Y4X1;
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DA1 HUMAN
                                                                                                                                                                                                                           Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseesisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 BIWLIRTYWDPBFPRPYLPN-FBFVGGLHCKPAKPLPKEMBBFIQSSGKNGVVVFSLGSM 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAFHALQIEGVIVDQMEPAGAVVAEASGLPF-----VSVACA---LPLNREPGL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 PLAVMPFBYGTSDAARE--RYTTSEKIYDWLMRRHDRVIAHHACRWGLAPREKLHHCFSP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 ---LOGHRYGLFRTLAKACEEVDAQLLLAHCGGLSATQAGELARGGDIQVVDFADQSAAL 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 S--QAQLTITHGGMNTVLDAIASRTPLLALPLAFDQPGVASRIVYHGIGKRASRFT-TSH 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 VKNLTBEKANL---LASALAQIPQKVLWRYKGKKPAT-----LGNNTQLFDWIPQNDLE 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 GHPKTKAFITHGGTNGIYEAIYHGVPMVGVPMFADQPDNIAHMKAKGAAVEVNIATMTSV 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------FFOOHDCKALV 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 604716; -.

MIM; 604716; -.

GO; GO:0008152; P:metabolism; TAS.

GO; GO:0009593; P:perception of chemical substance; TAS.

InterPro; IPR002213; UDP_gluco_trans.
Pfam; PF00201; UDPGT; 1.

PROSITE; PS00375; UDPGT; 1.

Transferase; Glycosyltransferase; Glycoprotein; Transmembrane; Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                       = UDP + acceptor
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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odorant molecules from the sensory epithelium.
-!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptants of a glucurons of a glucurons of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a glucular of a gluc
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20.9%; Pred. No. 0.00018;
ive 78; Mismatches 196; Indels
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313 313 N-
347 347 N-
527 AA; 59872 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ006054; CAB41974.1; -. Genew; HGNC:12542; UGT2A1.
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9 4 4 9 -
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                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 PPGSL-----SHLLHLAAHPLGPSMLRLINEMARTSDMLCRELPAAFHALQIEGVIVD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 LSGDVFQQSSIMSKIFNTDSDPYQDBYTNMCEEMVTNKELIBKLKKEKFDA----YFGE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 EKIYDWLMRR-----HDRVIAHHACRMGLAPREKLHHCFSPLAQISQLI-----PELDFP 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 AKNPVLQMAHIRDEYRDVVLTNDMFKKNFGSD----FPCVEFLAKTSDLIFVSTDELLEIQ 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---HRYGLFRTJAKACEEVDAQLLLAHCGGLSATQAGELARG-GDIQVVDFADQSAALSQ 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QMEPAGAVVAEASGLP--FVSVACALPLNREPGL----PLAVMPFEYGTSDAARERYTTS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 APTLSNVVH-IGGLGSEGGGLDEKFVKIMEKGKGVILFSLGTIANTTNLPPTIMENIM 297
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δ
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                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; istrovall.

Pfam: PF00201; UDGGT; 1.

PROSITE; PS00375; UDGGT; 1.

Hypothetical protein; Transferase; Glycosyltransferase; Glycoprotein; Hypothetical protein; Transmembrane; Signal; Multigene family.

Transmembrane; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                      Caenorhabditis elegans.
Sukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                 nitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CANALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor
beta-D-glucuronoside.
SIMILARITY: Belongs to the UDP-glycosyltransferase family.
01-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative UDP-glucuronosyltransferase UGT15 precursor (EC 2.4.1.17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 RKALPDCFHAVGPLRQPQGTPGSSTSYFPSPDKPR--IFASLGTLQG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                          Gattung S.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7A469450EFCDBB3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.7%; Score 150.5; DB 1
20.4%; Pred. No. 0.00035;
                                                                                                                                                                                                                                                                                                                                                                                        WormPep; C18C4.3; CE27363.
InterPro; IPR002213; UDP_gluco_trans.
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37
284
492
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505 AA;
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                                                                                                                                  SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                            JGTIS OR C18C4.3
                                                                                                                                                                                                         Waterston R.;
Submitted (OCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91;
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Best Local S
Matches 91
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                                                                        318 AQLT--ITHGGMNTVLDAIASRTPLLALPLAFDQPGVASRIVYHGIGKRASRF---TTSH 372
-----RRSFDLAEGLSNVLVVDWVPQTAVLAH 343
                                                                                                                     Gong Q.H., Cho J.W., Huang T., Potter C., Gholami N., Basu N.K., Kubota S., Carvalho S., Pennington M.W., Owens I.S., Popescu N.C.; "Thirteen UDP-glucuronosyltransferase genes are encoded at the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gholami N.; (UGT1A9) gene isozyme exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: UDPGT is of major importance in the conjugation and subsequent elimination of potentially toxic xenobiotics and endogenous compounds. This isoform has specificity for phenols.

-!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor beta-D-glucuronaide.

-!- SUBCELLULAR LOCATION: Microsomal.

-!- ALTERNATIVE PRODUCTS:

EVENT.=ALTERNATIVE PRODUCTS:

EVENT.=Alternative splicing; Named isoforms=1;

Comment=A number of isoforms may be produced. Isoforms have a different W-terminal domain and a common C-terminal domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       060656; Q9HAXO; 10-0CT-2003 (Rel. 42, Created) 10-0CT-2003 (Rel. 42, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) UDP-glucuronosyltransferase 1-9 precursor, microsomal (EC 2.4.1.17) (UDP-glucuronosyltransferase 1A9) (UDPCT) (UGT1*9) (UGT1-9) (UGT1-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISOId-060656-1; Sequence-Displayed;
-!- TISSUE SPECIFICITY: Liver.
-!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ciotti M., Potter C., Owens I.S.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           530 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [3]
SEQUENCE OF 1-285 FROM N.A.
OWENS I.S., Gong Q., Cho J.W., Potter C., '
"Human phenol UDP-glucuronosyltransferase
                                                                                                                                                                                                                        373 ALARQIRSLLTNTDYPORMTKIQAALR 399
                                                                                                                                                                                                                                                                  |: :| | :: :| 404 AIEGAIKEILVNPTYOEKANRLKKUMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=21327373; PubMed=11434514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pharmacogenetics 11:357-368(2001)
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       298 KITQKFKDYEFIIKV-DKFD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF297091; AAG29816.1;
Genew; HGNC:12541; UGT1A9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UGT1 gene complex locus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UGT1A9 OR UGT1 OR GNT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 residues;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---PAAFHALOIBGVIVDOMEPAGAVVAEASGLPFVSVA-------CALPLNRE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 PGLPLAVMPFEYGTSDAARERYTTSEKIYDWIMRRHDRVIAHHACRMGLAPREKLHHCFS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GSSTSYFPSPDKPRIFASIGTLQGHRYGLFRTIAKACBEVDAQLLLAHCGGL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 HGIVVFSLGSMVSEIPEKKAMALADALG-------KIPQTVLWRYTG-- 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 SATOAGELARGEDIQVVDFADOSAALS--OAQLTITHGGMNTVLDAIASRTPLLALPLAF 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 VIAPPPFSHVRALQNLAQELVARGHRVTFFQQHDCKALVTGSDIGFQ----TVGLQTHP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 LVVPMDGSFWFTMRSVVEKLIIRGHEV------VVVMPBVSWQLGRSLNCTVKTY- 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PGSLSHLIH------LAAHPLGPSMLRLINEMARTS-----DML---CREL----- 97
CO. GO.0008152; P:metabolism; TAS.

CO. GO.0008152; P:metabolism; TAS.

PROSITE: PEO02013; UDP_Gluco_trans.

PROSITE: PSO0375; UDPGT; 1.

PROSITE: PSO0375; UDPGT; 1.

Transferace; Glycosyltransferace; Glycoprotein; Transmembrane; Signal; Multigene family; Microsome; Alternative splicing.

SIGNAL

CHAIN 25 SJO UDP-GLUCURONOSYLTRANSFERASE 1-9.

TRANSNEM 488 504 POTENTIAL.

CARBOHYD 71 71 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 392 292 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 344 344 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 344 344 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 344 344 N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.7%; Score 150.5; DB 1; Length 530;
Best Local Similarity 19.4%; Pred. No. 0.00037;
Matches 91; Conservative 81; Mismatches 163; Indels 135; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DQPGVASRIVYHGIGKRASRP-TTSHALARQIRSLLTNTDYPQRMTKIQA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 PLAQ-----ISQLIPELDPPRKALPDCFHAVGPLRQPQGTP
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bb time : 10.264 secs

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.; Search time 28.6159 Seconds (without alignments) 3180.293 Million cell updates/sec
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2231
1 MSHFAVIAPPFFSHVRALQN.......EQAMRTCQPVLSGQDYATAL
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| cgn2_6/prodata/2/pubpaa/USO7_PUBCOMB.pep:*
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| cgn2_6/prodata/2/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*
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| cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*
                       version 5.1.6
- 2004 Compugen Ltd.
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                                                                                                                                                   2004, 14:51:24
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                         GenCore (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 28, Appli Sequence 14886, A Sequence 14886, A Sequence 4, Appli Sequence 4, Appli Sequence 522, Appli Sequence 522, Appli Sequence 522, Appli Sequence 522, Appli Sequence 522, Appli Sequence 522, Appli Sequence 522, Appli Sequence 522, Appli Sequence 522, Appli Sequence 522, Appli Sequence 522, Appli Sequence 522, Appli Sequence 522, Appli Description US-09-941-947A-28 US-10-1218-118-4 US-10-156-761-14886 US-09-740-020-4 US-09-962-67-68-2 US-09-962-65-67-68-2 US-09-98-52-2 US-10-175-737-522 US-10-175-737-522 US-10-175-738-522 US-10-175-738-522 US-10-175-738-522 US-10-175-738-522 US-10-175-738-522 US-10-175-738-522 四 Length Query Match 1 2231 2231 2531 247 167 167 167 167 167 167 167 ssult 8

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US-10-176-757-522 US-10-176-913-522 US-10-180-552-522 US-10-180-552-522 US-10-180-552-522 US-10-173-700-552 US-10-174-579-522 US-10-174-579-522 US-10-174-579-522 US-10-174-579-522 US-10-176-488-522 US-10-176-488-522 US-10-176-488-522 US-10-176-987-522 US-10-176-987-522 US-10-176-987-522 US-10-176-987-522 US-10-176-987-522 US-10-176-992-522 US-10-176-992-522 US-10-176-992-522 US-10-176-992-522 US-10-176-992-522 US-10-176-992-522 US-10-176-992-522 US-10-176-992-522 US-10-176-992-522 US-10-178-695-522 US-10-178-695-522 US-10-173-695-522 US-10-174-585-522 US-10-174-585-522	ALIGNMENTS 1947A a C. PRODUCTION FROM A 09/941,947A 9,907 9,858	100.0%; Score 2231; DB 10; 100.0%; Pred. No. 4.4e-218; ive 0; Mismatches 0; SHVRALQNIAQELVARGHRVTFFQQHDCI
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361 IGKRASRFTTSHALARQIRSLLINTDYPQRMTKIQAALRLAGGTPAAADIVBQANRTCQP 420
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                                                                   GDIQVVDFADQSAALSQAQLTITHGGMNTVLDAIASRTPLLALPLAFDQPGVASRIVYHG
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                                           GDIQVVDFADQSAALSQAQLTITHGGMNTVLDAIASRTPLLALPLAFDQFGVASRIVYHG
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Sequence 14886, Application US/10156761
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: SHIRAW, HINOSHI
APPLICANT: SHIRAW, HINOSHI
APPLICANT: SHIRAW, HORIKAWA, HINOSHI
APPLICANT: SHIRAW, HORIKAWA, HINOSHI
APPLICANT: SHIRAW, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TOSHIYUKI
APPLICANT: SHIRA, TOSHIYUKI
APPLICANT: ALAYORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PLILING DATE: 2001-05-30
PRIOR PLILING DATE: 2001-05-30
PRIOR PLILING DATE: 2001-06-30
PRIOR PLILING DATE: 2001-06-30
PRIOR PLILING DATE: 2001-08-02
SRQ ID NOS: 15109
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Matches 115; Conservative
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                                                                                            IAHHACRMGLAPREKLHHCFSPLAQISQLIPELDPPRKALPDCFHAVGPLRQPQGTPGSS
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Sequence 4, Application US/10218118
Publication No. US20030148319A1
GENERAL INPORMATION:
APPLICANT: Brzostowicz, Patricia
APPLICANT: Rovelowicz, Patricia
APPLICANT: Rovelowicz, Patricia
APPLICANT: Cheng, Qiong
TITLE OF INVENTION: Genes Encoding Carotenoid Compounds
TITLE OF INVENTION: Genes Encoding Carotenoid CURRENT APPLICATION NUMBER: 60/312,646
PRIOR APPLICATION NUMBER: 60/312,646
PRIOR PILING DATE: 2001-08-15
RUMBER: Microsoft Office 97
SOFTWARE: Microsoft Office 97
LENGTHIA. A.A.
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100.0%; Pred. No. 4.4e-218;
tive 0; Mismatches 0;
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ORGANISM: Pantoea stewartii
S-10-218-118-4
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Matches 431; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 HFAVIAPPFFSHVRALQNLAQELVARGHRVTFFQQHDCKALVTGSDI--
                                                                                                                                                                                                                                            APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: SHIRBA, JUN
APPLICANT: BSHIRAMA, JUN
APPLICANT: BSTAKAI, YOSHILALICANT: BAPLICANT: BAPLICANT: BARAKI, YOSHILALICANT: BARAKI, YOSHILALICANT: HATTORI, MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
RIOR PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR PRIOR DATE: 2001-06-30
SEQ ID NO 8483
LENGTH: 412
                                                                                                                                                                        Sequence 8483, Application US/10156761
Publication No. US200301190:8A1
GENERAL INFORMATION:
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400 LAGGTPAAADIVE 412
                           |||::||||:|
371 AAGGSESAADRLE 383
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3SULT 5 3-09-740-029-4 Sequence 4, Application US/09740029

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 SDAARERYTTSEKIYDWIM-RRHDRVIAHH-------ACR-MGLAPREK 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312 SAALS--QAQLTITHGGMNTVLDALASRTPLLALPLAFDQPGVASRIVYHGIGKRAS-RF 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 LEHCESPLAQISQLIPELDPPRKALPDCFHAVGPL--RQPQGTPGSSTSYPPSP--DKPR 251
                                                                                                                                                                                                                                                                                                                                                                                                                             13 SHVRALQNLAQELVARGHRVTFFQQHDCKALVTGSDIGFQTVGLQTHPP-----GSLSHL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SHWINLKVILEBLOLRGHEITVLVPSP-SLLLDHTKIPFNVEVLQLQVTKETLMBELNTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 TSGLTDNMSFVQRLKNWLLYLMNDMMFSHFMLSEWDEYYSKVLGRRTTICEIMGKAEMWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 IFASLGTLOGHRYGLFRTIAKACEBVDAQLLLAHCGGLSATQAGBLARGGDIQVVDFADQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09962678

Sequence 2, Application US/09962678

Patent No. US2002015549941

GENERAL INFORMATION:

APPLICANT: Lebly, Kavin R.

TITLE OF INVENTION: AND UDP-GLUCURONOSYL

TITLE OF INVENTION: AND UDP-GLYCOSYL TRANSFERASE AND USES THEREOF

FILE REPERENCE: 1044-804-004-01

CURRENT FILING DAIE: 2001-09-25

PRIOR FILING DAIE: 2000-09-25

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

ILENGTH: S27

TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Patent No. US20020082194A1

GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al

TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING

TITLE OF INVENTION: PROTEINS, NICLEIC ACID MOLECULES ENCODING HUMAN

TITLE OF INVENTION: AND USES THEREOF

FILE REPREMENT AND USES THEREOF

FILE REPREMENT SCHOOS28

CURRENT APPLICATION NUMBER: US/09/740,029

WUMBER OF SEQ ID NOS: 4

SOCTHARD: FASISEQ FOR Windows Version 4.0

SEQ ID NO 4.
                                                                                                                                                                                                                                                                                                                                                                                            98;
                                                                                                                                                                                                                                                                                                                                                  Length 477;
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7.9%; Score 177; DB 9; Length 477
Best Local Similarity 21.5%; Pred. No. 6.1e-09;
Matches 96; Conservative 75; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 ITSHALARQIRSLLTWIDYPORMTKI 394
                                                                                                                                                                                                                                                                                              ; ORGANISM: Oryctolagus cuniculus
US-09-740-029-4
                                                                                                                                                                                                                                                         477
                                                                                                                                                                                                                                                                                TYPE: PRT
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                                                                                       21;
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                                                                                                                                                                                                                                86 ENEIFVDLALNVLPGLSTWQSVIKLNDFFVEIRGTLRYMCESFIYNQTLMKKLQETNYDV 145
                                                                                                                                                                                                                                                                                 109 VIVDOMEPAGAVVAEASGIPFV---SVACALPINREPG---LPLAVMPFEY-GTSDAARE 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                      180 VIAHHACRMGLAPREKLHHCFSPLAQISQLIPELDFPRKALPDCFHAVGPL--RQPQGTP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 GSSTSYFPSPDKPRIFA-SLGTL-QGHRYGLFRTIAKACBEVDAQLLLAHCGGLSATQAG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      288 KEMENFVQSSGEDGIVVFSLGSLFONVTEEKANIİASALAQIPQKVLWRYKĞKKPST--- 344
                                                                                                                                                    :: | | : | : | | | :: 27 LVWPCDMSHWIAVYVILEBLIVRGHEVTVIL-THSKPSKIDYRKPSALKFEVVHMPQDRTE 85
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                                                                                                                            6 VIAPPFPSHVRALQNLAQELVARGHRVTFPQOHDCKALV---TGSDIGFQTVGLQTHPPG
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                                                                                         Indels 140;
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                                                     Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 2434655CD1
US-09-981-353-166
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Sequence 166, Application US/09981353
Satent No. US20020160382A1
GENERAL INFORMATION:
APPLICANT: Lasek, Amy W.
TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER FILE REPERVE: PA-0038 US
CURRENT PRILING DATE: 2001-10-11
CURRENT FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
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7.5%; Score 167; DB 9; Lv
Best Local Similarity 20.8%; Pred. No. 7.4e-08;
Matches 99; Conservative 79; Mismatches 159;
                                                7.5%; Score 167; DB 9; I
20.8%; Pred. No. 7.4e-08;
tive 79; Mismatches 159;
                                                       Query Match
Best Local Similarity 20.8
Matches 99; Conservative
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ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
IS-09-962-678-2
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: BCREETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P9430RACI
CURRENT PILING DATE: 2002-01-15
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
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PRIOR FILING DATE: 1997-10-28
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PRIOR PLING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR PLING DATE: 1997-10-28
PRIOR PLING DATE: 1997-10-28
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PRIOR PLING DATE: 1997-10-28
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PRIOR PLING DATE: 1997-10-28
PRIOR PLING DATE: 1997-10-28
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                                                                                                                                                                                                                                                                                                                                                                238 GSSTSYFPSPDKPRIFA-SLGTL-QGHRYGLFRIIAKACEEVDAQLLLAHCGGLSATQAG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 BLARGGDIOVVDFADQSAALS--QAQLTITHGGMATVLDAIASRTPLLALPLAFDQ---- 349
                                                                                                                                                                                                                                                                                                                                                                                                                        288 KEMENFVQSSGEDGIVVFSLGSLFQNVTEEKANIIASALAQIPQKVLWRYKGKKPST--- 344
109 VIVDOMEPAGAVVAEASGLPPV---SVACALPLNREPG---LPLAVMPFEY-GTSDAARE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 -----POPEFPOPYOPN - PEFVGGLHCKPAKALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 -----PGVASRIVYHGIGKRASRFTTSHALARQIRSLLTNTDYPQRMTKIQAALRLA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         402 AHMKAKGAAVEINF-----KTWISEDLIRALRIVIIDSSYKEN-----AMRLS 444
                                          146 MLIDPVIPCGDLWAELLAVPEVLTLRISVGGNWERSCGKLPAPLSYVPVPMTGLTD---
                                                                                                                            162 RYTTSEKI -----YD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 522, Application US/10052586
Publication No. US20020127584A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-10-31
APPLICATION NUMBER: 60/064103
FILING DATE: 1997-10-31
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K.
Wood, William I.
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PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/06412
PRIOR PLING DATE: 1997-11-13
PRIOR PLING DATE: 1997-11-20
PRIOR PLING DATE: 1997-11-20
PRIOR APPLICATION NUMBER: 60/06472
PRIOR PLING DATE: 1997-11-20
PRIOR PLING DATE: 1997-11-21
PRIOR PLING DATE: 1997-12-11
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PRIOR PLING DATE: 1997-12-18
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PRIOR PLING DATE: 1998-03-10
PRIOR PLING DATE: 1998-03-10
PRIOR PRING APPLICATION NUMBER: 60/07763
PRIOR PLING DATE: 1998-03-10
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PRIOR FILING DATE: 1998-05-17
PRIOR APPLICATION WUMBER: 60/085579
PRIOR APPLICATION WUMBER: 60/085580
PRIOR APPLICATION WUMBER: 60/085581
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
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, ORGANISM: Homo Sapien
US-10-174-590-522
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin L.
APPLICANT: Pan, James
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin I.
APPLICANT: Zhang, Zemin I.
APPLICANT: Zhang, Zemin I.
APPLICANT: Zhang, Zemin I.
APPLICANT: Zhang, Zemin I.
APPLICANT: APPLICANT: ALIBER I.
FILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1642
CURRENT FILLING DATE: 2002-06-18
CURRENT FILLING DATE: 2002-06-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 VEVDOMEPAGAVVAEASGLPFV---SVACALPLNREPG---LPLAVMPFEY-GTSDAARE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 RYTTSEKI-----WIMRRHDR 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 KEMENFVQSSGEDGIVVFSLGSLFQNVTEEKANIIASALAQIPQKVLWRYKGKKPST--- 344
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                                                                                                                                                                                                                                                                                                                                                                                                     350 -----PGVASRIVYHGIGKRASRFTTSHALARQIRSLLTNTDYPQRMTKIQAALRLA 401
                                                                                                                                                                                                                                                        ch 7.5%; Score 167; DB 13; Length 527; Similarity 20.8%; Pred. No. 7.4e-08; 99; Conservative 79; Mismatches 159; Indels 140;
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NUMBER OF SEQ ID NOS: 612
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08959
PRIOR FILING DATE: 1998-06-17
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LENGTH: 527
TYPE: PRT
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Best Local S
Matches 99
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPREDICE: P943-9016120-4
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT PILING DATE: 2002-06-21
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                                                     Indels 140;
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7.5%; Score 167; DB 14; Length 527;
Best Local Similarity 20.8%; Pred. No. 7.4e-08;
Matches 99; Conservative 79; Mismatches 159; Indels 14
Length 527;
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 522
LENGTH: 527
7.5%; Score 167; DB 14;
20.8%; Pred. No. 7.4e-08;
tive 79; Mismatches 159;
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APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
                              l Similarity 20.8
99; Conservative
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US-10-176-758-522
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APPLICANT:
APPLICANT:
     Query Match
Best Local Si
Matches 99,
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202 RAFFLERVKNSMLSVLFHFWIQDYDYHFWERFYSKALGRPTTLCBTVGKAEIWLIRTY-- 259
                                                                                                                                                                                                                                              ---WLMRRHDR 179
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                    109 VIVIXMEPAGAVVAEASGLPFV---SVACALPIAREPG---LPLAVMPFEY-GISDAARE 161
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                                                146 MEIDPVIPCGDLMAELLAVPFVLTLRISVGGNMERSCGKLPAPLSYVPVPMTGLTD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 -----PGVASRIVYHGIGKRASRFTTSHALARQIRSLLTNTDYPQRMTKIQAALRLA 401
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APPLICANT: Zhang,Zemin
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERBACE: P94.5071LC7
CURRENT APPLICATION NUMBER: US/10/173,706
CURRENT APPLICATION NUMBER: 2002-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 SLSHLIHLAAHPI-----GPSMLRIIN---EMARTSDMLC-----RELPAAFHALQIEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 140;
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SEQ ID NO 522
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20.8%; Pred. No. 7.4e-08;
tive 79; Mismatches 159;
                                                                                                                      RYTTSEKI------YD----
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Publication No. US20030022293A1
GENERAL INFORMATION:
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
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, ORGANISM: Homo Sapien
US-10-173-706-522
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Matches 99; Conserv
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US-10-173-706-522
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APPLICANT:
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APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Mod, William I.
APPLICANT: Mod, William I.
APPLICANT: Mod, William I.
APPLICANT: ALANG, Zemin
TITLE OF INVENTION: SCHEETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 19430R.C50
CURRENT APPLICATION NUMBER: US/10/175,737
CURRENT PILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 522
LENGTE: 527
                                                                                                                                                                                                                                                                                                                                                                                                                        238 GSSTSYFPSPDKPRIFA-SLGTL-QGHRYGLFRTIAKACEEVDAQLLLAHCGGLSATQAG 295
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                                                                                                                           146 MIJDPVIPCGDLMAELLAVPPVLTLRISVGGNMERSCGKLPAPLSYVPVPMTGLTD--- 201
                                                                                                                                                                                                                                                                                       RYTTSEKI-----WLAMRHUR 179
                                                                                                                                                                                                                                                                                                                                      202 RMTFLERVKASMLSVLFHFWIQDYDYHFWEEFYSKALGRPTTLCETVGKAEIWLIRTY-- 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 ELARGGDIQVVDFADQSAALS--QAQLTITHGGMNTVLDAIASRTPLLALPLAFDQ---- 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 KEMENFVQSSGEDGIVVPSLGSLFÖNVTEEKANIIASALAQIPQKVLWRYKGKKPST--- 344
                            VIAPPPFSHVRALQNLAQELVARGHRVTFFQQHDCKALV---TGSDIGFQTVGLQTHPPG 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 522, Application US/10175737
Publication No. US20030013153A1
GENERAL INFORMATION:
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Godowski, Paul J.
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Best Local Similarity 20.8'
Matches 99; Conservative
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ORGANISM: Homo Sapien
S-10-175-737-522
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S-10-175-737-522
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APPLICANT:
APPLICANT:
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238 GSSTSYFPSPDKPRIFA-SLGTL-QGHRYGLFRTIAKACBEVDAQLLLAAHCGGLSATQAG 295
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CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.5%; Score 167; DB 14;
20.8%; Pred. No. 7.4e-08;
tive 79; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 522, Application US/10175752 Publication No. US20030022295A1 GENERAL INFORMATION:
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Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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; ORGANISM: Homo Sapien
US-10-175-752-522
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Best Local Similarity
Matches 99; Conserv
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                                                                                                                                        238 GSSTSYFPSPDKPRIFA-SLGTL-QGHRYGLFRTIAKACEEVDAQLLLAHCGGLSATQAG 295
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             202 RMTFLERVKNSMLSVLFHFWIQDYDYHFWEEFYSKALGRPTTLCETVGKAEIWLIRTY-- 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  402 AHMKAKGAAVEINF------KTMTSEDLIRALRTVITDSSYKEN-----AMRLS 444
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APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Paul June
APPLICANT: Paul June
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P9430NIC45
CURRENT APPLICATION NUMBER: US/10/175,738
CURRENT FILING DATE: 2002-06-19
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                                                                              180 VIAHHACRMGLAPREKLHHCFSPLAQISQLIPBLDFPRKALPDCFHAVGPL--RQPQGTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 522, Application US/10175738
Publication No. US20030022294A1
GENERAL INFORMATION:
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Goddard, Audrey
Godowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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; ORGANISM: Homo Sapien
JS-10-175-738-522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RYTTSEKI ---
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APPLICANT: GodOwski, Paul J.
APPLICANT: GoLOWSki, Paul J.
APPLICANT: GoLOWSki, Paul J.
APPLICANT: Pau, James
APPLICANT: Pau, James
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVERTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVERTION: SECRETED AND TRANSMEMBRANE
FILE REFERENCE: P3430R1C70
CURRENT APPLICATION NUMBER: US/10/176,482
CURRENT APPLICATION NUMBER: US/200-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
LENGTH: 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 ELARGGDIQVVDFADQSAALS--QAQLTITHGGWNTVLDAJASRTPLLALPLARFDQ---- 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 SLSHILHLAAHPL-----GPSMIRLIN---EMARTSDMLC-----RELPAAFHALQIEG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 VIVDOMEPAGAVVAEASGLPFV---SVACALPINREPG---LPLAVMPFEY-GTSDAARE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 MIIDPVIFCGDLWABILAVPFVLTLRISVGGNWERSCGKLPAPLSYVPVPWHTGLTD---- 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----WLWRRHDR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 VIAHHACRMGLAPREKLHHCFSPLAQISQLIPELDFPRKALPDCFHAVGPL--RQPQGTP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 GSSTSYFPSPDKPRIFA-SIGTL-QGHRYGLFRTIAKACEEVDAQLLLAHCGGLSATQAG 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345 ---LGANTRLYDWIPQNDLLGHPKTKARITHGGANGIYEAIYHGVPANGVPIFGDQLDNI 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 VIAPPFFSHVRALONLAQELVARGHRVTFFQQHDCKALV---TGSDIGFQTVGLQTHPPG 62
                                     402 AHWXAKGAAVIINF-----KTWISEDLIRALRIVITDSSYKEN-----AMRLS 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 -----PGVASRIVYHGIGKRASRFITSHALARQIRSLLINTDYPQRWTKIQAALRLA 401
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350 -----PGVASRIVYHGIGKRASRFTTSHALARQIRSLLTNTDYPQRWTKIQAALRLA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Pest Local Similarity 20.8%; Pred. No. 7.4e-08;
Matches 99; Conservative 79; Mismatches 159; Indels 140; Gaps
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                                                                                                                                                                                                   Sequence 522, Application US/10176482
Publication No. US20030022296A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     Desnoyers, Luc
Goddard, Audrey
                                                                                                                                                                                                                                                                                          APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo Sapien
3-10-176-482-522
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3-10-176-482-522
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APPLICANT:
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:arch completed: February 29, 2004, 15:27:58
ib time : 32.6159 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.		February 29, 2004, 14:34:14; Search time 11.9967 Seconds (without alignments) 3455.835 Million cell updates/sec	
GenCore version 5.1.6 c) 1993 - 2004 Compuç	sw model	14:34:14 ; (u) 34	
GenCor (c) 199	using	2004,	7A-28
Copyright	1 protein - protein search, using sw model	February 29,	US-09-941-947A-28
	4 protein	ın on:	itle:

sylect score: 2231
1 MSHFAVIAPPFFSHVRALQN........EQAMRTCQPVLSGQDYATAL 431 BLOSUM62 Gapop 10.0 , Gapext 0.5 coring table:

283366 seqs, 96191526 residues sarched: 283366 stal number of hits satisfying chosen parameters:

ost-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries inimum DB seq length: 0 iximum DB seq length: 2000000000

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* tabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	protein -		zeaxanthin glucosy	zeaxanthin glucosy	probable glycosyl	glycosyltransferas	glycosyltransferas	macrolide glycosyl	probable glycosylt	macrolide glycosyl	glycosyl transfera	zeaxanthin glucosy	2-hydroxyacylsphin	probable glycosyl	probable transfera	hypothetical prote	flavonol 3-0-gluco	2-hydroxyacylsphin	UDP-glucuronosyltr			hypothetical prote	probable transfera			flavonol 3-0-giuco	probable glycosyl	P glucuronosyltr	glucuronosyltransi
	ĕ	crtX	ģ	265	zeg	pro	91,	91,	mac	pro	mag	9]	269	2-7	ď	pr	Ę.	ΕΊ	2-1	Ē	gJı	5	Ę,	ŭ	mak	ŭ	£1.	ŭ	ġ.	Ę
	ы	\$52583	B37802	S52980	S74500	T37104	S33184	T51110	C69851	F75587	90669H	JS0636	A46292	JC5423	C97234	B70878	T03890	XUBHFG		872936	157961		-	D70723	A6978	•	S0832	AB024	JC565	S17512
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	Length	431	431	413	419	407	430	424	392	418	287	418	54	541	407	388	611	455	541	392	535	449	533	414	381	428	473	395	530	. 530
01 0	Query Match	80.4	80.2	45.7	25.0	11.7	30.2	7.6	9.1	ω 6.	æ.	8.1	8.1	7.9	7.8	7.7	7.6	7.5	7.4	7.4	7.3	7.2	7.2	7.1		•		9.9	•	9.9
	Score	1794	1790	1018.5	558.5	262	228.5	217	204	198.5	195.5	181.5	180	175.5	175	172	168.5	167	164.5	164	162	160.5	160	158	154.5	149	148.5	147.5	147.5	146.5
	esult No.		7	٣	4	Ŋ	vo	7	ထ	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	flavonor 3-0-gruco	CONTR-O-C TORONDIT	glucuronosyltranst	probable glycosylt	glucuronosyltransf	glucuronosyltransf	glycosyltransferas	hypothetical prote	glucuronosyltransi	probable glycosyl		hypothetical prote	hypothetical prote	glucuronosyltransf	hypothetical prote	
T23893	S01037	SULUSZ	S15089	A97146	A48633	A35343	T44860	T34458	A39092	T46519	T24309	T27582	F87565	807390	T33980	
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745	471	7 / 5	527	398	530	531	408	533	533	382	535	532	361	530	531	
6.0	9 9	6.4	6.3	6.2	6.2	6.2	6.2	6.2	6.1	6.1	6.1	6.1	6.0	0.9	6.0	
146	145.5	143.5	139.5	138.5	138.5	138	137.5	137.5	137	136	135	135	133.5	133.5	133	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1

\$52583	1
crtX p	rocei
C;Species:	cies: Brwinia herbicola n. 15.1.1.1-1995 #semience revision 01-Sep-1995 #text change 22-Jun-1999
C: Acce	10-cut 13/3 #Stydemed-restored to the management of the styles in the second styles in the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second se
R;Lin,	Lai, E.M.
Mol.	7-423, 1994
A, Titl	A,Title: Transcriptional activation for tlanking sequences by intuou insertion.
A; RELE	. S52583
A;Status:	
A; Molecule	
A;Resi	A;Residues: 1-431 <lin> b. ross.refarances: RMRL:M90698: NTD:q148393: PIDN:AAA21261.1; PID:g148395</lin>
C', Supe	
One	80.4%; Score 1794
Best	Similarity 82.4%; Fred. No. 3 5; Conservative 19; Mismatch
È	SHVRALQNLAQELVARGE
q	
Š	61 PGSLSHILHLAAHPIGPSWIRLINEMARTSDWLCRELPAAFHALQIEGVIVDQMEPAGAV 120
ą	61 SGSLSRLLHIAAHPLGPSMLRLINEMARTSDMLCLALPRAFNDLAIDGVIVDQMEPAGAL 120
Š	121 VAEASGLPPVSVACALPLAREPGLPLAVMPPEYGTSDAARERYTTSEKIYDMLMRRHDRV 180
셤	
ŝ	181 IAEHACRMGLAPREKLHHCFSPLAQISQLIPELDFPRKALPDCFHANGPLRQPQGTPGSS 240
qq	:
ò	241 TSYPPSPDKRIFASLGTLQGHRYGLFRTIAKACBEVDAQLLLAHCGGLSATQAGELARG 300
qG	241 PLYFSPSEKPRIFASLGTLQGHRYGLFKALVKACBEIDGQLLLAHGGRLTAFQAEBLARS 300
ζ	301 GDIQVVDFADQSAALSQAQLTITHGGNNTVLDALASRTPLLALPLAFDQPGVASRIVYHG 360
g	301 RHTQVVDFADQSAALSQAQLAITHGGMNTVLDAINYRTPLLALPLAFDQPGVASRIVSHG 360
ð	
QD	361 IGKRASRFTTSHALARHWRALLTNVDYPQRWTKIQTALRLAGGTWAAADIVEQAMRTGQP 420

421 VLSGQDYATAL 431 || | | || || 421 VLXGSGYATAL 431

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Mon Mar

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Rikaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N., K.; Kaneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-419 <KAN>
A;Cross-references: EMEL:D90899; GB:AB001339; NID:g1651550; PIDN:BAA16652.1; PID:g16517;
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                           58 THP-PGSLSHLIHLAAHPLGPSMLRLINEMARTSDMLCRELPAAFHALQIEGVIVDQMEP 116
                                                                                                                                                                                                                                                                                                   52 FYPLPASVQQAQRINVQQQSNGRLLRLIAAMSSLTDVLCQQLPAILQRLAVDALIVDENRP 111
                                                                                                                                                                                                                                                                                                                                                                    117 AGAVVARASGLPFVSVACALPLNREPGLPLAVMPFEYGTSDAARERYTTSEKIYDWLMRR 176
                                                                                                                                                                                                                                                                                                                                                                                                     177 HDRVIAHHACRWGLAPREKLHHCFSPLAQISQLIPELDFPRKALPDCFHAVGPLRQPQGT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 SATQAGBLARGGDIQVVDFADQSAALSQAQLTITHGGMNTVLDAIASRTPLLALPLAFDQ 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 PGSSTSYPPSP-----DKPRIFASLGTLQGHRYGLFRTIAKACEEVDAQLLLAHCGGL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 -----YQPPPQVBRSPRSTPRIFASLGTLQGHRLRLFQKIARACASVGAEVTIAHCDGL 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 TPAQADSLYACGATEVVSFVDQPRYVAEANLVITHGGLMTVLDALAAATFVLAVPLSFDQ 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 PGVASRIVYHGIGKRASRFTTSHALARQIRSLLTNTDYPQRMTKIQAALRLAGGTPAAAD 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSHFAVIAPPFFSHVRALQNLAQELVARGHRVTFFQQHDCKALVTGSDIGF---QTVGLQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: $74500
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                                                                    Gabs
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NAlternate naces, hypothetical protein slr1125
C;Species: Synechocystis sp.
A;Variety: PCC 6803
                                                                 31;
48.7%; Score 1018.5; DB 2; Length 413; 48.8%; Pred. No. 8.8e-72; live 62; Mismatches 128; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.0%; Score 558.5; DB 1; Length 419; Best Local Similarity 31.7%; Pred. No. 6.8e-36; Matches 132; Conservative 81; Mismatches 196; Indels 7;
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A; Status: nucleic acid sequence not shown; translation not shown
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Query Match
Best Local Similarity 48.88
Matches 211; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410 IVECAMRICOPV 421
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                                                                                                                                                                                                                 :Misawa, N.; Nakagawa, M.; Kobayashi, K.; Yamano, S.; Izawa, Y.; Nakamura, K.; Harashim Bacteriol. 172, 6704-6712, 1990
.Title: Blucidation of the Erwinia uredovora carotemoid biosynthetic pathway by function. Reference number: A37802; MUID:91072214; PMID:2254247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zeazanthin glucosyl transferase - Erwinia herbicola
C;Species: Erwinia herbicola
C;Species: Erwinia herbicola
C;Species: IS-7ul-1995 #sequence_revision 01-Sep-1995 #text_change 22-Jun-1999
C;Accession: S52980
R;Hundle, B.; Alberti, M.; Nievelstein, V.; Beyer, P.; Kleinig, H.; Armstrong, G.A.; Bur Mol. Gen. Genet. 245, 406-416, 1994
A;Title: Functional assignment of Erwinia herbicola Eho 10 carotenoid genes expressed in A;Reference number: S52976; MUID:95107236; PMID:7808389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 SRYFISSEKPRIFASLGILGGHRYGLFXTIVKACEEIDGGLLLAHCGRLIDSQCEELARS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 RHTQVVDFADQSAALSQAQLAITHGGMNTVLDAINYRTPLLAIPLAFDQPGVASRIVYHG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PGSLSHLIHLAAHPLGPSMLRLINEMARTSDWLCRBLPAAFHALQIEGVIVDQMEPAGAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 VAEASGLPFVSVACALPLNREPGLPLAVMPFEYGTSDAARERYTTSEKIYDWLARRHDRV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 IAHHACRMGLAPREKLHHCFSPLAQISQLIPELDFPRKALPDCFHAVGPLRQPQGTPGSS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 TSYPPSPDKPRIFASLGTLQGHRYGLFRTIAKACEEVDAQLLLAHCGGLSATQAGELARG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 GDIQVVDFADQSAALSQAQLTITHGGMNTVLDAIASRTPLLALPLAFDQPGVASRIVYHG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGKRASRFTTSHALARQIRSLLTNTDYPORNTKIQAALRLAGGTPAAADIVEQAMRTCQP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                         rtX protein - Erwinia uredovora
Species: Erwinia uredovora
;Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 20-Jun-2000
;Accession: B37802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSHFAVIAPPFFSHVRALQNLAQELVARGHRVTFFQQHDCKALVTGSDIGFQTVGLQTHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSHFAAIAPPFYSHVRALQNIAQBLVARGHRVTFIQQYDIKHLIDSBTIGFHSVGTDSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-413 <HUN>
A;Cross-references: EMBL:MB7280; NID:g148404; PIDN:AAA64979.1; PID:g148410
                                                                                                                                                                                                                                                                                                                                                                                                                                                   yResidues: 1-431 <MIS>
yCross-references: GB:D90087; NID:g216681; PIDN:BAA14125.1; PID:g216683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
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80.2%; Score 1790; DB 2; Length 431;
Best Local Similarity 80.3%; Pred. No. 6.38-132;
Matches 347; Conservative 29; Mismatches 55; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLSGQDYATAL 431
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                                                                                                                                                                                                                                                                                                                                                                                                  .;Status: preliminary .;Molecule type: DNA
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jycosyltransferase (BC 2.4.1.-) ole! [validated] - Streptomyces antibioticus (ATCC 11891 C; Species: Streptomyces antibioticus
C; Species: Streptomyces antibioticus
A; Variety: ATCC 11891
C; Date: 2.1-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C; Accession: T5:110
R; Quiros, L.M.; Aguirrezabalaga, I.; Olano, C.; Mendez, C.; Salas, J.A.
A; Reference number: 225300
A; Accession: T5:110
A; Accession: T5:110
A; Accession: T5:110
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A; Accession: T5:110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 QTHPPGSESHILHLAAHPLGPSMLRLINEMARTSDMLCRRLP--AAFHALQIEGVIVDQM 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 R--KALPDCFHAVGPLRQPQGTPGSSTSYFPSPDKPRIFASLGTLQGHRYGLFRTIAKAC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 BEVDAQLLLAHCG-GLSATQAGELARGGDIOVVDFADQSAALSQAQLTITHGGMNTVLDA 333
                                                                                                                                                  Glycosyltransferase (EC 2.4.1.-) - Streptomyces antibioticus CiSpecies: Streptomyces antibioticus CiSpecies: Streptomyces antibioticus CiSpecies: Streptomyces antibioticus CiSpecies: Streptomyces antibioticus CiAccession: S3184

R;Hernandez, C.; Olano, C.; Mendez, C.; Salas, J.A.

R;Hernandez, C.; Olano, C.; Mendez, C.; Salas, J.A.

R;Hernandez, C.; Olano, C.; Mendez, C.; Salas, J.A.

A;Description: Characterization of a Streptomyces antibioticus gene cluster A; Reference number: S3182

A;Description: S3184

A;Molecule type: DNA

A;Molecule type: DNA

A;Residues: 1-430 AHRN-
A;Residues: 1-430 AHRN-
A;Cross-references: RMB::Z22577; NID:g404284; PIDN:CAA80301.1; PID:g581564
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 B--PAGAVVAEASGLPFVSVA------CALPLNREPGLPLAVMPFEYGTSDAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----RQTBRGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 HADRVDEDVYTFVGACQGDRAEEGGWQR--PAGAEKVVIVSLGSAFTKQPAFYRECVRAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 IASRIPLLALPLAFDQPGVASRIVYHGIG---KRASRFITSHALARQIRSLLTNTDYPQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 SHFAVIAPPFFSHVRALQNLAQELVARGHRVTF----FQQHDCKALVTGSDIGFQTVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 HSTLPGP-----DADPEAWGSTLLDNRRTFLNDAI-QALPQLADAYADDIPDLVLHDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 ERYTTSEKLYDWL----MRRHDRVIAHHACRMGLAPREKLHHCFSPLAQISQLIPELDFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 430;
Query Match 10.2%; Score 228.5; DB 1;
Best Local Similarity 25.3%; Pred. No. 3.8e-10;
Matches 112; Conservative 67; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Start codon: GTG
C,Superfamily: glycosyltransferase
C,Keywords: glycosyltransferase, hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391 MTKIQAALRLAGGTPAAADIVE 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   obable glycosyl transferase - Streptomyces coelicolor
Species: Streptomyces coelicolor
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
Accession: T37104
Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, Ibmited to the EMBL Data Library, August 1999
Accession: T37104
Accession: T37104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Residues: 1-407 <SAU>
Cross-references: EMBL:AL109950; PIDN:CAB52955.1; GSPDB:GN00070; SCOEDB:SCJ4.21
Experimental source: strain A3(2)
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                                239
                                                                                                                                                  240 STSYFPSPDKPRIFASLGTLQGHRYGLFRTIAKACEEVDAQLLLAHCGGLSATQAGELAR 299
                                                                                                                                                                                                                                                                                                                                   300 GGDIQVVDFADQSAALSQAQLTITHGGMNTVLDAIASRTPLLAIPLAIPLAFDQPGVASRIVYH 359
                                                                                                                                                                                                                                                                                                                                                                   HPPGSLSHLLHLAAHPL--GPSMLRLINEMARTSDMLCRELPAAFHALQIEG---VIVDQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 MEPAGAVVAEASGLPFVSVACALPLNREPGLPLAVMPFEYGTSDAARERYTTSEKIYDWL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 MRRHDRVIAHHACRMGLAPREKLHHCFSPLAQISQL----IPBLDFPRKALPDCFHAVGP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----LAD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----PDKPR-----IFASLGTLQG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :||||:
178 IRQPINLVYISRAFQPAVEEFDRSYRFVGPSIGARPDDPSFPVNRLRDPVLYASLGTVFN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HRYGLFRTLAKACEEVDAQLLLAHCGGLSATQAGELARGGDIQVVDFADQSAALSQAQLT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 ADPLILRTRATALSPL-AGTVVVSTCQTDPAALGELP--GNVLARRSVPQLEVLDRAALF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 ITHGGMNTVLDAIASRTPLLALPLAFDQPGVASRIVYHGIGK--RASRFT--TSHALARQ 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVAEASGLPFVSVACALPLANREPGLPLAVMPFBYGTSDAARERYTTSBKIYDWLMRRHDR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 DFPWEQLTDQPIIYASLGTIQNQLMSTPKIIAEACMDLDAQLIIS-LGGAKLESMPALP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 GVGEFIPLSKINTNN-LRAALEKVLTBDSYKRNTLOLOGOAIKTAGGLTKAADIIEQ 412
                                                                                                                                                                                                                                                                                                                                                                                                                                               360 GIGK--RASRFTTSHALARQIRSLLTNTDYPQRNTKIQAALRLAGGTPAAADIVEQ 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165, Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACPMGALAARVLGLPAVSSFTTFAYNRHVPSP-----TRASRE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.7%; Score 262; DB 2; Length 407; 26.8%; Pred. No. 8.7e-13; ive 59; Mismatches 165; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----LLAGAAR----PRNLAGYVGARLALRRRPAATGVPLVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
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Best Local Similarity 26.8
Matches 123; Conservative
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J.D.; Dodson, R.J.;
T.; Zalewski, C.; Ma
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                           A;Cross-references: GB:Z99110; GB:AL009126; NID:g2633472; PIDN:CAB13079.1; PID:g2633576
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Deinococcus radiodurans
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C; Accession: F75887
R;White, Co.; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Praser, C.M.
Science 286, 1571-1577, 1999
A; Paterence number: A75250; MUID:20036896; PMID:10567266
A; Accession: F75887
A; Accession: F75887
A; Accession: F75887
A; Residuals type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 VALAGKLIPABKLINVPVIKLCSSYAQNBS------PQLGNBDMLKKIRBABABFKAYL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 MRRHDRVIAHHACRMGLAPREXCHHCFSPLAQISQLIPELDFPRKALPDCFHAVGPLRQP 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 EQEKLPAVSFEQ----LAVPEALNIVFMP------KSPQIQHETFDDRFCFVGPSLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 QGTPGSSTSYFPSPDKPRIFASLGTLQGHRYGLFRTIAKACEEVDAQLLLAHCGGLSATQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRIVYHGIGKRASR-FTTSHALARQIRSLLTWTDYPQRMTKIQAALRLAGGTPAAADIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 VGLQTHPPGSLSHLIHLAAHPLGPSMLRLINEMARTSDMLCRELPAAFHALQIBGVIVDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 AGBLARGGDIQVVDFADQSAALSQAQLTITHGGMNTVLDALASRTPLLALPLAFDQPGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 HFAVIAPPFFSHVRALQNIAQELVARGHRVTF-----FQQHDCKALVTGSDIGFQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ::| | : | | : | | ::| | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| 
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
9.1%; Score 204; DB 1; Length 39
Best Local Similarity 19.8%; Pred. No. 2.8e-08;
Matches 84; Conservative 82; Mismatches 206; Indels
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C,Superfamily: glycosyltransferase
                                                                                                                                                                                                                                            A.Gene: yjiC
C.Superfamily: glycosyltransferase
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A; Experimental source: strain Rl
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Species: Bacillus subtilis:
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Species: Branceson, B.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter S.; Bron, S.; Bronillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd. S.; Enrich, S.D.; Emmerson, P.T.; Entian, K.D.; Erington, J.; Pabret, C.; Ferrari, E. Getter, B.; Capuano, V.; Carter, N.M.; Chd. Species: B.; Bronger, C.; Ferrari, E. S.; Hollow, B.; Getter, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler tech. J.; Harwood, C.R.; Hematut, A.; Hilbert, H.; Holappel, S.; Hollow, M.F. Goetter, D.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, J.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, M.; Ronger, M.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, Matchors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror Meuchi, M.; Tamaka, T.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchlyama, T.; Whiters, P.; Wipat, A.; Yamanoto, H.; Yamane, K.; Yata, K.; Yata, K.; Yata, K.; Yoshikaw, H.P.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
Title: The complete genome sequence of the Gram-posttive bacterium Bacillus subtilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 THPPGSLSHLLHLAAHPLGPSMLRLINEMARTSDMLC---RELPAAFHALQIEG---VIV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----ILPEEFNPEELLAEDQGSRWACSLAEAFRVLPQLRTATPTTGRDLIVY 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 DQMEPAGAVVAEASGLPFV----SVACA----LPLNREPGLPL---AVMPFEYGTSDA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 ARERYTTSEKIYDWLMRRHDRVIA----HH-----ACRMGLAPREKLHHCFSPLAQISQLI 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 GD-----TVGDNYTFVGPTYGDRSHQGTWEGPGHG------RPVLLIALGSAFTDHL 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGMNTVLDAIASRTPLLALPLAFDQPGVASRIVYHGIGKRASR-FTTSHALARQIRSLLT 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
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9.7%; Score 217; DB 2; Length 42.
Best Local Similarity 24.7%; Pred. No. 3e-09;
Matches 111; Conservative 69; Mismatches 185; Indels
                                                i,Residues: 1-424 <QUI>
I,Cross-references: EMBL:AF055579; PIDN:AAC12648.1
I,Experimental source: ATCC 11891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPGVAERLAAVRQEIREAGGARAAADILE 417
, Molecule type: DNA
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Db 174 LEILKRASLFVTHGGMNSTSEGLYFETPLVVIPMGGDQFVVADQVEKVGAGKVIKKEELS 233 Qy 372 HALARQ-IRSLLTNTDYPQRMTKIQAALRLAGGTPAAADIVEQAMR 416 1 :: :: :: :: :	Streptomyces lividans on 30-Jun-1992 #text_change 22-Jun-1999 n of two genes from Streptomyces lividan .04506; PMID:1761231 j153345; PIDN:AAA26780.1; PID:g153347 ncose from UDP-glucose to macrolide antib cosyltransferase ore 181.5; DB 2; Length 418; ed. No. 1.76-06;	Wative 6 PFSHVRALQN CHCHVNPSLE CHCHVNPSLE CHCHVNPSLE CHCHCVNALQN CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCHCVNALA CHCNALA CHCHCVNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCNALA CHCN
5 IASQPIAGHVLPLREIARELARRGHELRWYTGRKFRPQVEAAGAVWEGPVHARDYDDA 62 7 63 SLSHLLHLAAHPLGPSMLRLINEMARTSDWLCRELPAAFHALQIEGVIVDQWE 115	116 PAGAVVAEASCLPFVSVACALPLNREPGLPLAVMPFEYCTSDAARERYTTSE 167	STUTY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY 10 STORY

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probable glycosyl transferase from UDP-glucuronosyltransferase family CAC2716 [imported C) Species: Clostridium acetobutylicum
C) Species: Clostridium acetobutylicum
C) Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C) Accession: C97234
R.Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Balty, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
A, Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clothacterion: 193, 4823-4839, 2001
A, Fitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clothacterion: Comparative Analysis of the Solvent-Producing Acterium Clothacterion: C10314
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: B70878
R;Cole, S T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 ANKTAGNRSYADIITKIIGMTECEIEDILKKIKGMKEDYVUHCSMFCAGNIIAQILKVPS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 ISSFAVFATRKE-----VMKMQYSPITEKELESNPIVSRAYSEAKSRIEKRYFVKMPAI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----DFADQSAALSQAQLTITHGG 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327 MNTVLDAIASRTPLLALPLAEDQPGVASRIVYHGIGKRASR-FTTSHALARQIRSLLTNT 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 VSVACALPINREPGLPLAVMPPEYG------TSDAARERYTTSEKIYDWLMRRH 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 SELM---ACRGDIAIANTAK-------EFVSNIEY----YDDSFKFIGPPIYKRK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 QGTPGSSTSYFP---SPDKPRIFASLGTL----QGHRYGLFRTIAKACBEVDAQLLLAHC 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE001437; PIDN:AAX80662.1; PID:g15025750; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
324 SGPKPKNLGNNTKLIEWLPQNDLLGHSKIKAFVSHGGLNSIFETMYHGVPVVGIPVFGDH 383
                                                                                                 350 PGVASRIVYHGIGKRAS-RFTTSHALARQIRSLLTNTDYPQRMTKIQAALRLAGGTP 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 PFFSHVRALQNIAQELVARGHRVTFFQQHDCKALVTGSDIGFQTVGLQTHPPGSLSHLLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 PGYGHVNPTLGLVDELVKRGZEVYYPCTDEFKESIZAAGAKFISYGER-----MSNFKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 DRVIAHHACR--MGLAPREKLHHCFSPLAQISQLIPBLDFPRKALPDCFHAVGP--LRQP
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Best Local Similarity 20.0%; Pred. No. 5.3e-06;
Matches 89; Conservative 69; Mismatches 178; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 ENLD ----- PPPEKLKNKKVIYISLGTVPNNTNSNLYNIP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 GCLSATQAGELARGGDIQVV-----
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A,Molecule type: DNA
A,Residues: 1-407 <KUR>
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      임
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;Kapitonov, D.; Yu, R.K.
iochem. Biophys. Res. Commun. 232, 449-453, 1997
;Tille: Cloning, characterization, and expression of human ceramide galactosyltransfera
;Telle: Cloning, characterization, and expression of human ceramide galactosyltransfera
;Reference number: JC5423; MUID:97242209; PMID:9125199
      Jitle: Functional expression of zeaxanthin glucosyltransferase from Brwinia herbicola Reference number: A46292; MUID:93028456; PMID:1409639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Experimental source: fetal glioma cell : Comment: This enzyme catalyzes the final step of galactosylceramide synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 FNSTTSDAFLOSKMRNIFSGRLTAI------ELFDILDHYTKNCDMM-----VGNH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 ALOIBG-----VIVDOMEPAGAVVAEASGLPFVSVACALPINNEPG--LPLAVMPFR 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 YGTSDAARERYTTSEKIYDWLMRRHDRVIAHHACRMGLA----PREKLHHCFSPLAQISQ 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LDFPRKALPDCFHAVGPLRQPQGTPGSSTSYPPSPD 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 LLPEKSMYDLVHGSSLWMLCTDVALEPPRPTLPNVVTVGGILTKPAS------PLPE 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 KPRIFASLGTLOGHRYGLFRTIAKACEBVDAQLLLAHCGGLSATQAGBLAR----- 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275 DLQRWVNGANEHGFVLVSFGAGVRYLSEDIÅNKL.------ÄGALGRLPQKVIWRF 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---GGDIQVVDFADQSAALSQAQLT--ITHGGMNTVLDAIASRTPLLALPLAFDQ 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 IIVPPIMPESHMYIFKTLASALHERCHHTVFL----LSEGRDIAPSNHYSLQRYPGI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -hydroxyacylsphingosine 1-beta-galactosyltransferase (BC 2.4.1.45) - human hydroxyacylsphingosine 1-beta-galactose:ceramide galactosyltransferase hallow sapiens (man) species: Homo sapiens (man) species: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 26-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 VIAPP--FESHVRALQNIAQELVARGHRVTFFQQHDCKALVTGSDIG-PQTVGLQTHP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              306 VDFADQSAALSQAQLTITHGGMNTVLDAIASRTPLLALPLAFDQPGVASRIVYH 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VSFVDQPRYVAEANLVITHGGINTVLDALAAATPVLAVPLSFDQPAVAARLVYN
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                                                                                                 Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                     Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.9%; Score 175.5; DB 2; Length 5 20.1%; Pred. No. 7e-06; tive 71; Mismatches 173; Indels
                                                                                                                                                                                                                                                                               Query March
8.1%; Score 180; DB 2; Length 54
Best Local Similarity 61.1%; Pred. No. 1.6e-07;
Matches 33; Conservative 12; Mismatches 9; Indels
                                                                                                                                                                                      Note: sequence extracted from NCBI backbone (NCBIP:115898); Superfamily: glycosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Matcn
Best Local Similarity 20.1*
Watches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,Molecule type: mRNA
,Residues: 1-541 <KAP>
,Cross-references: GB:U62899
                                                                                                                                  Molecule type: nucleic acid
Residues: 1-54 <HUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 LIPE----
                                                                              Accession: A46292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,Accession: JC5423
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thors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
thors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
tele. Deciphering the biology of Mycobacterium tuberculosis from the complete genome
ference number: A70500; MUID:98235987; PMID:9634230
cession: B70878
atus: preliminary; nucleic acid sequence not shown; translation not shown
lecule type: DNA
sidues: 1-388 cCDL.
sidues: 1-388 cCDL.
perimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 RISDMLCRELPAAFHALQIEGVIVDQMEPAGAVVAEASGLPFVSVACALPLNREP----- 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 ELLTRADLVICGGGHGMVAKTLLAGVPMVVVPGGGGDQWEIANRVVRQG-SAVLIRPLTAD 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 KGLPPIGSGLAAGTGIRGRLRDATMRALTGRSWRAGLRQRAAVRVBIGLPARDP----G 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 PLAQISQLIPELDFPRKALPDCFHAVGPLRQPQGTPGSSTSYFPSPDKPRIFASLGTLQG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 HRYGLFRTIAKACEEVDAQLLLAHCGGLSATQAGELA----RGGDIQVVDFA----DQS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 GTAGL-----TEVALÓSLTP---GETVPSGSRLVVSRLSGADLTVPPWÄVAGLGSQA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313 AALSQAQLTITHGGMNTVLDALASRTPLLALPLAFDQPGVASRIVYHGIGKRASRFTTSH 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 -GLPLAVMPPEYGTSDAARERYTTSEKIYDWIMRRHDRVIAHHACRMGLAPREKLHHCFS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345 ALVAAVNEVLSSPRFR-----EAARRAAASVAGAADFV----RVCHDALA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373 ALARQIRSLLTNTDYPORMTKIQAALRLAGGTPAAADIVEQAMRTCQPVLS 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ery Match 7.7%; Score 172; DB 2; Length 388; st Local Similarity 25.6%; Pred. No. 8.6e-06; tches 90; Conservative 40; Mismatches 169; Indels 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                perfamily: glycosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                             Rv273.9c
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ch completed: February 29, 2004, 14:52:45 time : 14.9967 secs

Sequence

Sequence Sequence Sequence

1,629, A 4, Appli 2, Appli 4, Appli 8, Appli 8, Appli 8, Appli 25844, A 15, Appli 22, Appli

Sequence Sequence Sequence Sequence

Sequence 8 Sequence 8 Sequence 2 Sequence 2 Sequence 1 Sequence 1

Sequence Sequence

Sequence

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DB 1; Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/07783705A; Sequence 2, Application US/07783705A; Sequence 2, Application US/07783705A; Sequence 2, Application US/07783705A; Sequence 2, Application: Natural Sequence 2, Application: Missis, No. 5429939ihiko APPLICANT: Missis, No. 5429939ihiko APPLICANT: Missis, No. 5429939ihiko APPLICANT: Missis, No. 5429939ihiko APPLICANT: Natura, Kateumi APPLICANT: Natura, Kateumi APPLICANT: Natura, Kateumi APPLICANT: Natura, Synthesis OF CAROTENOIDS NUMBER OF SEQUENCES: 18
CONTREPT: 26 West 61 Street
CITY: New York:
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CALK: 10023
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720Kb storage COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/783,705A
FILING DATE: 19911023
             US-09-603-207-17
US-09-603-207-17
US-09-813-918-2
US-09-252-9918-1
US-08-926-327-2
US-08-926-327-2
US-08-926-327-2
US-09-036-987A-8
US-09-036-987A-8
US-09-036-987A-8
US-09-180-852-2
US-09-180-852-2
US-09-252-991A-25844
US-09-252-991A-25844
US-09-252-991A-25844
US-09-252-991A-25844
US-09-284-693A-12
                                                                                                                                                                                                                                                                                                              US-09-284-768A-4
US-09-284-768A-7
PCT-US92-00282-5
                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/07/09,000
CLASSIFICATION 435
PRIOR APPLICATION DATA.
APPLICATION NUMBER: JP 1-103078
FILING DATE: 21-APR-1999
APPLICATION NUMBER: JP 2-5325
FILING DATE: 02-VAR-1990
APPLICATION NUMBER: US 07/519,011
FILING DATE: 19-APR-1990
APPLICATION NUMBER: US 07/519,011
FILING DATE: 19-APR-1990
APPLICATION NUMBER: US 07/519,011
FILING DATE: 212-VAR-1990
ATORNEY/AGENT INFORMATION:
NAME: Schwadron, Janet I.
REGISTATION NUMBER: 33,778
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-246-5959
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 431 amino acids
AMINO ACID
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Query Match
    Sequence 1, Appli
Sequence 1, Appli
Sequence 8, Appli
Sequence 20, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                              2231
1 MSHFAVIAPPFFSHVRALQN.......EQAMRTCQPVLSGQDYATAL 431
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Sequence 11
Sequence 6,
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Sequence 2
Sequence 2
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/cgm2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgm2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgm2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgm2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgm2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-096-623A-20

US-08-108-09-11

US-08-111-731A-6

US-09-105-537-20

US-09-105-537-20

US-09-105-537-4

US-09-105-537-4

US-09-105-537-4

US-09-105-537-4

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US-09-105-537-4

US-09-105-537-5

US-09-105-212-2

US-09-105-212-2

US-09-105-212-2

US-09-105-212-2

US-09-105-212-2

US-08-22-02-28-2

US-08-22-02-28-2

US-08-22-02-28-2

US-08-22-02-28-2

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US-08-22-02-28-2
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US-09-356-806-8
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Maximum Match 100%
Listing first 45 summaries
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Best Local Similarity 48.6%; Pred. No. 9.5e-92;
Matches 204; Conservative 58; Mismatches 124; Indels
                                PILING DATE: 03-AUG-1990
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/525,551
FILING DATE: 18-MAY-1990
PRIOR APPLICATION NUMBER: US 07/487,613
PILING DATE: 02-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 29,381
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TYPE: amino acid
STRANDEDNES:
TOPOLLGY: linear
MOLECULE TYPE: protein
APPLICATION NUMBER:
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APPLICANT: Ausich, Rodney L.
APPLICANT: Ausich, Reichelm L.
APPLICANT: Michael, Indrani
APPLICANT: Proffitt, John H.
APPLICANT: Yarger, James G.
APPLICANT: Yarger, James G.
APPLICANT: Yen, Huei-Che B.
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                                                                                                                                      1 MSHFAVIAPPFFSHVRALQNLAQELVARGHRVTFFQQHDCKALVTGSDIGFQTVGLQTHP
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,623A
FILING DATE: 2-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/805,061
RILING DATE: 09-DEC-1991
PRIOR APPLICATION NUMBER: US 07/662,921
PRIOR APPLICATION NUMBER: US 07/662,921
FILING DATE: 28-FEB-1991
PRIOR APPLICATION DATA:
    80.5%; Pred. No. 1.7e-178; tive 29; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUNKESSEE: Welsh & Katz, Ltd.
STREET: 120 S. Riverside Plaza, 22nd Floor CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/08096623A Patent No. 5684238 GENERAL INFORMATION:
         Best Local Similarity 80.5
Matches 347; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLSGQDYATAL 431
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                          58 THP-PGSLSHILHLAAHPLGPSMLRLINEMARTSDMLCRELPAAFHALQIEGVIVDQMEP 116
                                                                                       111
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                           51
                   177 HDRVIAHHACRMGLAPREKLHHCFSPLAQISQLIPELDFPRKALPDCFHAVGPLRQPQGT
                                                                                                                                                                                                 290 SATOAGELARGGDIOVVDPADOSAALSQAQITITHGGMNTVLDAIASRTPLLALPLAFDQ
                                                                                                                                                                                                                                                                                                                      1 MSHFAVIAPPFFSHVRALQNIAQELVARGHRVTFFQQHDCKALVTGSDIGF---QTVGLQ
                                                                                                                                                                                                                                             237 PGSSTSYFPSP-----DKPRIPASLGTLQGHRYGLFRTIAKACEEVDAQLLLAHCGGL
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TOPOLOGY:
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                                                    STATE: V
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-750-524-1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 IFASLGTLOGHRYGLFRTIAKACEEVDAQLLLAHCGGLSATQAGELARGG----- 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92 MLCRELPAAFHALQIEGVIVDQMEPAGAVVAEASGLPFVSVACAL------PLNREP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 GLPLAVMPFEYGTSDAARERYTTSEKIYDWL----MRRHDRVIAHHACRWGLAPREKLHH 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 CRSPLAQISQL----IPELDFPRKALPDCFHAVGPLRQPQGTPGSSTSYFPSPD--KPR 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 VEVTOG------TVANDAE----RLLLPAIRALAARDVLVVATTGAPLELEPMPA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 DIQVVDFADQSAALSQAQLTITHGGMNTVLDAIASRTPLLALPLAFDQPGVASRIVYHGI 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 VATTPGDGHVNPMVPVAQEMVSRGHEVRWYTGKAFRSTVERTGARHEPMRDAHDFGGMPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 ---FQQHDCXALVTGSDIGFQTVGLQTHPPGSLSHLLHLAAHPLGPSMLRLINEMARTSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KALSUhisa KOJIRI, et al.
TITLE OF INVENTION: GENE ENCODING GLYCOSYLTRANSFERASE AND ITS
TITLE OF INVENTION: USES
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 414;
            MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: Dell System 210; Intel 80 286 Microprocessor OPERALING SYSTEM: MS DGS 6.2 SOFTWARE: WORD PETFCT, Version 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/337,913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 7.7%; Score 171.5; DB 1; Similarity 21.4%; Pred. No. 2.9e-09; 96; Conservative 68; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 GKR-ASRFTTSHALAROIRSLLTNTDYPQ 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 VIAPPFFSHVRALQNLAQELVARGHRVTP-
                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/337,913
FILING DATE: December 12, 1996
ATTONEY/AGENT INFORMATION:
NAME: RICHARD NUMBER: 26,588
REGISTRATION NUMBER: 26,588
REPRENCE/DOCKET NUMBER: S-2401
TELECOMMUNICATION INFORMATION:
TELEFRAM: (703) 849-2282
TELEFRAM: (703) 849-2282
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Patent No. 5861293
GENERAL INFORMATION:
APPLICANT: Katsuhisa KOJIRI, et
                                                                                                                                                                                                                                                                                                                                                                                                : 414 amino acids
amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
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                                                                                                                                         FILING DATE:
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Best Local S
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103 ALLEDFPA-----DVLVTDETFFGAGFVSERTGIPVAMIATSITVFSSRDTAPLGL-- 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---- 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 ---FQQHDCKALVTGSDIGFQTVGLQTHPPGSLSHLLHLAAHPLGPSMLRLINEMARTSD
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                                                                                                                           ZIP: 22314
COMPUTER READABLE FORM: 5.25 inch, 360 kb storage MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: Dell System 210: Intel 80 286 Microprocessor OPERATING SYSTEM: NS DOSS 6.2
OPERATING SYSTEM: NS DOSS 6.2
ADDRESSEE: Law Office of Sherman and Shalloway STREET: 413 N. Washington Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68; Mismatches 156;
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Similarity 21.4%; Pred. No. 2.9e-09;
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                                                                                                                                                                                                                                               SOFTWARE: Word Perfect, Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,524
FILING DATE: December 12, 1996
ATTORNEY AGENT INFORMATION:
NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588
REFERRNCE/DOCKET NUMBER: 2-401
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
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Patent No. 658326
GENERAL INFORMATION
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 414 amino acids
amino acids
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                                              Alexandria
: Virginia
RY: USA
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us-09-941-947a-28.rai

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Sequence B, Application US/09320878A Patent No. 6117659
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SEQ ID NO 8
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Best Local Similarity 23.1;
Matches 109; Conservative
                                                                                                                                                                             GENERAL INFORMATION:
                                                   419
                   397 ALR 399
                                                417 CLR
                                                                                                                           US-09-320-878-8
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NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 SLSHLLH--LAAHPLGPSMIRLINEMARTSDMLCRELPAAFHAL-------- 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 HD-RVIAHHACRMGLAPREKLHHCFSPLAQISQLIPELDFPRKALPDCFHAVGP-LRQPQ 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 HGLSSLGRNLCRIFTDGDHTLY-----ADVPELMPTYD-----LPANHEYLGPVLMSPA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 GTPGSSTSYFPSPDKPRIFASLGTLQGHRYGLFRTIAKACBEVDAQLLLAHCGGLSATQA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 GELARGGDIQ-----VVDFADQSAALSQAQLTITHGGMNTVLDAIASRTPLLALPLAF 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348 DOPGVASRIVYH------GIGKRASRFTTSHALARQIRSLLTWTDYPORMTKIQA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 PPFPSHVR-----ALQNLAQELVARGHRVTFFQQHDCKALVTGSDIGFQTVGLQTHPPG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.2%; Score 160.5; DB 4; Length 452; Best Local Similarity 19.3%; Pred. No. 4.7e-08; Matches 93; Conservative 67; Mismatches 154; Indels 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 PPVASEVRGDAAISTTPDAAPGLAARRRRILFVAE----AVT-----
                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IS PORTION:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGRYT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REGISTRATION NUMBER: 31,616
REGISTRATION NUMBER: 31,616
                                                                                        E: WOLF, GREENFIELD & SACKS, P.C. 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYCOBACTERIUM TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET UNMERS: C004
TELECOMMUNICATION INFORMATION:
TELEFRAM: 617/720-3500
TELEFAX: FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 452 amino acids
amino acid
                                                                                                STREET: 600 ALCITY: BOSTON
STATE: MASSACHUSETTS
TTATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 M------BP---AGAVVARASGLPFVSVACALPLAREFGLPLAVMPFEYGTS 156
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23.1%; Pred. No. 3.3e-06;
iive 42; Mismatches 182; Indels 139;
APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: McDart.
APPLICANT: TANG, Li
TITLE OP INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/320, 873A
CURRENT APPLICATION NUMBER: US/09/320, 873A
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: US/09/320, 873A
EARLIER APPLICATION NUMBER: US/09/31,538
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER APPLICATION NUMBER: 60/109,880
EARLIER APPLICATION NUMBER: 60/100,880
EARLIER FILING DATE: 1998-09-22
EARLIER FILING DATE: 1998-09-22
NUMBER OF SEQ ID NOS: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------VALRDRQPPEHREDPTAE--WLTWTLDRYGASFEEE 199
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Patent No. 6503741
GENERAL INFORMATION:
APPLICANT: AFFLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary
APPLICANT: BAPLACH, Mary
APPLICANT: TANG, Li
TILE OF INVENTION: Combinatorial Polyketide Libraries Produced Using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 SHVRALQNIAQELVARGHRVTFFQQHDCKALVTGSDIGFQTVGLQTHPPGSLSHILH---
361 FFLPPAELTPQAVRDAVVRILDDPSVATAAHRLREETFGDPTPAGIVPELER 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 6.4%; Score 142.5; DB 3; Length 426; al Similarity 23.0%; Pred. No. 3.3e-06; 107; Conservative 42; Mismatches 191; Indels 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 LARQ-IRSLLTN-TDYPORMTKIQAALRLAGGTPAAADIVEQAMR 416
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                                                                                                                                                                                                                                                                           APPLICANT: Zhao, L.
TITLE OF INVEXTION DA encoding methywycin and pikromycin
FILE REFERENCE: 600.4380%1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILMG DATE: 1998-06-26
NUMBER OF FILMG DATE: 1998-06-26
SOFTWARE: FactSEQ for Windows Version 3.0
LENGTH: 426
TYPE: PRT
                                                                                                                                Sequence 20, Application US/09105537A Patent No. 6265202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptomyces venezuelae
S-09-105-537-20
                                                                                                                                                                                                        APPLICANT: Sherman, D.H. APPLICANT: Liu, H. APPLICANT: Xue, Y.
                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                           09-105-537-20
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S-09-141-908-8
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Best Local Si
Matches 107,
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70 --LAAHPLGPSMIRLINEMARTSDMLCRSLPAAF-HALQIBGVI--------VDQ 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 6.4%; Score 142.5; DB 4; Length 426; al Similarity 23.1%; Pred. No. 3.3e-06; Conservative 42; Mismatches 182; Indels 139;
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APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Molanie C.
APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, Li
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REPERBNCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/657,440
CURRENT FILLING DATE: 1999-05-27
PRIOR PILLING DATE: 1999-05-27
TITLE OF INVENTION: Modular PKS Gene Cluster as Scaffold
CURRENT APPLICATION NUMBER: US/09/141,908
CURRENT FILING DATE: 1998-08-28
EARLIER PILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: PROV. 60/076,919
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1998-03-05
EARLIER PILING DATE: 1998-03-05
EARLIER PILING DATE: 1998-03-05
EARLIER PILING DATE: 1998-03-05
EARLIER PILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 31
SSOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT; ORGANISM: Streptomyces venezuelae
US-09-141-908-8
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160 -SARKKF------
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US-09-657-440-8
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Best Local S:
Matches 109,
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70 --LAAHPLGPSMLRLINEMARTSDM-----LCRELPAAFHALQIEGVIVDQM-----166 VRMAGEP-RENHEALAFDEARPEPLDWDHALGIBAILAPYFHILANNDSMVDDLVDFARS 115 -----EP---AGAVVAEASGLPFVSVACALPINREPGLPLAVMPFEYGTSDAARERY 164 TISEKIYDWLMRRHDRVIAHHACRMGLAPREKLHHCFSPLAQISQLIPELD----FPRK 568 -------WITWTLDRYGASPEE 219 ALPDCFHAVGP----IRQPQGTPGSSTSYPP-----SPDKPRIFASLGTL--

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                                                                                                                                                                                                                            Query Match
6.4%; Score 142.5; DB 4; Length 426;
Best Local Similarity 23.1%; Pred. No. 3.3e-06;
Matches 109; Conservative 42; Mismatches 182; Indels 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09105537A
Patent No. 6265202
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Xue, Y.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT PILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
PRIOR APPLICATION NUMBER: CIP OF 09/141,908
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 8
IENGTH: 426
TYPE: PRT
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US-09-105-537-4
                                                                                                                                                  ORGANISM: Streptomyces venezuelae
JS-09-657-440-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -SARKE-----
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NGTH: 3782
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US-09-105-537-4
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314 ALSQAQLTITHGGMNTVLDALASRTPLLALPLAFDQPGVASRIVYHGIGKRASRFTTSHA 373

260 -----QGHRYGLFRTIAKACEEVDAQLLLAHCGGLSATQAGELAR-GGDIQVVDFADQSA 313

661 EVLGGDGVSQG---DILEALADLDIELVAT----LDASQRAEIRNYPKHTRFTDFVPMHA

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601

999

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Sequence 7, Application US/08311731A
Patent No. 6583266
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAC, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR THIE OF INVENTION: DIAGNOSTICS AND THERAPBUTICS
NUMBER OF SEQUENCES: 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
                                                                                                                                                                                                                              GREENFIELD & SACKS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C0044/7125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
ATTORNEY AGENT INFORMATION:
AMAGE: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFRENCE/DOCKET NUMBER: C004*
TELEPHONE: 617/720-3500
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Floppy disk COMPUTER: IBM PC compatible ODERATING SYSTEM: PC-nnc/vm SOPTIMEND
                                                                                                                                                                                                                                                  600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 463 amino acids
amino acid
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SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acid
                                                                                                                                                                                                                                                                          CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: prot
HYPOTHETICAL: YES
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TELEFAX: 61
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13 SHVRALQNIAQELVARGHRVTFFQQHDCKALVTGSDIGPQTVGLQTHPPGSLSHLLH---

Query Match 6.4%; Score 142.5; DB 3; Length 3782; Best Local Similarity 23.0%; Pred. No. 0.0001; Matches 107; Conservative 42; Mismatches 191; Indels 125;

Gaps

DD 137 LPAAFHALQIBGYLVDRAYGVSRNTFWSYFSQLQBLCWBYYDYSNKLCKDAULNKK 136 97 LPAAFHALQIBGYLVDRAYABASGLPFVSVACALPINREPGLPLA 147 137 LAMKLQBSKFDVILADALNPCGBLLAELFNIPFLXSLRFSVGYTFERWGGGFLFPFSYVP 196 137 LAMKLQBSKFDVILADALNPCGBLLAELFNIPFLXSLRFSVGYTFERWGGGFLFPFSYVP 196 148 WAPFEYGTSDAARERYTTSEKIYDNLMRRHDRVIAHHACRMGLA 191	RESULT 13 PCT-US92-00282-6 ; Sequence 6, Application PC/TUS9200282 ; Sequence 6, Application PC/TUS9200282 ; GENERAL INFORMATION: APPLICANT: OWENS, IDA S. ; APPLICANT: STTTEM, OSSENT K. TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION ; TITLE OF INVENTION: THEREIN. ; NUMBER OF SEQUENCES: 40 ; CORRESPONDENCE ADDRESS:	STATE: D.C. COUNTRY: WASHINGTON STATE: D.C. COUNTRY: U.S.A. ZID: 20036-5601 COMPUTER: READABLE FORM: MEDIUM TYPE: RIOPPY disk COMPUTER: IBM FC Compatible COMPUTER: IBM FC COMPATIBLE COMPUTER: PC-DOS/MS-DOS SOFTWARE: PETCHTON DATA: CORRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US92/00282 FILING DATE: 19920110 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: SCOTY WATSON T. REGISTRATION NUMBER: 26581 REFERENCE/DOCKET NUMBER: 91532-PCT TELEPHONE: 202-861-3000 TELEPHONE: 202-861-3000 TELEPHONE: 202-861-3000 TELEPHONE: 202-861-3000 TELEPAX: 202-822-0944 TELEPHONE: CONSH INFORMATION POR SEG ID NO: 6: SEQUENCE CHARACTERISTICS:	LENGTH: S13 am.no acids TYPE: AMINO ACID TYPE: AMINO ACID TYPE: AMINO ACID STRANDEDNESS: single TYPE: DrobLogy: linear TYPE: protein MULECULE TYPE: protein PCT-US92-00282-6 Cuery Match 6.2%; Score 138; DB 5; Length 531; Best Local Similarity 19.2%; Pred: No. 1.4e-05; Matches 91; Conservative 72; Mismatches 169; Indels 142; Gaps 20;
ORIGINAL SOURCE: ORGANISM: MYCOBACTERIUM TUBERCULOSIS -08-311-731A-7 Cwery Match Best Local Similarity 21.5%; Score 142; DB 4; Length 463; Best Local Similarity 21.5%; Pred. No. 4.2e-06; Matches 98; Conservative 69; Mismatches 188; Indels 100; Gaps 22; 20 NLAQELVARGHRVTFFQQHDCKALVTGSDIGFQTVGLQTHPPGSLSHLLHLAAMP 74 21 NAAPEPVARRQRILFYGGAATLAHVVRFVLARSLDPSREVHFACDF 68 75LGF	274 CEEVDAQLILAHCGGLSATQAGELARCGDIQVVDFADQSAALSQAQLTITHGGANTVL 331 289 LADLPVTVIAATAGRNHLKNVPANAFVADYLPGEAAARRAVVCNGGSPTTQ 341 332 DALASRTPLLALPLAFDQPGVASRIVYHGIGKRASRFTTSHALARQIRSLLTNTDYPQ 389 1342 QALAAGVPVIGLPSNMDQHLNMEALERAGAGVLLRTERLAT-BGVAAAVKQVLSGABFR- 399 390 RWIKIQAALKLAGGTPAAADIVEQAMRTCCPVLSG 424 400QAARRLPKPSDQTLPDSRSTSKVRCG 425	SSGUTT 12 3-09-356-806-113 Sequence 113, Application US/09356806 Batent No. 6586775 GENERAL INFORMATION: APPLICANT: Penny, Laura APPLICANT: Penny, Laura APPLICANT: Reidy, Michael APPLICANT: Reidy, Michael APPLICANT: Reidy, Michael APPLICANT: Reidy, Michael APPLICANT: Miler, Andrew APPLICANT: Miler, Andrew APPLICANT: Miler, Andrew APPLICANT: SEQ-22PRV2 CURRENT FRIMOWING: 2B15 (UGT2B15) Genes FILE OF INVENTION: UDP-Glucuronosyltransferase 2B4 (UGT2B4), 2B7 (UGT2B7) and FILE REFERENCE: SEQ-22PRV2 CURRENT FILING DAFE: 1999-07-20 NUMBER OF SEQ ID NOS: 164 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 113 LENGTH: 530 TYPE: PRT ORGANISM: H. sapiens	Query Match 6.2%; Score 138.5; DB 4; Length 530; Best Local Similarity 20.2%; Pred. No. 1.2e-05; Matches 91; Conservative 75; Mismatches 193; Indels 91; Gaps 18; 6 VIAPPPESHYRALQNIAQBIVARGHRVTFPQQHDCKALVTGSDIGFQTVGLQTHPPGSLS 65 1

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ATTORNEY/AGENT INFORMATION:
                                            Query Match
Best Local Similarity 24.34
Matches 109; Conservative
MOLECULE TYPE: protein
     US-08-926-258-2
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                                                                                                               72 FTLQTYAFPYTKEEYQREILGNAKKGFEPQHFVKTFFETMASIKKFFDLYANSCAALLHN 131
                                                                                                                                                                                                                                                                                  --DFPRKALPDCFHAVG-----232
                                                                                                                                                                                                                                                                                                                 234 ELLOREMSLVEVISHASVWEFRGDFVFDYPPPIMPNMVFIGGINCVIKKPLSQEFEAYVN 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      336 TC----TRPSNLAK--NTILVKWLPQNDLIGHPKARAPITHSGSHGIYEGICNGVPMVMM 389
                                                                                                                                                 103 -----ALQIEGVIVDQMBPAGAVVAEASGLPFV---SVACAL-----PLNRE 141
                                                                                                                                                                               132 KTLIQQLNSSFDVVLTDPVFPCGALLAKYLQIPAVFFLRSVPCGIDYBATQCPKPSSVI 191
                                                                                                                                                                                                                  PGLPLAVMPFBYGTSDAARERYTTSEKIYDWLMRRHDRVIAHHACRMGLAPREKLHHCFS 201
                                     VIAPPFFSHVRALQNLAQELVARGHRVTFFQQHDCKALVTGSDIGFQTVGLQTHPPGSLS 65
                                                                                                                                                                                                                                     344 PLAFDOPGVASRIVYHGIGKRASRF-TTSHALARQIRSLLTNTDYPQRMTKIQA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2. Application US/08926258
Patent No. 5871983
GENERAL INFORMATION:
APPLICANT: Solenberg, Patricia J.
APPLICANT: Treadway, Patri J.
TITLE OF INVENTION: Glucosyltransferase Gene gtfE From TITLE OF INVENTION: Amycolatopsis orientalis
NUMBER OF SEQUENCES:
ADDRESSEE: Eli Lilly and Company
                                                                                                                                                                                                                                                                                                                                                                                     294 ASGEHGIVVFSLGSMVSEIPEKKAMEIAEALG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/926,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFRENCE/DOCKET NUMBER: P-10430
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 AGE---LARG-GDIQVVD-----FA----DQSAALSQAQLTITHGGMNTVLDAIASRTPL 340
                                                                                                                                                                                                                                                                                                                                                                                 118 İPYPYGFHCPSYVPSPYYAPPPLGEPPAPDGİDIQALWERNNQS------AYRKYGEPL 171
                                                                                                                                                             99
                                                                                                                                                                                                                                                                                                                                                                                                                                           182 AHHACRMGLAPREKLH-HCPSPLAQISQLIPELDPPRKALPDCFHAVGPLRQPQGTPGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 NSRRAAIGLPPVEDIFGHGYT------DHPWMAADP---VLAPL-QPTDLDAVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : | | : : | | 216 TGAWILPDERPISAELEAFLDAGAPPVYLGFGSLRAPADAA-KVAIBAIRAH------
                                                                                                              15 VRALQNIAQELVARGHRVTFFQQHDCKALVTGSDIGFQTVGLQTHPPGSLSHLIHLAAHP
                                                                                                                                                             14 VEPLVALAVRLRERGAEVRMCAPPDCADRLAEVDVPHLPLGASARPSAG-----QAKP
                                                                                                                                                                                                                    75 L-GPSMLRLINEMARTSDMLCRELPAAFH---ALQIEGVIVDQMEPAGAV----VABASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 TSYPPSPDKPRIFASLGTLQGH-----RYGLFRTIAKACBEVDAQLLLAHCGGLSATQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 LALPLAFDOPGVASRIVYHGIGKR----ASRFTTSHALARQIRSLLTNTDYPQRMTKIQA
Length 408;
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6.2%; Score 137.5; DB 2;
24.3%; Pred. No. 1e-05;
tive 43; Mismatches 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Baltz, Richard H.
APPLICANT: Solenberg, Patricia J.
APPLICANT: Tracadway, Patri J.
TITLE OF INVENTION: Glucosyltransferase Gene STITLE OF INVENTION: Amycolatopsis orientalis NUMBER OF SEQUENCES: AMYCOLATORICE ADDRESS: ADDRESSEE: Eli Lilly and Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397 ALRL--AGGTPAAADIVEQAMRTCQPVL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379 VAETVQTDGAAVAADLLFAAVTGNOPAV 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis STATE: Indiana COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/926,258
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09120053; Patent No. 5932464; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Webster, Thomas D. REGISTRATION NUMBER: 39,872
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us-09-941-947a-28.rai

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Query Match 6.2%; Score 137.5; DB 2; Length 408;
Best Local Similarity 24.3%; Pred. No. 1e-05;
Matches 109; Conservative 43; Mismatches 201; Indels 95; Gaps 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 LTAEDMLRETTETIATQ---FERIPAAAEGCAAVVTTGLL-----AAAIGVRSVAEKUG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|| | : | : | : | : | 112 NSRRAAIGLPPVEDIFGEGYT--------DHPWMADP----VLAPL-QPTDLDAVQ 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 TGAWILPDERPISAELEAFLDAGAPPVYLGFGSLRAPADAA-KVAIEAIRAH----- 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 L-GPSMIRLINEMARTSDMLCRELPAAFH---ALQIEGVIVDQMEPAGAV----VAEASG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 LP-FVSVACALPIAR---EPGLPLAVMPFEYGTS-DAARERYTTSEKIYDWLMRRHDRVI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 IPYFYGFHCPSYVPSPYYAPPPFLGBPPAPDGTDIQALWERNNQS-----AYRRYGBPL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 AHHACRMGLAPREKLH-HCFSPLAQISQLIPELDFPRKALPDCFHAVGPLRQPQGTPGSS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSYPPSPDKPRIFASLGTLQGH-----RYGLFRTIAKACEEVDAQLLLAHCGGLSATQ 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 VRALQNIAQELVARGHRVTFFQQHDCKALVTGSDIGFQTVGLQTHPPGSLSHLLHLAAHP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99
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REFERENCE/DOCKET NUMBER: P-10430
TELECOMMUNICATION INPORMATION:
TELEPHONE: 317-276-334
TELEPHONE: 317-276-3361
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: procein
-09-120-053-2
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)b time : 16.0973 secs

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GenCore version 5.1.6
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                    Copyright
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protein - protein search, using sw model

February 29, 2004, 14:26:38; Search time 50.9584 Seconds (without alignments) 2389,754 Million cell updates/sec on:

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2231 1 MSHFAVIAPPFFSHVRALQN........EQAMRTCQPVLSGQDYATAL 431 US-09-941-947A-28 tle: rfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 oring table:

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1586107 segs, 282547505 residues arched: 1586107 tal number of hits satisfying chosen parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

	Description	Aae22312 Pantoea s		Pantoea			Zea	Aab61974 S. avermi	Abul1976 M. echino					Abu89759 Protein d	•	2 Saccha		S. fra	4 Human	Aau77927 Human dru	7 Human	4 Human	Abu58660 Human PRO	Abu88208 Novel hum	Abu84523 Human sec	Abr66397 Human sec
SOFFEE	ŒĨ	AAE22312	AA016018	ABP96686	AAR07464	AAW87890	AAR13989	AAB61974	ABU11976	ABM69288	ABP57697	ABB64912	AAB84216	ABU89759	ADD48913	AAR93982	ABU54566	AAY83786	AAU29284	AAU77927	ABP71237	AAE15434	ABU58660	ABU88208	ABU84523	ABR66397
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ALIGNMENTS

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Carotenoid; isopentenyl pyrophosphate; antheraxanthin; astaxanthin; diet; anti-oxidant; steroid; flavour; fragrance; electro-optic application; aquaculture; enzyme; zeaxanthin glucosyl transferase; CrtX.
                                                             Pantoea stewartii zeaxanthin glucosyl transferase (CrtX) enzyme.
                                                                                                                                                                                                          (DUPO ) DU PONT DE NEMOURS & CO E I.
                AAE22312 standard; protein; 431 AA.
                                                                                                                                                                                 01-SEP-2000; 2000US-0229858P.
01-SEP-2000; 2000US-0229907P.
                                                                                                                                                                  04-SEP-2001; 2001WO-US027420.
                                                 (first entry)
                                                                                                                 Pantoea stewartii.
                                                                                                                                 WO200218617-A2.
                                                 25-JUL-2002
                                                                                                                                                  07-MAR-2002.
                                AAE22312;
RESULT 1
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Koffas M, Miller ES; Brzostowicz PC, Cheng Q, Dicosimo DJ, Odom JM, Picataggio SK, Rouviere PE;

2002-351711/38. WPI; 2002-351711, N-PSDB; AAD35510 Producing carotenoid compounds e.g. antheraxanthin and astaxanthin, by using microorganisms having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolize single carbon substrates.

Claim 25; Page 136-137; 156pp; English.

The invention relates to a method for producing carotenoid compounds. The method comprises a transformed metabolising host cell, comprising suitable levels of isopernenyl pyrophosphate and a nucleic acid molecule encoding an enzyme in the carotenoid biosynthetic pathway, under the control of regulatory sequences, and contacting the host cell with carbon substrate to produce a carotenoid compound. The method is useful for producing carotenoid compounds such as antheraxanthin and astexanthin, by using microorganism having a nucleic acid molecule encoding enzymes in

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the carotenoid biosynthetic pathway and which metabolise single carbon substrates. The carotenoids have potent anti-oxidant properties useful in diet, and aquaculture elements. The carotenoids are also useful as intermediates in the synthesis of steroids flavours and fragrances and compounds for potential electro-optic applications. The present sequence is Pantoea stewartii zeaxanthin glucosyl transferase (CrtX) enzyme used
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                                                                                                                                              100.0%; Score 2231; DB 5; Length 431;
100.0%; Pred. No. 4.4e-215;
ive 0; Mismatches 0; Indels 0;
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                                                                             is Pantoea stewarin the invention
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                                                                                                                        Sequence 431 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid useful e.g. to engineer host cells with the ability to produce particular carotenoids and polypeptides useful in cell-free systems to make particular carotenoids.
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                                                                                                              The invention comprises the amino acid and coding sequence of a number carotenoid (crt)-related proteins. The crt-related DNA and protein sequences of the invention are useful for engineering cells which are able to produce carotenoids. The present amino acid sequence represents crt-related protein of the invention
                                                                                                                                                                                                                                                                                                                                    361 ICKRASRFTTSHALARQIRSLLTWTDYPQRMTKIQAALRLAGGTPAAADIVEQAMRTCQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stewartii; carotenoid biosynthetic enzyme; crtX; crtX; crtY;
rtB; crtZ; zeaxanthin glucosyl transferase; enzyme; phytoene;
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                                                                                                                                                                                                                    100.0%; Score 2231; DB 6; 100.0%; Pred. No. 4.4e-215;
                                                                                                                                                                                                                                                Mismatches
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                                                                                              Claim 7; Page 58-59; 74pp; English
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          2003-075455/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes Pantoea stewartii carotenoid biosynthetic enzymes (1). More specifically described are the geranylgeranyl pyrophosphate synthase (crtB), zeazanthin glucosyl transferase (crtX), lycopene cyclase (crtX), phytoene desaturase (crtI), phytoene synthase (crtB) and beta-carotene hydroxylase (crtZ) enzymes (see ABP96685 to ABP96680) encoded by ACC44759 to ACC44764. (1) can be used for regulating carotenoid biosynthesis in an organism, by over-expressing (1) in an organism. (1) and the genes encoding (1) are useful for converting phytoene to the carotenoids, for creating recombinant organisms that have the ability to produce various carotenoid compounds, and also for enhancing or manipulating carotenoid compounds. (1) can also be used for producing gene products having enhanced or altered activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 VAEASGLPFVSVACALPLAREPGLPLAVMPFSYGTSDAARERYTTSEKIYDWLMRRHDRV 180
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                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acid molecule isolated from Pantoea stewartii encoding carotenoid biosynthetic enzyme, useful for regulating carotenoid biosynthesis in an organism.
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                                                                                                                                                                                                             Rouviere PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 2231; DB 6; 100.0%; Pred. No. 4.4e-215;
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                                                                                                                                                                                                             Picataggio SK,
                                                                                                                                                 (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 59-60; 68pp; English
                                                                                        15-AUG-2001; 2001US-0312646P.
                                  15-AUG-2002; 2002WO-US026647
                                                                                                                                                                                                         Cheng Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLSGODYATAL 431
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                                                                                                                                                                                                                                                                     2003-268323/26.
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431; Conserv
                                                                                                                                                                                                                                                                                                  N-PSDB; ACC44760
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                                                                                                                                                                                                             Brzostowicz PC,
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                                                                                                                                       with enzymatic activity for the conversion of zeaxanthin into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene products are useful for the synthesis of carotenoids, useful as food coloring, vitamin A precursor, and possibly in prevention of cancer. See also AAQ06293-9. (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA sequences encoding enzymes for carotenoid biosynthesis - for prodn. of carotenoid cpds. e.g. beta-carotene, lycopene, phytoene, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGSLSHLIHEAAHPLGPSMLRLINEMARTSDMLCRELPAAFHALQIEGVIVDQMEPAGAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 IGKRASRFTTSHALARQMRSLLTNVDFQQRMAKIQTALRLAGGTMAAADIIEQVMCTGQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 IAHHACRMGLAPREKLHHCPSPLAQISQLIPELDFPRKALPDCFHAVGPLRQPQGTPGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 TSYFPSPDKPRIFASLGTLQGHRYGLFRTIAKACEEVDAQLLLAHCGGLSATQAGELARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDI QVVDFADQSAALSQAQLTITHGGMNTVLDAIASRTPLLALPLAFDQPGVASRIVYHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 431;
                                                                                                                                                                                                    Carotenoid biosynthesis; vitamin A; cancer; food coloring
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80.5%; Pred. No. 9.2e-171;
ive 29; Mismatches 55;
AAR07464 standard, protein, 431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Fig 2; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                           89JP-00103078.
                                                                                                                                                                                                                                                                                                                                                                     90EP-00107493
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 347; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misawa N, Kobayashi K,
                                                                                                                                                             zeaxanthin diglucoside
                                                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KIRI ) KERIN BEER KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1990-322212/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                Pantoea ananatis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 431 AA;
                                                                                                                                                                                                                                                                                                                                                                     20-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                05-MAR-1990;
                                                                            24-OCT-2003
28-JAN-1991
                                                                                                                                           Polypeptide
                                                                                                                                                                                                                                                                                                                              24-0CT-1990.
                                                                                                                                                                                                                                                                                     EP393690-A.
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                                         AAR07464;
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24-OCT-2003
25-MAR-2003
26-NOV-1991
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                                                                                                                                                                                                                                                                                                                                                                     04-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                         02-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                18-MAY-1990;
                                                                                                                                                                                                                                                                                                                              WO9113078-A.
                                                                                                                                                                                                                                                                                                                                                 05-SEP-1991
                                                                                                                                                                                                           AAR13989;
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                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a protein involved in carotenoid biosynthesis. The specification describes astaxanthin diglucosides and adonixanthin-3'-glucosides. The specification also describes a method for the preparation of a carotenoid glycoside, in Which all, or part of, carotenoid biosynthesis genes crtE, crtB, crtI, crtY, crtZ, crtX or crtW are introduced to a microbe or plant and expressed. The transformed organism is cultured and astaxanthin diglucosides, adonixanthin-3'-glucosides, and/or astaxanthin monoglucoside are collected. The carotenoid glucosides are used as food additives. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGSLSHILHLAAHPLGPSMLRLINEMARTSDMLCRELPAAFHALQIEGVIVDQMEPAGAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAEASGIPFVSVACALPINREPGIPLAVMPFEYGTSDAARERYTTSEKIYDWLMRRHDRV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                  Carotenoid biosynthesis; astaxanthin diglucoside; crtE gene; crtE gene; crtI gene; adonixanthin-3'-glucoside; astaxanthin monoglucoside; carotenoid glycoside; crtY gene; crtZ gene; crtX gene; crtM gene; food additive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
80.2%; Score 1790; DB 2; Length 431;
Best Local Similarity 80.5%; Pred. No. 9.2e-171;
Matches 347; Conservative 29; Mismatches 55; Indels (
                                                                                                                                 Protein encoded by the carotenoid biosynthesis gene crtX.
                                                                                                                                                                                                                                                                                                                                                              New carotenoid glucoside(s) - used as food additives
                                                                                                                                                                                                                                                                                                    (KIRI ) KIRIN BREMERY KK.
(KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Page 20-21; 26pp; Japanese.
                                                                AAW87890 standard; protein; 431 AA
                                                                                                                                                                                                                                                                97JP-00140460.
                                                                                                                                                                                                                                                                                  97JP-00140460.
                                                                                                                 (first entry)
421 VLSGODYATAL 431
                421 VLSGSGYATAL 431
                                                                                                        (revised)
                                                                                                                                                                                                                                                                                                                                 WPI; 1999-099030/09.
                                                                                                                                                                                                       Pantoea ananatis.
                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAV84082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 431 AA;
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                                                                                                                                                                                                                         JP10327865-A.
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                                                                                                      17-0CT-2003
10-MAR-1999
                                                                                                                                                                                                                                            15-DEC-1998
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There are a total of six relevant genes in a 7900 bp region that cause E. coli cells to produce GGPP and the carotenoids phytoene through caxoarathin diglucoside, which is the final prod. identified in the carotenoid pathway contd. in plasmid pARG376 (contg. a ca. 13 kb chromosomal DNA fragment isolated by Perry et al., J. Bacteriol. 168:607 (1986). The genes for geranjugaranty pyrophosphate (GGPP) synthase, phytoene synthase, phytoene dehydrogenase-4H, lycopene cyclame, betacarotene hydroxylase, and zeaxanthin glycosylase are represented in ARG13719, ARG13719, ARG13722, ARG13724 and ARG13726 in Espectively. Recombinant expression plasmids can be used to produce large amts. of the enzymes and hence large amts. of the carotenoids which they synthesise. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated standardise OS field)
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                                                                                                                                                                                                                                                                                                                    420
                                                                                                                                                                                                                                                                                                                                                   361 IGKRASRFTTSHALARQMRSLLTHVDFQQRMAKIQTALRLAGGTWAAADIIEQVMCTGQP 420
181 IAEHSHRMGLAPRQKLHQCFSPLAQISQLVPELDFPRKALPACFHAVGPLRETHAPSTSS 240
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                                                                241 SRYFTSSEXPRIFASLGTLQGHRYGLFKTIVKACEEIDGQLLLAHGGRLTDSQCBELARS
                                                                                                                                                                                       301 GDIQVVDFADQSAALSQAQLTITHGGMNTVLDAIASRTPLLALPLAFDQPGVASRIVYHG
                                                                                                                                                                                                                            361 IGKRASRFTTSHALARQIRSLLTNTDYPQRMTKIQAALRLAGGTPAAADIVEQAMRTCQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yarger JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pantoea agglomerans; EHO-10 (E. vulneris - ATCC 39368).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ausich RL, Brinkhaus FL, Mukharji I, Proffitt JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGPP; carotenoid; phytoene; zeaxanthin; lycopene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 25(1-3); 313pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zeaxanthin glycosylase - engineered.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR13989 standard; protein; 399 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-00487613.
90US-00525551.
90US-00562674.
91US-00662921.
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(revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 VLSGQDYATAL 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 VLSGSGYATAL 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1991-281410/38.
N-PSDB; AAQ13726.
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WO200279465-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a 10 kb genomic DNA isolated from S. avermitilis that contains genes encoding proteins for glycosylation of avermectin
                                                                                                                                                                                                             117 AGAVVAEASGLPFVSVACALPLNREPGLPLAVMPFEYGTSDAARERYTTSEKIYDWLMRR 176
                                                                                                                                                                                                                              236
                                                                                                                                                                                                                                                                                              224
                                                                                                                                                                                                                                                                                                                           289
                                                                                                                                                                                                                                                                                                                                                      278
                                                                                                                                                                                                                                                                                                                                                                                  290 SATQAGELARGGDIQVVDFADQSAALSQAQLFITHGGMNTVLDAIASRTPLLALPLAFDQ 349
                                                                                                                                                                                                                                                                                                                                                                                                            337
                                                                                                                                                                                                                                                                                                                                                                                                                                         PGVASRIVYHGIGKRASRFTTSHALARQIRSILITNTDYPQRMTKIQAALRLAGGTPAAAD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAVAARLVYNGLGRRVSRPARQETLADELAQLLGDETLHERVATAQQQLNDAGGTPRCGD 397
                                                                                                                                                      58 THP-PGSLSHILHLAAHPLGPSMLRLINEMARTSDMLCRELPAAFHALQIEGVIVDQMEP 116
                                                                                                                                                                                 52 FYPLPASVQQAQRNVQQQSNGNLLRLIAAMSSLTDVLCEQLPAILQRLAVDALIVDEMEP 111
                                                                                                                1 MSHPAIVAPPLYSHAVAVHALALQMAQRGHRVTF-----IFGNVASLARQETERVA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acid fragments of Streptomyces avermitilis genome useful for enzymatic, biochemical, biosynthetic and diagnostic purposes.
                                                                                                MSHFAVIAPPFFSHVRALQNLAQELVARGHRVTFFQQHDCKALVTGSDIGF---QTVGLQ
                                                                                                                                                                                                                                                                     177 HDRVIAHHACRMGLAPREKLHHCFSPLAQISQLIPELDFPRKALPDCFHAVGPLRQPQGT
                                                                                                                                                                                                                                                                                                                                                      -----YQPPPQVERSPRSTPRIFASLGTLQGHRLRLFQKIARACASVGAEVTIAHCDGL
                                                                                                                                                                                                                                                                                                                                                                                                 237 PGSSTSYFPSP-----DKPRIFASLGTLQGHRYGLFRTIAKACEEVDAQLLLAHCGGL
                                                                     34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aglycone; biocatalysis; antibiotic;
                                       ; Score 945; DB 2; Length 399;
Pred. No. 6.9e-86;
59; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycosylation, avermectin, aglycone, biocata oleandrose, ORF2; AvrB; glycosyl transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S, avermitilis ORF2 (AvrB) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 20; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gewain KM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB61974 standard; protein; 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-2000; 2000WO-US020331
                                          42.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry
                                                       Local Similarity 47.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macneil DJ, Occi J,
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                Ą,
                Seguence 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B61974
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aglycones. The polypeptides can be expressed by standard recombinant methodology. The gene and the encoded polypeptides together with other enzymatically active polypeptides, are useful to perform combinatorial biocatalysis in vitro and in vivo in a host cell. They are useful for performing biotransformations on macrolide compounds including avermectin or other macrolide aglycones. The sequences are also useful in vivo in a bacterial host, in vitro in combination with an actinomycete polypeptides that are not from the avermectin biosynthetic pathway to effect the synthesis of a pharmaceutically active compound, e.g. an antibiotic. Sequences AABS1973-981 represent polypeptides in the avermectin biosynthetic pathway, involved in the synthesis and/or addition of oleandrose to avermectin aglycones. The present sequence is the S. avermetilis ORF2 (AvrB) polypeptide having the activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----DPPRKALPDCFH-----AVGPLRQPQGTPGSSTSYFPSPDK 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 ITBPVDDFLSGPEDFNLVCLPRAFQYAGDTFDERFAFVGPCLGKRRGLGEWTP--PGSGH 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -------PDSAQVSAPPPR-----FSEQMELFGLGALVPRLAELLVSRG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVVLISLGTVFNRQLSFFRTFVRAFTDVPVHVVIS------LGKGVDPDVLRPL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---IQVVDFADQSAALSQAQLTITHGGMNTVLDAIASRTPLLALPLAPDQPGVASRIVYH 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biosynthetic gene cluster; aryltetrasaccharide; aglycone; resistance; nonchromoprotein enediyne; enediyne resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIGKRAS-RFTTSHALARQIRSLLTNTDYPQRMTKIQAALRLAGGTPAAADIVEQAMR 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 ---GEQTVCLQTHPPGSLSHLLHLAAHPLGPSMLRLINEMA--RTSDMLCRELPAAFHAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 QIEGVIVDOMEPAGAVVAEASGLPFVSVACALPLAREPGLPLAVMPFEYGTSDAARERYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSEKIYDWLMRRHDRVIAHHACRMGLAPREKLHHCFS---PLAQISQLIPEL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 HPLFMSAPFWGHVFPSLAVABELVHRGHHVTF------VTGAEMADAVRSVGADFLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cch 11.1%; Score 247; DB 4; Length 412;
al Similarity 21.3%; Pred. No. 1e-15;
102; Conservative 76; Mismatches 162; Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIFASLGTLOGHRYGLFRTIAKACEEVDAQLLLAHCGGLSATQAGELARGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 HFAVIAPPFFSHVRALQNLAQELVARGHRVTFFQQHDCKALVTGSDI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M. echinospora calicheamicin biosynthesis protein CalM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Micromonospora echinospora; spp. calichensis
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycosyl transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 TMOSVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 412 AA;
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13-FEB-2003
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358 AVAADPALLARVEAMRGHVRRAGGAARAADAVE 390

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Novel nucleic acid molecule from nonchromoprotein enediyne biosynthetic gene cluster from Micromonospora echinospora useful for conferring calicheamicin resistance on a subject.
                                                                                                                                                                                   (SLOK ) SLOAN KETTERING INST CANCER RES
                                                   28-NOV-2001; 2001WO-US044285.
                                                                                                                            28-NOV-2000; 2000US-00724797.
                                                                                                                                                                                                                                                                                                                      2003-092897/08.
10-0CT-2002.
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The present invention relates to the isolation of the Micromonospora echinospora spp. calcichensis calicheamicin biosynthetic gene cluster encoding proteins and enzymes used in the biosynthetic production of calicheamicin, including aryltetrasacharide and adjycome. The gene cluster also includes the gene encoding for the protein that confers calicheamicin, resistance. The calicheamicin biosynthetic gene cluster is a nonchromoprotein enediyne biosynthetic gene cluster. Expression vectors containing genes from the biosynthetic gene cluster are also disclosed.

The expression vectors are useful for producing calicheamicin provides an approach for gene therapy, for example, by introduction of enediyne resistance genes into bone marrow cells, thus increasing resistance and allowing tolerance to chemotherapeutic doses of calicheamicin. Abull 964-Abul 2010 represent proteins and enzymes encoded by genes in the M. Abul 2010 represent proteins and enzymes encoded by genes in the M. Abul 2010 represent proteins and enzymes encoded by genes in the M. Abul 2010 represent proteins and enzymes encoded by genes in the M. Abul 2010 represent proteins and enzymes encoded by genes in the M. Claim 25; Page 100-101; 179pp; English 2003 to standardise OS field)

Seguence 397 AA;

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GGMNIVLDALASRIPLLALPLAFDQPGVASRIVYHGI-----GKRASRFITSHALARQIR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----FQIAGDIFDÖRFVFVGPCFDDRRFLGEWTR--PADÖLPVVLVSLGFIFNDRP 243
                                                                                                                                                                                                                                                                                                                                                                                           204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPFRDCARAFDGQPWEVVWTLGGQVDPAALGDLP--PNVEAHRWVPHVKVLBQATVCVTH 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGMGTLMEALYWGRPIVVVPQSFDVQPMARRVDQLGLGAVLPGEKADGDT----LLAAVG 357
                                                                                                                                                                                                                                                                                                                                                      98 PAAFHALQIEGVIVDQME-PAGAVVAEASGLPFVSVACALPLNREPGL------ 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QISQLIPELDFPRKALPDCFHAVGPLRQPQGTPGSSTSYFPSPDKPRIFASLGTLQGHRY 264
                                                                                                                                                                         1 MAHLLIVNVASHGLILPTLTVVTELVRÄGHRVSYVTAGGFAEPVRAAGATVVPYÖSEIID 60
                                                                                                                                                                                                                                                                               61 ADAAEVPGSDDLGVR------PHLMYIREN------VSVLRATAEALDGDV 99
                                                                                                                     38 ---FQQH--- 38
                                                                                                                                                                                                                                    39 -DCKALVTGSDIGFQTVGLQTHPPGSLSHLLHLAAHPLGPSMLRLINEMARTSDMLCREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 PLAVMPFEYGTSDAARERYTTSEKIYDWLMRRHDRVIAHHACRMGLAPREKLHHCFSPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265 GLFRTIAKACEEVDAQLLLAHCGGLSATQAGELARGGDIQVVDFADQSAALSQAQLTITH
Ouery Match

9.0%; Score 201; DB 6; Length 397;
Best Local Similarity 21.2%; Pred. No. 4.1e-11;
Matches 96; Conservative 69; Mismatches 184; Indels 104; Gaps
                                                                                                                           1 MSHFAVIAPPFFSHVRALQNLAQBLVARGHRVTF----
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The invention relates to the isolation of genes and their encoded corteins from Photorhabdus luminescens. The isolated sequences are proteins from Photorhabdus luminescens. The isolated sequences are sources of probas and primers for detection; the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polypeptides encoded by the genes are used for detection/identification of the genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that compines or microorganisms other than P. luminescens and are able to alter response or sensitivity to coxins and antibiotics produced by P. creombinant production of the proteins, particularly toxins and carried antibacterials useful as insecticides, bactericides and fungicides. The creombinant production of the proteins, particularly toxins and carried that the respective to P. luminescens end the proteins or antibiotics and as some constitute to P. luminescens and the proteins are also useful the properticides, bactericides and fungicides. The biopesticides, Other uses of the genes and the proteins are as virulence factors and for identifying tragets of human diseases for which P. contains a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AVIAPPFFSHVRALQNIAQELVARGHRVTFF------QQHDCKALVTGSDIGFQTVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
8.2%; Score 183; DB 6; Length 432;
Best Local Similarity 21.8%; Pred. No. 3e-09;
Matches 99; Conservative 62; Mismatches 175; Indels 118; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Danchin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kunst F,
                                                                                                                                      Photorhabdus luminescens protein sequence #2385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Frangeul L,
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               ABM69288 standard; protein; 432
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LQTH-----PPGSLSHILHLAAHPLGPSMIRLINEMARTSDMLCRELPAAFHALQIEG 108
                                                                       ------KÖFFČSPIP--FLDRÖLGQ 103
                                                                                                                                                                                                                                                                                                   ----AARERYTTSEKIYDWLMRR-----HDRVIAHHACRMGLAPREKLHHCFSP-- 202
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                                                                   65 LKORFPDRAHLPPGNLOMALAF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 RGL--AGDÓVLVVATTGREGVDLGYVP--DNARVASFLPYRELMPKLAAVVTNGGFGTVQ
                                                                                                                     Gaps
microorganisms. The present sequence represents one of the butenyl-spinosyn biosynthetic polypeptides of the invention
                                                                                                                                                    1 MSHFAVIAPPFFSHVRALQNLAQELVARGHRVTFFQQHDCKALV--TGSDIGFQTVG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila, developmental biology; cell signalling, insecticide;
                                                                                                                   72;
                                                                                    Length 470
                                                                                  8.2%; Score 183; DB 6; Length 47
21.0%; Pred. No. 3.3e-09;
tive 80; Mismatches 212; Indels
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                                                                                                                                                                                                                                                                                                                                                               172 WLMRRHDRVIAHHACRMGLAPREKLHHCF
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB10702). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                         Disclosure; SEQ ID NO 21528; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 540 AA
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19;
                                                                                                                                                                                                                                                                                                                                                                                                                             92 QFFDALGDKWREGVLVSTIFYNVSHAI-----LINNWGVQ---MLMRDKSIRFDMIMVEA 142
                                                                                                                                                                                                                                                                        143 SHLDALYG----LAEFYNATLLGISCMHMTWHIDYLAGNLAPSVYEPISPNGFALDNTFL 198
                                                                                                                                                                                                                                                                                                                                                           253
                                                                                                                                                                                                                                                                                                                                                                                                 P----RKALPDCFHAVG-PLROPQGTPGSS-TSYFPSPDKPRIFASLGTLQGHRYGLFRT 269
                                                                                                                                                        49 IGFQTVGLQTHPPGSLSHLLHLAAHPLGPSMLRLINEMARTSDMLCRELPAAFHALQIEG 108
                                                                                                                                                                                                                                      109 VIVDQMEPAGAVVARASGLPFVSVACA-----LPINRRPGLPLAVMPFFYGTSDAAR 160
                                                                                                                                                                                                                                                                                                                     ER----YTTSEKIYDWLMRRHDRVIAHHACRWGLAPREKLHHCFSPLAQISQLIPELDF 215
                                                                                                                  16
                                                                              -----SD 48
                                                                                                                                                                                                                                                                                                                                                  SRWSNWIYITEEKLLERLVFRPAQVRLFK--KFFGYPAEKLDBL---RARFSVILVNSHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 IAKACEEVDAQLLLAHCGGLSATQ----AGELA----RGGDIQVVDFADQSAALS--QAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---LPENMQKQLLLVF---LQMKQRVIWKSELSMLANKSENIYVMJKVPQRMVLAHPNLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIITHGGMNTVLDAIASRIPLLALPLAFDQPGVASRIVYHGIGKRAS-RFTTSHALARQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFITHGGLQSVMEAIDNGVPMLGLPLFFDQFNNIHRVQLAGMAKVLDPNDLNADTLIETI
                                                                                                                  36 IPSPF----QMVRPLIKALVERGHKVTMVTPADYPAKIDGVRHIRVPMLNQLMQNLMKND
                                        Gaps
                                      83;
DB 4; Length 540;
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSLLINIDYPQRMTKIQAALRLAGGIPAAADI--VEQAMR 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KELLENPSYAQRAKEMAASPRDRPMSPLDTAIWWTBYALR 462
                                      66; Mismatches 202;
                                                                              7 IAPPFFSHVRALQNLAQELVARGHRVTFFQQHDCKALVTG
Query Match
8.1%; Score 181.5; DB 4
Best Local Similarity 23.7%; Pred. No. 5.8e-09;
Matches 109; Conservative 66; Mismatches 202
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standard; 06-AUG-2001 AAB84216 AAB84216;

Amino acid sequence of an UDP-glucose:aglycon-glucosyltransferase entry) (first

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protein; 492

UDP-glucose:aglycon-glucosyltransferase; UDP-GAG; cyanohydrin; terpenoid; glucose; transgenic plant; cyanogenic glucoside biosynthesis; pathogen resistance; herbivore response.

Sorghum bicolor

WO200140491-A2

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The present sequence represents a UDP-glucose:aglycon-glucosyltransferase (UDP-GAG) polypeptide. The enzyme conjugates a cyanohydrin, terpenoid, phenylderivative or hexanolderivative to glucose. UDP-GAG polymucleotides are useful for producing transgenic plants having modified cyanogenic glucoside biosynthesis. Constitutive, inducible or tissue-specific expression of UDP-GAG is useful for obtaining transgenic cyanogenic plants with altered resistance to pathogens and herbivore responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 -VIVDOMEPAGAVVARASGLP----PVSVACAL--PLAREPGLPLAVMPFEYGTSDAARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 DGKPAGSVVYVNFGSM-----AVMTAAQAREFALGLASCGSPFLWVKRPDVVEGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --LSATQAGELARGGDIQVVDFADQSAALSQAQ--itithggmntvldalasrtplladp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :| :: | :: | :: | :: | CHGEQTINCRQLCEVWGNGAQLPREVESGAVARLVREWAVGDLGKEKRAKAAEWKAAAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 CVVGDVVMTPAAAAREAGIPEVQPPTASACGLLGYLHYGELVERGLVPFR-DASLLADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RYTTSEKIYDWL-----MRRHDRVIAHHACR------MGLAPREKLHHCPSPLAQISQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYELE---KOVVDALAAFFPPIYTVGPLAEVIASSDSASAGLAAMDISIWQEDTRCLSWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAPDQPGVASRIV-YHGIGKRASRFTTSHALARQIRSLLTNTDYPQRMTK-----IQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 HPAVIAPPFFSHVRALQNLAQBLVARGHRVTF-FQQHDCKALVTGSDIGFQTVGLQTHPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 GSLSHLLHLAAHPLGPSMLRLINEMARTSDMLCRELPAAFHAL-----QIEG-----
                                                                                                                                                                                                                      DNA molecule coding for UDP-glucose.aglycon-glucosyltransferase conjugating cyanchydrin, terpenoid or phenylderivative to glucose, producing transgenic plants having modified cyanogenic glucoside biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --KPR---IFASLGTLOGHRYGLFRTIAKACEEVDAQLLLAHCGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.0%; Score 178.5; DB 4; Length 23.2%; Pred. No. 1e-08; tive 73; Mismatches 191; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 IPELDFPRKALPDC-----FHAVGPLRQPQGTPGSSTSYFPSPD
                                                                                                                     UNIV ROYAL VETERINARY & AGRIC.
                                                                                                                                                                                                                                                                                                             Claim 7; Page 27-29; 31pp; English
                                                                                                                                                     Jones PR;
                                         2000WO-EP011982.
                                                                         99EP-00123838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 23.2%
Matches 113; Conservative
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                                                                                                                                                   Hoej P, Moeller BL,
                                                                                                      (LUMI-) LUMINIS PTY
                                                                                                                                                                                 2001-374846/39
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                                                                                                                                                                                                    N-PSDB; AAF90242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 492 AA;
                                           29-NOV-2000;
                                                                         01-DEC-1999;
             07-JUN-2001
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108 125 161

61 9 209 239

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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence unjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more
                                                                                                                                                                          ------GGDIQVVDFADQSAALSQAQLT--ITHGGANTVLDAIASRTPLLALPLAFDQ 349
                                                                                                                                                                                                       324 SGPKPKNLGNNTKLIBWLPQNDLLGHSKIKARLSHGGLNSIPETWYHGVPVVGIPLFGDH 383
275 DIQRWYNGANEHGFVLVSFGAGVKYLSEDIANKL-----AGALGRLPQKVIWRF 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                        : | : | : | | | : : | | | : : | | | 384 YDTWTRVQAKGMGILLEWKTVTEKELYEALVKVINNPSYRQRAQKLSEIHKDQPGHP 440
                                                                                                                                                                                                                                                                        350 PGVASRIVYHGIGKRAS-RFTTSHALARQIRSLLTNTDYPQRMTKIQAALRLAGGTP 405
                                                                            249 KPRIFASLGTLQGHRYGLFRTIAKACBEVDAQLLLAHCGGLSATQAGBLAR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Protein Q16880, SEQ ID NO 14624.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-033347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-2002; 2002WO-US025765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Woolf C, D'urso D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FARE ) BAYER AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                              ADD48913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 LIPE-------LOPPRKALPDCFHAVGPLRQPQGFPGSSTSYFPSPD 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     angina, ischemia, myocardial infarction or arteriosclerosis by detection of a polynucleotide in a biological sample comprises detecting a hybridization complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 FNSTTSDAFLQSKMRNIFSGRLTAI------RLFDILDHYTKNCDLM-----VGNH 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- PGSLSHLLHLAAHPLGPSMLRLINEMARTSDMLCRELPAAFH
                                                                                                                                                                                                                                                   Cardiovascular disease, arteriosclerosis; ischaemia; angina pectoris; myocardial infarction; cardiant; antiarteriosclerotic; antianginal; gene therapy; differential gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 VIAPP--FFSHVRALQNIAQELVARGHRVTFFQQHDCKALVTGSDIG-FQTVGLQTHP--
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                                                                                                                                                                                                         Protein differentially expressed in cardiovascular disease #53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schmitz G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 406-408; 454pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wick M,
                                                         ABU89759 standard; protein; 541
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Best Local Similarity 20.19
Matches 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         WO2003031650-A2.
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                                                                                                           ABU89759;
               SULT 13
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aerocolonigenes (ATCC 39243). The glycosyl transferase (GT) may be from any organism of the order Actinomycetales. GT is used in a method of glycosylating indolopyrrolocarbazole derivs. Glycosylated indolopyrrolocarbazole derivs. are useful as anti-tumour agents. GTs can be made by recombinant means using new GT-producing strains Streptomyces lividans TX21 (pNGT207) FERM BP-5091 and S. morbaraensis BA 13793 (pNGT207) FERM BP-5091 and S. worbaraensis CA (field)

AAR93982 is a glycosyl transferase enzyme derived from Saccharothrix

- useful in glycosylation of

Gene coding for glycosyl transferase indolo:pyrrolo carbazole derivs.

Claim 4; Page 4-6; 45pp; Japanese

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Suda

'n Kondo

Suzuki H,

Kojiri K,

WPI; 1996-049691/05. N-PSDB; AAT29923.

(BANY) BANYU PHARM CO LTD

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polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g., spinal segmental nerve injury (Chung), chronic construction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g., gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                               77 FNSTTSDAFLQSKMRNIFSGRLTAI------BLFDILDHYTKNCDLM-----VGNH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GGDIQVVDFADQSAALSQAQLT--ITHGGMYTVLDAIASRTPLLALPLAFDQ 349
                                                                                                                                                                                                                                                                                                                                                        -----PGSLSHLTHLAAHPLGPSMIRLINEMARTSDMLCRELPAAFH 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIPEKSMYDEVHGSSLWMLCTDVALEPPRPTLPNVVYVGGILTKPAS-----PLPE 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 KPRIFASLGTLQGHRYGLFRTIAKACEBVDAQLLLAHCGGLSATQAGBLAR----- 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------LDFPRKALPDCFHAVGPLRQPQGTPGSSTSYFPSPD 248
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                                                                                                                                                                                                                                                                                                                                                                                                                             ALQIEG------VIVDQMEPAGAVVAEASGLPFVSVACALPLNREPG--LPLAVMPFE 152
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                                                                                                                                                                                                                                                                                     6 VIAPP--FFSHVRALQNIAQBLVARGHRVTFFQQHDCKALVTGSDIG-FQTVGLQTHP-- 60
                                                                                                                                                                                                                                                                                                                 24 IIVPPIMPESHMYIPKTLASALHERGHHTVPL-----LSBGRDLAPSNHYSLQRYPGI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGVASRIVYHGIGKRAS-RFTTSHALARQIRSLLTNTDYPQRMTKIQAALRLAGGTP 405
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                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                 / Match 7.8%; Score 174.5; DB 7; Length 541; Local Similarity 20.1%; Pred. No. 2.9e-08; hes 96; Conservative 71; Mismatches 173; Indels 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycosyl transferase; glycosylating; indolopyrrolocarbazole; Actinomycetales; cancer treatment; anti-tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 CFSPLAQISQL-----IPELDPPRKALPDCFHAVGPLRQPQGTPGSSTSYFPSPD--KPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 VHVTQG------TVANDAE----RLLLPAIRALAAEDVLVVATTGAPLELEPMPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 DIQVVDFADQSAALSQAQLTITHGGMNTVLDAIASRTPLLALPLAFDQPGVASRIVXHGI
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                                                                                                                                                                                                                                                           Length 414;
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21.4%; Pred. No. 4e-08;
tive 68; Mismatches 156; Indels
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		Description	Q8gcs4 pantoea ste	Q47842 pantoea agg	Q8vuj8 pantoea agg	Q93ci9 xanthobacte	P94788 flavobacter	Q9k969 bacillus ha	Q9kix4 bradyrhizob	Q8xx94 ralstonia s	Q9sxz6 daucus caro	Q9zu77 arabidopsis	Q8nwd6 staphylococ	Q9lia0 arabidopsis	Q99tx2 staphylococ	QBlsc4 cistus inca	Q91hr4 arabidopsis	Q7w7q1 bordetella	
SUMMARIES		CI.	Q8GCS4	Q47842	Q8VUJ8	Q93CI9	P94788	69K36Ö	Q9KIX4	Q8XX94	95XZ6	09ZU77	QBNWD6	O9LIA0	Q99TX2	Q8LSC4	Q91.HR4	Q7W7Q1	
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364	363.5	363.5	362.5	361	360.5	36	360	59.	59.	359.5	359	359	358.5	358.5	358.5	357.5	357.5	357.5	356.5	355.5	355	354	m	52	m	351.5	349	347	
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ALIGNMENTS

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Best Local Similarity 99.3%; Pred. No. 1.4e-114;

Matches 301; Conservative 1; Mismatches 1; Indels 0; Gaps

1 LIVCAKKHVHLTGISAEQLLADIDSRLDQLLPVQGRADCVGAANREGTLAPGKRIRPMLL
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
NCBI_TaxID=66269;
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deSouza M.L., Kollmann S.R., Schroeder W.A.;

deSouza M.L., Kollmann S.R., Schroeder W.A.;

"Carotenoid Biosynthesis (WO 02/079395 A2).";

submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AY166713; AAN85596.1; -

CO; OC:0008299; P:isopremoid biosynthesis; IEA.

InterPro; IPR000994; Polypremyl synt.

InterPro; IPR000994; Polypremyl synt.

Pram; PF00348; polypremyl synt.

PROSITE; PS00744; POLYPREMYL SYNTHET.1; 1.

PROSITE; PS00744; POLYPREMYL SYNTHET.2; 1.

SEQUENCE 303 AA, 32430 MW; SCBEFB68PD7B432B CRC64;
                                                                                                                                                                                                                                                                                                  01-NAR-2003 (TEMBLrel. 23, Last sequence update) 01-NAR-2003 (TEMBLrel. 25, Last annotation update) Geranylgeranyl pyrophosphate synthase. CRTE.
                                                                                                                                      303 AA
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01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                             PRT;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
NCBI_TaxID=182454;
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InterPro; IPR0008949; Terpenoid synth.
Pfam; PP00348; polyprenyl synt; 1.
PR05ITE; PS0043; POLYPRENYL SYNTHET 1; 1.
SEQUENCE 303 AA; 32504 MW; 605183FDC0A5816D CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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Best Local Similarity 78.2%; Pred. No. 1.9e-87;
Matches 237; Conservative 24; Mismatches 41
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Q93CI9;
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MEDLINE-9423627; PubMed-8180698;

MEDLINE-9423627; PubMed-8180698;

A TO K.Y., Lai S.T.,

Chang Y.S., Liu S.T.;

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IT Exwinta herbicola Encod.";

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RMEL; M90699; AAA21260.1;

RMEL; M90699; AAA21260.1;

RMEL; M90699; Polypenyl synt.

RGG, GO:0008299; Pisoprenoid biosynthesis; IEA.

InterPro; IPR00099; Polypenyl synt.

InterPro; IPR00099; Polypenyl synt.

InterPro; IPR00099; Polypenyl synt.

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RR Pfan; PF00344; POLYPRENYL SYNTH.

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MEDILINE=33371414; PubMed=8395826;
Liu S.T.
"Carotenoid-biosynthesis genes as a genetic marker for the purpose of
                                 Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
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Last sequence update)
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Biochem. Biophys. Res. Commun. 195:259-263(1993)
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01-NOV-1996 (TrEMBLrel. 01, Cr
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                                                                                                                                                                                                                                                                                                                                                                                  196 ASTOMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTDT---GKDINQDAGKSTL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 LRAVIDRRLGLLVPPAASHPAVLHAAMRHIILSPGKRLRPLLTLAAAIQINA--SEHAVL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                      138 AEGLTPIAKTRAVSELSTAIGMOGLVOGOFKDL--SEGDKPRSADAILLTNOFKTSTLFC 195
                                                                                                                                                                                                                                                                                                                                 77
                                                                                                                                                                                                                                                                                                                                 19 LLADIDSRLDQLLPVQGBRDCV-GAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                        Xanthobacter sp. (strain Py2).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Byphomicrobiaceae; Xanthobacter.
VGBI_TaxID=78245;
                                                                                                                                                                                                                                                                          32.1%; Score 490; DB 2; Length 359; 44.9%; Pred. No. 2.2e-31; ive 41; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Flavobacterium sp. ATCC 21588.
Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
Flavobacteriaceae; Flavobacterium.
                                                                                                                                            Larsen R.A., Metcaif W.W.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF408847; AAL019981; -
GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
                                                                                                                                                                                              InterPro; IPR000092; Polyprenyl_synt.
InterPro; IPR008949; Terpenoid synth.
Pfam, PF00348; Polyprenyl_synt; 1.
SEO01EE; PS0044; POLYPENYL SYNTHET 2; 1.
SEQUENCE 359 AA; 37348 MW; AE33F9D22D4B727D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Geranylgeranyl synthase.
01-DEC-2001 (TrEMBirel. 19, Last sequence update)
01-OCT-2003 (TrEMBirel. 25, Last annotation update)
Geranylgeranyl diphosphate synthase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 IASLGA----PRAR---KLLSEHLAGA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                      Matches 120; Conservative
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                                                                                                                    SEQUENCE FROM N.A.
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                                       CRTE.
Xanthobacter
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                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 G--IDLACAIEMIHTYSLIHDDLPSMDDDDIRRGKPTNHKVFGEAHAILAGDALLTYSFE 124
                                                                                                                                                                                                                                                                                                                                                                     64 AWVDAACAVEMVHAASLIFDDMPCMDDARTRRGQPATHVAHGEGRAVLAGIALITEAMRI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CASTOMASIAANASCEARENLHRPSLDLGQAFQLLDDLTDGMTD---TGKDINQD-AGKS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 VAGLEMLSIIKGLDKAETEQLMAFGRQLGRVFOSYDDLLDVIGDKASTGKDTARDTAAPG 240
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                                                                                                                                                                                                                                              76 -LLDLACAVEMVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 IABABGLTPIAKTRAVSBLSTAIGMQGLVQGQFKDLSEGDKPRSADAILLTNQFKTSTLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
BMBL; AR001516; BAB06500.1; -. PIR; E83997; E83997; E83997.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008299; P:isopremoid biosynthesis; IEA.
InterPro; IPR000092; Polypremyl_synt.
InterPro; IPR0009949; Terpenoid synth.
Defam. DP00148. "Alvarent" ent.
                                                                                                                                                Gaps
                                                                                                                                                                                                              23 IDSRIDQLIPVQGERDCV----GAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGG-
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STRAIN=C-125 / JCM 9153;
MEDLINEL=20512582; Pubmed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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                                                                                          DB 2; Length 295;
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                                                                                          27.9%; Score 425; DB 2; Length 29
39.6%; Pred. No. 3e-26;
ive 37; Mismatches 102; Indels
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NCBI_TaxID=86665;
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PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.
SEQUENCE 295 AA; 31332 MW; 849AC89EECEAECO1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 TLVNLLGSGAVEERLRQHLRLASEHLSAACQNGHSTTQLF 290
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Last annotation update)
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PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.
PROSITE; PS0044; POLYPRENYL SYNTHET 2; 1.
Transferase; Complete protecme.
SEQUENCE 294 AA; 32653 MW; 3B2942868A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sed
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                                                                                          125 IVAKMKGVDPAKTLCLIBELARAAGPEGMVGGQVADIBGENQKLTVEGLEYIHHHKTGAL
                                                                                                                                                      194 FCASTQMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGWTD---TGKDINQDAG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes from the photosynthetic bacterium Bradyrhizobium sp. strain ORS278.";
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CRTE.
Tradyrhizobium sp. ORS278.
Bradyrhizobium sp. ORS278.
Bradyrhizobiaceae, Bradyrhizobium.
OCBI_TaxID=114615;
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CO:0008299; P:isopyrenoid biosynthesis; IEA.
GO: CO:0008299; P:isopyrenoid synt.
InterPro; IPR0009949; Terpenoid synt.
Pfam; PR00348; polyprenyl synt. 1.
Pfam; PR00348; polyprenyl synt. 1.
PROSITE; PS0444; POLYPENYL SYNTHET 2: 1.
PROSITE; ABA; 33713 MW; 9921ABD798A3FP16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                   245 KSTYPSILITLEGAKEKLHIHTILLAKBYLYSVQMN 278
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SEQUENCE FROM |
STRAIN=ORS278;
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                                           134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244
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BEDI1MES-1681879; PubMed=11823852;

SAIDINES-1681879; PubMed=11823852;

SAIDINES-1681879; PubMed=11823852;

Arlat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Ellault A., Brottier P., Camus J.C., Cattolico L., Arlat M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Siguier P., Lavie M., Moisan A., Robert C., Sauxin W., Schiex T., Fielsenhach J., Boucher C.A.;

Weissenhach J., Boucher C.A.;

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

"Mature 415:497-622(2002).
01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
Probable geranyltransferase (Farnesyl-diphosphate synthase)
protein (EC 2.5.1.10)
                                                                                                                                                                                                                                                                            Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.6%; Score 391; DB 16; Length 299; 38.4%; Pred. No. 1.7e-23; ive 43; Mismatches 104; Indels 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AL646668, CAD15929.1; -. GO, GO:0004337, F:geranyltranstransferase activity; IEA GO; GO:0004337, F:geranyltranstransferase activity; IEA. GO; GO:0016740; F:transferase activity; IEA. GO; GO:0008299; P:isopranoid biosynthesis; IEA. InterPro; IPR000992; Polyprenyl synt. InterPro; IPR008999; Terpenoid_synth.
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01.MAY-2000 (TrEMBLrel. 13, Last sequence update)
01.OCT-2003 (TrEMBLrel. 25, Last annotation update)
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PROSITE; PS00723; POLYPRENYL SYNTHET 1: 1.
PROSITE; PS00444; POLYPRENYL SYNTHET 2: 1.
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ISPA OR RSC2222 OR RS01377.
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Best Local Similarity 38.4%
Matches 108; Conservative
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Daucus carota (Carrot)
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(MAR-2000) to the EMBL/GenBank/DDBJ databases.
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ISPA OR MW1474.
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Best Local
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.
Cronin L.A., Shen M., Vanken S.E., Umayam L., Tallon L.J., Gill J.E.
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Bisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                           Gaps
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NCBI_TaxID=3702,
                                                                                                                                                                                                                                                                                                                                                                                 23 IDSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGGL
                                                                                                                                                                                                                                                                                                   25.3%; Score 385.5; DB 10; Length 367; 37.2%; Pred. No. 6.3e-23;
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                                                                                                             to the EMBL/GenBank/DDBJ databases.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative geranylgeranyl pyrophosphate synthase.
ATC318620.
Arabidopsis thaliana (Mouse-ear cress).
                                                     TISSUB=Root;
Uno T., Sankawa U.;
Uno T., Sankawa U.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ datak
EMBL; AB027706; BAA78047.1;
EMBL; AB027706; BAA78047.1;
EG) GO:0008299; P:isoprenoid biosynthesis; IEA.
InterPro; IPR008949; Pisoprenoid synth.
InterPro; IPR008949; Terpenoid-synth.
PROSITE; PS00723; POLYPRENYL, SYNTHET 1; 1.
PROSITE; PS00723; POLYPRENYL, SYNTHET 1; 1.
PROSITE; PS00444; POLYPRENYL_SYNTHET 1; 1.
                                                                                                                                                                                                                                                                                                                                           49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 LVNLLGSGAVEERLRQHLRLASBHLS 277
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                                                                                                                                                                                                                                                                                                                                           99; Conservative
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STRAIN=cv. Columbia;
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                                         SEQUENCE FROM N.A.
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   NCBI_TaxID=4039;
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183 PARVVRAIGELAKAIGSKGLVAGQVVDLTSGGMDQNDVGLEVLEFIHVHKTAVLLEAATV 242
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Baba T., Takeuchi F., Kuroda M., Yuzawa E., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
                                                                                                                                                                                                                                                                                                                                          11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 24.7%; Score 376.5; DB 16; Length 293; Local Similarity 35.5%; Pred. No. 2.5e-22; nes 98; Conservative 44; Mismatches 119; Indels 15;
                                                                                                                                                                                                                                                                                    DB 10; Length 347;
                                                                                                                                                                                                                                                                                                                                             89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _
::
EMBL; AC006135; AAD12206.1; -
PIR; E84566; E84566
GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
InterPro; IPR00092; Polyprenyl synt.
InterPro; IPR009849; Terpenoid synth.
Pfam; PF00348; polyprenyl synt; i.
PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.
SEQUENCE 347 AA; 37390 MW; CCGSCDID22FF8840 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293 AA; 32778 MW; 4A1920D61BB2CA7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus (strain MW2).
Bacteria, Firmicutes, Bacillales, Staphylococcus
                                                                                                                                                                                                                                                                                                               .6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DATES: AP004827; BABS5339-1; ...
GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
GO; GO:0008299; P:isoprenoid biosynthesis; IEA.
InterPro; IPR0008949; Perpenoid synth.
PEAR: PF00348; polyprenyl synt; 1.
PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.
PROSITE; PS00444; POLYPRENYL_SYNTHET 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                          48; Mismatches
                                                                                                                                                                                                                                                                                 24.7%; Score 377.5; 37.6%; Pred. No. 2.6
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01-OCT-2002 (TrEMBLES). 22,
01-OCT-2003 (TrEMBLES). 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lancet 359:1819-1827(2002)
                                                                                                                                                                                                                                                                                                                                             89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                               Similarity
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300 GKDVMAGKLIYPRLIGLERSREVAEKLR---REAAEQL 334
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                                                                          Q99TX2
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QBLSC4
                                             RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --GVIAEAEGLTPIAKTRAVSELSTAIGMQGLVQGQFKDL-SEGDKPRSA--DAILLTNQ 187
    INTEYELG--MKSAIALEMIHTYSLIHDDLPAMDNDDYRRGKLTNHKVYGEWTAILAGDA 114
                                 LLSKAFGVIAEAEGLTPIAKTRAVSELSTAIGMOGLVOGOFKDLSEGDKPRSADAILLTN 186
                                                          115 LLIKAFELISSDDRLIDEVKIKVLORLSIASCHVGMVGGOMLDMQSEGOPIDLETLEMIH 174
                                                                                                            "Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
TAC and BAC clones."
DNA Res. 7.217-221 (200)
BNBS, AP001309; BAB02589.1; -.
GO; GO:0006299; P:isoprenoid biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 IDSRIDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLLL----LTARDLGCAISHGGLLD
                                                                                         ...TGKDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                Geranylgeranyl pyrophosphate synthase.
Arabidopsis thaliana (Mouse-ear oress).
Sparayota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NOBI_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAINE-COlumbia;
Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LACAVEMVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAP-
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                                                                                         187 QEKTSTLFCASTOMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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41A40566CC8962F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKST------LVNLLGSGAVEERLROHLRLASEHL 276
                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84;
                                                                                                                                                                   235 GSDLENNKSTYVSLLGKDGAEDKLTYHRDAAVDELT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.7%; Score 376.5; DB 1
37.1%; Pred. No. 3.3e-22;
                                                                                                                                                    244 NODA--GKSTLVNLLGSGAVEERLROHLRLASEHLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00348; polyprenyl synt; 1.
PROSITE; PS00723; POLYPERNYL SYNTHET 1, 1.
PROSITE; PS00444; POLYPERNYL SYNTHET 2; 1.
SEQUENCE 357 AA; 38502 MW; 41A40566CC8
                                                                                                                                                                                                                                                          357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000092; Polyprenyl synt.
InterPro; IPR008949; Terpenoid synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Columbia;
MEDLINE=20363099; PubMed=10907853;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakamura Y.;
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Best Local S
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                                                                                                                                                                                                                              ESULT 12
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INTEYELG -- VKSAIALEMIHTYSLIHDDLPAMDNDDYRRGKLTNHKVYGEWTAILAGDA 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QFKTSTLFCASTQMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTD---TGKDI 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 LGCAISHGGLLDLACAVEMVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVA
                                                                                                                                                                                                                                                                                                                                      SPECIES—S. aureus (strain Mb16), and S.aureus (strain N315);
MEDLINE=21311952; PubMed=11418146;
MEDLINE=21311952; PubMed=11418146;
Minda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goro S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba
'Mkhole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETAFFBBBA868F7D8 CRC64;
                                                 or-oct-2003 (TrEMBLrel, 25, Last sequence update) IspA protein (Geranyltranstransferase homolog). ISPA OR SAVI521 OR SAI352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.6%; Score 375.5; DB 16; 35.5%; Pred. No. 3e-22; iive 44; Mismatches 119;
                                                                                                                                                                                              Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBL_TaxID=158878, 158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 NODA--GKSTLVNLLGSGAVEERLRQHLRLASEHLS
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GO; GO:0016740; F:transferase activity; IEA
GO; GO:000299; P:isoprenoid biosynthesis;
InterPro; IPR000092; Pelyprenyl gynt.
InterPro; IPR0009949; Terpenoid_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PĒGM; PP00348; polypreny<u>l</u> synt; 1.
PROSITE; PS00723; POLYPRENYL_SYNTHET 1; 1.
PROSITE; PS00444; POLYPRENYL_SYNTHET 2; 1.
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SECUENCE 293 AA; 32746 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lancet 357:1225-1240(2001).
EMBL; AP003362; BABS7683.1; -.
EMBL; AP003134; BAB42614.1; -.
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QBLSC4;
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 35.5%
Matches 98, Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 AA;
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Search completed: February 29, 2004, 14:50:49 Job time : 28.9147 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 DQMADSVNQALESAVSLR-EPLKIHEAMRYSLLAGGKRVRPLLCIAACELVGGDVSVA-- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 MPAACAVEMIHTMSLIHDDLPCMDNDDLRRGKPTNHKAFGEDIAVLAGDALLSFAFEHVA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 -EAEGLIPIAKTRAVSELSTAIGMOGLVOGOFKOL-SEGDKPRSADALLLINOFKTSTLF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CASTQMASIAANASCEARENLHRFSLDLGQAPQLLDDLTD---GMTDTGKDINQD--AGK 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 BAAVVIGAILGGGTDEEVBRIRKFAICIGLLFQVVDDILDVTKSSVELGKTAGKDLVADK 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 EQLIADIDSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGGL
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Geranylgeranyl pyrophosphate synthase.
GGSPS2.
Cistus incanus subsp. creticus.
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spernatophyta; Magnoliophyta; endicotyledons; core endicots; rosids;
eurosids 11; Malvales; Cistaceae; Cistus.
NCBI_TaxID=191224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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01-0CT-2000 (TrEMBLEE]. 25, Last annotation update)
Geranylgeranyl pyrophosphate synthase.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota, Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids 11; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 STLVNLLG---SGAVEERLR----QHLR-----LASEHLSAACQN 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320 VIYPKIMGLEKSREFAEKIRDDAVEQLRVFDQVKAAPLIALAHYIAYRQN 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 369;
                                                                                                                                                                                                                                                                                     Pateraki I., Kanalis A.K.;

"Cloning of Cistus creticus subsp. creticus geranylgeranyl
"Cloning of Cistus creticus subsp. creticus geranylgeranyl
pyrophosphate synthase cDNA."

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AF492023; AAM21639.1; ---
CO; GC:000829; P:isoprenoid biosynthesis; IEA.

Interpro; IPR008949; Terpenoid_Synt.

Pram; PP00348; polyprenyl synt.
PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.

PROSITE; PS00744; POLYPRENYL SYNTHET 2; 1.

SEQUENCE 369 AA; 39735 MW; 3AB04635AE0F21A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.2%; Score 369.5; DB 10; Length
35.5%; Pred. No. 1.3e-21;
ive 49; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -OCT-2000 (TrEMBLrel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 35.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Nakamura Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09LHR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESULT 15
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99 MODAQMRRGRPTIHTQYGEHVAILAAVALLSKAF-----GVIABABGLTPIAKTRAV 150
                                                                                                                                                                                                                                       203
                                                                                                                                                                                                                                                                    SELSTAIGMOGLVOGOFKDL-SEGDKPRSA--DAILLINOFKTSTLFCASTOMASIAANA 207
                                                                                                                                                                                                                                                                                                  204 TELAKAIGTKGLVAGQVSDLCSQGLNPYDVGLERLEFIHLHKTAALLEAAAVLGAIIGGG 263
                                                                                                                                                                                                                                                                                                                                                            208 SCEARENLHRFSLDLGGAFQLLDDLTDGMTDTGKDINQDAGKST-----LVNLLGS
                                                                                                                                                                                                                        43 AMREGILAPGKRIRPMILL----LIARDLGCAISHGGLLDLACAVEMVHAASLILDDAMPC
                                                                                                   Gaps
                                                                                                   40;
                                                                  Length 360;
                                                                                                   Indels
POLYPRENYL SYNTHET 1; 1.
POLYPRENYL SYNTHET 2; 1.
38936 MW; 83A4F63A9E40CBC2 CRC64;
                                                                  24.1%; Score 368; DB 10; 37.6%; Pred. No. 1.6e-21;
                                                                                                     46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             259 GAVEERLRQHLRLASEHL 276
                                                                                                                                                                                                                                                                                                                                                                                                                                              323 REVAEKĹŘ---ŘEÁAEQĽ 337
                                                                      Query Match
Best Local Similarity 37.6
Matches 97; Conservative
     PS00723; PC
PS00444; PC
360 AA;
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PROSITE; E
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283366 seqs, 96191526 residues

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aximum DB seq length: 200000000

summaries ost-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

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4: Dirl:* atabase

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		crtB protein - Erw	phytoene synthase	geranyltranstransf	probable geranylge	hypothetical prote		geranylgeranyl pyr		geranylgeranyl pyr	probable geranyige	geranyltranstransf	geranyltranstransf	geranyltransferase	geranyltranstransf	๙	geranylgeranyl pyr	geranylgeranyi pyr		geranyltranstransf	farnesyltranstrans	farnesyltranstrans	geranyltranstransf	geranyltranstransf	geranyltranstransf	geranyltranstransf	geranyltranstransf	geranyltranstransf	geranyltranstransf
	ID	A37802	S52584	C39273	83	E84566	A89932	853722	P85434	T10452	T02429	G84566	D87505	JX0257	F97685	AH2910	AI3285	S71230	S74538	AE1833	A69961	T11021	T09966	A82267	AH0385	300665	AG1607	E81796	990	G85538
	DB	5	~	7	Ċ	Ċί	ĊV	7	7	Ŋ	N	N	N	7	N	N	N	N	N	7	۲,	N	(7	N	~	N	0	Ŋ	7	7
	Length	302	302	308	294	347	293	369	371	366	376	372	294	297	304	335	304	378	302	309	272	316	357	294	306	299	293	298	299	299
ر ورور ورور	-	88	84.		27.	24.		C	7	23.	7	23	23	23	23	N	23	23	23	23	22	(A	22	CA	22	21.	21.	14	21,	21.5
	Score	1344.5	1295.5	752	412.5	377.5	375.5	372	369	364.5	364	361	360.5	360.5	358.5	358.5	356.5	355	354	352	346.5	345.5	345.5	339	335.5	332	329	328.5	328	328
t Linear	No.		101	ო	4	ហ	9	7	80	σ		11			14	5	16	17	18				22				56		28	29

241 KOINQDAGKSTLVNLIKGSGAVEERLRQHLRLASEHLSAACQNGHSTTQLFIQAWFDKKLA 300

241 KOSNQDAGKSTLVNLLGPRAVEERLRQHLQLASEHLSAACQHGHA-TQHFIQAWFDKKLA 299

301 AVS 303 AVS 302

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RESULT 2

\$52584 crtE protein - Erwinia herbicola C;Species: Erwinia herbicola C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 24-Nov-1999 C;Accession: S52584

geranyltranstransf v4kU protein - Rhi	probable dimethyla	geranyltranstranst	tarnesyltranstrans	geranyltranstranst	tarnesyltranstrans	geranyltranstransi	geranylgeranyl pyr	geranyltranstransi	farnesyltranstrans	geranyltranstransi	geranyltranstransi	geranyltranstransi	phytoene synthase	geranyltranstransi
AG0554	140213	AC1245	T06969	D82778	T05674	C64123	849625	F81217	T50750	F98007	G95139	F83139	S04407	B81261
00	1 (1	N	N	N	N	N	N	~	7	N	0	7	~	7
900	332	293	300	291	326	295	288	259	288	291	291	295	289	281
21.1	20.7	20.6	20.5	20.5	20.5	20.3	20.2	20.1	20.1	20.0	19.9	19.8	19.5	19.4
322	316	314	313,5	313	313	309.5	308	307	307	305.5	303.5	301.5	297.5	296
30	⊣ (X) n m	33	34	35	36	37	38	6	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

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                                                                                                                                                                                                                                                               181 AILLTNOFKTSTLFCASTQMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTDTG 240
                                                                                                                                                                                                                                                                                                   61 LITARDIGCAVSHDGLIDLACAVEWVHAASLILDDMPCMDDAKLRRGRPTIHSHYGEHVA 120
                                                                                                                                                                                                                                                     9
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                                                                                                                                                                          1 LIVCAKKHVHLTGISAEQLLADIDSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLL
                                                                                                                                                                                    Gaps
                                                                                                                                                         1;
                                                                                                                                      Length 302;
                                                                                                                                     Query Match

88.1%; Score 1344.5; DB 2; Length

Best Local Similarity 88.4%; Pred. No. 1.7e-104;

Matches 268; Conservative 16; Mismatches 18; Indels
crtE protein - Erwinia uredovora
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2; Gaps

76 75

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C)Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 17-May-2002
C;Accession: B83997
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir. Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: GB:AP001516, GB:BA000004; NID:g10175192; PIDN:BAB06500.1; GSPDB:GN0
Experimental source: strain C-125
                                                                                                                                                                                                                                            77 IDLACAVBMVHAASLILDDMPCXDDAQMRRGRPTIHTQYGBHVAILAAVALLSKAFGVIA 136
                                                                                                                                                                                                                                                                    76 LDLACAVELTHTASLMLDDMPCMDNAELRRGOPTTHKKFGESVALLASVGLLSKAFGLIA 135
                                                                                                                                                                                                                                                                                                                                                                 137 BARGLIPIAKTRAVSELSTALGMOGLVQGQPKDLSEGDKPRSADAILLTNOFKTSTLFCA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 STQMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTDTGKDINQDAGKSTLVNLL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              geranyltranstransferase BH2781 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 GGLLDLACAVEMVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 G--IDLACAIEMIHTYSLIHDDLPSMDDDIRRGKPTNHKVFGBAHAILAGDALLTYSPE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 VIAEARGLTPIAKTRAVSELSTAIGMOGLVQGQFKDLSEGDKPRSADAILLTNQFKTSTL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 IVAKOKGVDPAKTLCLIEBLARAAGPBGOVGGQVADIBGBNQKLTVEGLEYIHHHKTGAL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 FCASTQMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTD---TGKDINQDAG-- 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 LSFAIVAGARLADĀSEQDIENIRRFSRELGLLFQIRDDILDVEGDQAAIGKPVGSDDGNQ 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 QLLADIDSRLDQLLPVQGER----DCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISH 73
                                                                                                                                                                                                                                                                                                                                                                                                   17 EQLLADIDSRLDQLLPVQGERDCVGAANREGTLAPGKRIRPMLLLLTARDLGCAISHGGL
                                                                                                                                                         Query Match
27.0%; Score 412.5; DB 2; Length 294;
Best Local Similarity 37.6%; Pred. No. 7.5e-27;
Matches 103; Conservative 47; Mismatches 113; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257 GSGAV-EERLRQHLRLASEHLSAACQNGHSTTQLFIQAWFDXXLA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 GADAARROKLREHIDSADKHLTFACPOGGAIRQ-FWHLWFGHHLA 299
55.8%; Pred. No. 4e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Superfamily: geranyltranstransferase
                                                        Matches 159; Conservative
                              Best Local Similarity
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A;Molecule type: DNA
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A;Molecule type: DNA
A;Residues: 1-308 <ARM>
A;Cossidues: 1-308 <ARM>
A;Cossidues: 1-308 <ARM>
A;Cossidues: 1-308 <ARM>
A;Note: the authors translated the codon CTC for residue 187 as Ala, ATT for residue 191
e 211 as Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O
D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phytoene synthase - Erwinia herbicola
C;Species: Erwinia herbicola
C;Species: Erwinia herbicola
C;Accession: C39273; C31120
R:Atmstrong, G.A.; Alberti, M.; Haarst, J.E.
Proc. Natl. Acad. Sci. U.5.A. 87, 9975-9979, 1990
A;Title: Conserved enzymes mediate the early reactions of carotenoid biosynthesis in a A;Reference number: A39273; MUID:91088634; PMID:2263648
                                                                                                                                                            4,Status: preliminary, nucleic acid sequence not shown; translation not shown 4; Molecule type: DNA 4; Residues: 1.302 - LINA 4; Residues: 1.302 - LINA 4; Cross-references: EMBL: M90698; NID:g148393; PIDN:AAA21260.1; PID:g148394 4; Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1992 2; Superfamily: geranyltranstransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLTARDLGCAISHGGLIDLACAVEMVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rilin, Y.P.; Lai, E.M.; To, K.Y.; Chang, Y.S.; Liu, S.T.
Wol. Gen. Genet. 245, 417-423, 1994
A;Title: Transcriptional activation of flanking sequences by Tn1000 insertion.
A;Reference number: S52583; MUID:95107237; PMID:7808390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LLTARDLGCAVSHEGLLDIACAVEMVHAASLILDDMPCMDDAQIVGGRPTVHCQYGEHVA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ILAAVALLSKAFGVIAEAEGLTPIAKTRAVSELSTAIGMQGLVQGQFKDLSKGDKPRSAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AILLINQFKTSTLFCASTQMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTDTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDINQDAGKSTLVNLLGSGAVEBRLRQHLRLASEHLSAACQNGHSTTQLFIQAWFDKKLA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 KDINQDEGKSTLVNLLGSRAVEERLRHSLKHASEHLSAACQNGKSTQQ-FIQAWFDKKLA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LTVCAKKHVHLTGISAEQLLADIDSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 84.9%; Score 1295.5; DB 2; Length 302; Best Local Similarity 86.1%; Pred. No. 2e-100; Matches 261; Conservative 14; Mismatches 27; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: the authors inserted as Arg after residue 261 in figure 3 R;Armstrong, G.A.; Alberti, M.; Hearst, J.E. submitred to the Protein Sequence Database, September 1990 A;Reference number: A33120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 AVS 303
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RESULT 3

11:

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probable geranylgeranyl pyrophosphate synthase (imported) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
```

49.3%; Score 752; DB 2; Length 308;

8 임

A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA

Experimental source: strain Eholo, ATCC 39368

A; Residues: 1-261,263-308 <AR2>

A,Gene: crtE C,Superfamily: geranyltranstransferase C,Keywords: carotenoid biosynthesis

Query Match

```
Agrical farmestransferase (BC 2.5.1.29) precursor - pepper
NyAlternate names: geranylgeranyl diphosphate synthase; geranylgeranyl pyrophosphate syn
CiSpecies: Capsitoum annuum (pepper)
CiSpecies: Capsitoum annuum (pepper)
CiAccession: 853722
CiAccession: 853722
Blant Mol. Biol. 27, 425-428, 1995
A;Title: Structure of a functional geranylgeranyl pyrophosphate synthase gene from Capsi
A;Reference number: 853722; MUID:95195169; PMID:7888631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cold Sprin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A)Residues: 1.369 <BAD>
A)Residues: 1.369 <BAD>
A)Cross-references: EMBL:X80267; NID:g643093; PIDN:CAA56554.1; PID:g643094
A)Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Accession: F85434
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Colature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: F85434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 TPSRIVGAVABLAKSIGTEGLVAGQVADIKCTGNASVSLETLEFIHVHKTAALLESSVVL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 ASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTDTGKDINQDAGKSTLVN----- 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 KTKTGALLTFAVMSAADIANVDDATKEHLBSYSYHLGMMFQIKDDLLDCYGDBAKLGKKV 234
LLTKAPELISSDBRLTDEVKIKVLQRLSIASGHVGWVGGQMLDMQSEGQPIDLETLEMIH 174
                                                                                              187 QFKTSTLFCASTQMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGWTD---TGKDI 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             geranylgeranyl pyrophosphate synthase [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-201 #sequence_revision 16-Feb-2001 #text_change 24-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 VENVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAR-GVIARAEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 IDSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGGLLDLACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Superfamily: geranyltranstransferase
;Keywords: carotenoid biosynthesis; chloroplast; chromoplast; transferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: S53722
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
24.4%; Score 372; DB 2; Length 36
Best Local Similarity 34.5%; Pred. No. 2.4e-23;
Matches 99; Conservative 52; Mismatches 108; Indels
                                                                                                                                                                                                                                                         235 GSDLENNKSTYVŞLLGKDGABDKLTYHRDAAVDELF 270
                                                                                                                                                                                                                   244 NODA--GKSTLVNLLGSGAVEERLRQHLRLASEHLS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325 LIGLEKAKBFAAELNREAKOOLEG-----
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A;Molecule type: DNA
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                                               115
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Jacuschi, Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
                            Accession: E84566
Jun, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
J. Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
ature 402, 761-768, 1999
Jitles Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
Accession: E84566
Accession: E84566
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v;Wolecule type: DNA
v;Wesidues: 1-293 <CUR>
v;Cresidues: 1-293 <CUR>
v;Cresidues: 1-293 <CUR>
v;Cross-references: GB:BA000018; PID:g13701320; PIDN:BAB42614.1; GSPDB:GN00149
v;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEMVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFGVIAEAEGLT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 VEMIHIMSLIHDDLPCMDNDDLRRGKPINHKVFGEDVAVLAGDALISFAFEHLATSTAVS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIAKTRAVSELSTAIGMOGLVQGQFKDLSEGDKPRS---ADAILLTNQFKTSTLFCASTQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 LGCAISHGGLLDLACAVEMVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 LLSKAFGVIAEABGLTPIAKTRAVSBLSTAIGMOGLVOGOPKOLSEGDKPRSADAILLTN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary
!Molecute type: DNA
;Residues: 1-347 <STO>
;Cross-references: GB:AB002093; NID:g4217998; PIDN:AAD12206.1; GSPDB:GN00139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 LGAIVGGGSDEEVEKLRRPARCIGLLFQVVDDILD-VTKSSEELGKTAGKDLIADKL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Staphylococcus aureus
;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
;Accession: A89932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTDTGKDINQDAGKSTLVNLL 256
                  Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
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1 Similarity 37.6%; Pred. No. 7.6e-24;
89; Conservative 48; Mismatches 89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: geranyltranstransferase
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene: At2g18620
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A; Molecule type: DNA
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A:Introns: 184/3
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'R. Bodfmann, B.; von Lintig, J.; Schledz, M.; Al-Babili, S.; Hobeika, B.; Klein At. J. Biochem. 247, 942-950, 1997
'Ritle: Chloroplast import of four carotenoid biosynthetic enzymes in vitro reveals dif 'Areference number: Z17023; MUID: 97433278; PMID: 9288918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arnesyltranstransferase (BC 2.5.1.29) precursor, chloroplast - white mustard (Alternate names: geranylgeranyl-diphosphate synthase, geranylgeranyl-pyrophosphate synthase; Sinapis alba (white mustard); Species: Sinapis alba (white mustard); Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                   9
                      Cross-references: GB:NC_001268; NID:g7270630; PIDM:CAB80347.1; GSPDB:GN00140
                                                                                                                                                                                                                                                                                                                  VEMVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFGVIAEA---B 139
                                                                                                                                                                                                                                                                                                                                                                                                                        144 VEMIHTMSLIHDDLPCMDNDDLRRGKPTNHKVFGEDVAVLAGDALLSFAFFHLASATSSD 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 STOWASIAANASCEARENIARFSLDIGQAFQLLDDLTDGWTDTGKDINQDAGKSTLVNLL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 SAVLGAIVGGGSDDEIERLRKFARCIGLLFQVVDDILD-VTKSSKELGKTAGKDIADKL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 GLTPIAKTRAVSELSTAIGMQGLVQGQFKDL-SEGDKPRSA--DAILLTNQFKTSTLFCA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 VVSPVRVVRÁVGELAKÁIGTEGLÍVAGÓVVDISSEGLDLNDVGLEHLEFIHLHKTAALLEA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 --CAVEMVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFGVIAEA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 EG--LTPIAKTRAVSELSTAIGMQGLVQGQFKDL-SEGDKPRSA--DAILLTNQFKTSTL 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 LEASAVIGGIIGGGSDEBIERLRKFARCIGLLFQVVDDILD-VTKSSQBLGKTAGKDLIA 314
                                                                                                                                                                                                                                                                                   23 IDSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGGLLDLACA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 IDSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGGLLDLA-- 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.Residues: 1-366 <BON>
J.Cross-references: EMBL:X98795; NID:g1419757; FIDN:CAA67330.1; PID:g1419758
                                                                                                                                                                                                                                   10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 23.9%; Score 364.5; DB 2; Length 366;
Best Local Similarity 39.5%; Pred. No. 9.9e-23;
Matches 96; Conservative 42; Mismatches 88; Indels 17; Gaps
                                                                                                                                                                          24.2%; Score 369; DB 2; Length 371; 38.8%; Pred. No. 4.2e-23; tive 46; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;Genome: nuclear
2;Superfamily: geranyltranstransferase
2;Keywords: carotenoid biosynthesis; chloroplast; transferase
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                                                                                                Map position: 4 . Superfamily: geranyltranstransferase
                                                                                                                                                                                                                             93; Conservative
                                                                                                                                                                                                      Best Local Similarity
Residues: 1-371 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 NLL 256
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                                                                         Gene: AT4936810
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                                                                                                                                                                                Query Match
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geranylgeranyl pyrophosphate synthase (EC 2.5.1.-) - Arabidopeis thaliana
[K.Alternate names: pregeranylgeranyl pyrophosphate synthase; protein F27L4.2; protein F;
[K.Alternate names: pregeranylgeranyl pyrophosphate synthase; protein F27L4.2; protein F;
[K.Alternate names: pregeranylgeranyl pyrophosphate synthase; protein F27L4.2; protein F;
[K.Species: A.-Mar.1999 #text_change 02-Feb-2001
[K.Accession: T04499; #B4629
[K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, May 1998
[K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, May 1998
[K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, A.Bescription: Arabidopsis thaliana chromosome II BAC F27L4 genomic sequence.

A.Accession: T02429
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A; Crossidues: 1-336 <RGW>
A; Crossidues: 1-336 <RGW>
A; Crossidues: 1-336 <RGW>
A; Crossidues: 1-336 <RGM: AC004482; NID:g3152602; PIDN:AAC17084.1; PID:g3152605
A; Experimental source: cultivar Columbia
R: Lin, X.; Kaul, S.; Rounsley, S.D.; Shaa, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Kco, H.; Moffat, K.S.; Cronin, L.A.; Shan, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID:20083487; PMID:10617197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-376 <ROU>
A;Cossitues: 1-376 <ROU>
A;Coss-references: EMBL:AC004482; NID:g3152602; PIDN:AAC17083.1; PID:g3152604
A;Experimental source: cultivar Columbia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 KLTYPKLIGLEKSKBFVKRLTKDARQHL 353
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A; Status: translated from GB/EMBL/DDBJ
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Matches 102, Conserva
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A.Molecule type: DNA
A.Residues: 1-376 <STO>
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Geraryltransferase (AF203881) [imported] - Agrobacterium tumefaciens (strain C58, Cereon Geraryltransferase (AF203881) [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #text_change 18-Nov-2002 C;Accession: F97685
C;Accession: F97685
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97389; MUID:21608551; PMID:11743194
A;Accession: F97685
A;Accession: F97685
A;Accession: F97685
A;Molecule type: DNA
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N;Alternate names: farmesyl-diphosphate synthase
C;Species: Bacillus stearothermophilus
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Jun-2000
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Jun-2000
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Jun-2000
C;Date: 31-Dec-1993
A;KOyama, T; Obata, S; Osabe, M.; Takeshita, A.; Yokoyama, K.; Uchida, M.; Nishino, T.
J. Biochem. 113, 355-363, 1993
A;Alte: Thermostable farmesyl diphosphate synthase of Bacillus stearothermophilus: mole A;Reference number: JX0257; MUID:93252758; PMID:8486607
A;Accession: JX0257
A;Alte: DNA
A;Residues: 1-297 < KOV>
A;Conetics:
C;Genetics:
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                                                                                                                                                     64 DPAVG--LPVACAIEMIHTYSLIHDDLPSMDDLRRGKPTNHKVFGEAMAILAGDGLAT 121
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           131 AFGVIAEAEGLTP-LAKTRAVSELSTALGMQGLVQGQFKDLSBGDKPRSADALLINQFK 189
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                                                                                                                                                                                                                                 242 DINQDAGKSTLVNLLGSGAVEERL-----RQHLRL---ASEHLSAA 279
                                                                                                                                                                                                                                                                                      240 DAAK--GKANYVILLGIDAAKERVILLAEQIRSHLEIFGERAEHLRAS 285
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                                                                                                                        TSTLFCASTOMASIAANASCEARENLHRFSLDLGQAFQLLDDLTD
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C,Superfamily: geranylt:
C,Keywords: transferase
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Best Local Si
Matches 98;
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Species: Caulobacter crescentus;
Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Bisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Dodson, R.J.; Brablaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
J.; Brmolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Trill complete Genome Sequence of Caulobacter crescentus.
,Reference number: A87249; MuID:21173698; PMID:11259647
;Accession: G84566
Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
Liko, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
Lss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
sture 402, 761-768, 1999
Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
Reference number: A84420; WUID:20083487; PMID:10617197
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;Cross-references: GB:AE005673; NID:g13423548; PIDN:AAK24040.1; GSPDB:GN00148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLIPIAKTRAVSELSTAIGMOGLVOGORKDL-SEGDKPRSA--DAILLINOFKTSTLFCA 196
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                                                                                                                                                                                                                      Status: preliminary
Molecule type: DNA
Fesidues: 1-372 <5TO>
(Cross-references: GB:AE002093; NID:g4185130; PIDN:AAD08933.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 IDSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGG---LLDL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 ADIDS-RIDQLLP-VQGBRDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGGLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 ADIVTVALDELLERADGEESRLTEAMRYAALGEGKRLRPFFALET-----GKMFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.7%; Score 361; DB 2; Length 372; 37.4%; Pred. No. 2e-22; Live 47; Mismatches 101; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YPKVIGVEKSKEFVEKLKRDAREHL 349
                                                                                                                                                                                                                                                                                                                                                                                                Map position: 2
Superfamily: geranyltranstransferase
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Best Local Similarity 37.4%
Matches 99; Conservative
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223 GALLRPACEAGAIIAGSNQAERQRLRLFGEKIGLSFQLADDLLDLTADAATWGKATGKDA 282
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Karge, G.; Gillet, W.; Zhang, S.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   geranyltranstransferase [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C.Species: Agrobacterium tumefaciens C.Species: Agrobacterium tumefaciens C.Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ter, E.W.

'Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.

'Reference number: AB2577; MUID:21608550; PMID:11743193

'Accession: AH2910

'Status: preliminary

'Molecule type: DNA
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Cross-references: GB.AE008688; PIDN:AAL43702.1; PID:g17741230; GSPDB:GN00186
Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 GGLLDLACAVEMVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFG 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALLRFACEAGAIIAGSNQAERQRLRLFGEKIGLSFQLADDLLDLTADAATMGKATGKDA 251
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                                     A;Cross-references: GB:AE007869; PIDN:AAK88439.1; PID:g15157936; GSPDB:GN00169
1;Genetics:
4;Gene: AGR C 4933
1;Map position: circular chromosome
                                                                                                                                                                                                                                                             17 EQLIADI --- DSRLDQLLPVQGBRDCVGAAMREGTLAPGKRIRPMLLLTARDLGCAISH 73
                                                                                                                                                                                                                                                                                          20 BALLGHILSGEARADEITRPQNLIE----AMRHGVLNGGKRLRPFLVIESVALLGODAEA 75
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                                                                                                                                                                   Length 304;
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C;Superfamily: dimethylallyltranstransferase
                       Residues: 1-304 < KUR>
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1 LIVCAKKHVHLTGISAEQLL.......HSTTQLFIQAWFDKKLAAVS 303
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Copyright (c) 1993 - 2004 Compugen Ltd.
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-!- CATALYTIC ACTIVITY: Trans-trans-farnesyl diphosphate + isopentenyl diphosphate = diphosphate + geranylgeranyl diphosphate.
-!- PATHWAY: Carotenoid biosynthesis.
-!- SIMILARITY: Belongs to the FPP/GGPP synthetase family.
                                            ILAAVALLSKAFGVIAEAEGLTPIAKTRAVSELSTAIGMQGLVQGQFKDLSEGDKPRSAD
                                                                                                                      ALLINQFKTSTLFCASTQMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTDTG
                                                                                                                                                                KDINQDAGKSTLVNLLGSGAVEERLROHLRLASEHLSAACONGHSTTQLFIQAWFDKKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Armstrong G.A., Alberti M., Hearst J.E., Conserved enzymes mediate the early reactions of carotenoid blosynthesis in nomphocosynthetic and photosynthetic proc. Natl. Acad. Sci. U.S.A. 87:9975-9979 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.

PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.

Carotenot biosynthesis; Isoprene biosynthesis; Transferase.

SEQUENCE 307 AA; 33242 MW; 6A534C6194CE9F59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1991 (Rel. 19, Last sequence update)
10-COT-2003 (Rel. 42, Last annotation update)
Geranylgeranyl pyrophosphate synthetase (EC 2.5.1.29) (GGPP synthetase) (Farnesyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92357711; PubMed=1495965;
Math S.K., Hearst J.E., Poulter C.D.;
"The crtE gene in Erwinia herbicola encodes geranylgeranyl
                                                                                                                                                                                                                                                                                                                                  307 AA
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InterPro; IPR000092; Polyprenyl synt.
InterPro; IPR008949; Terpenoid synth.
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EMBL; M87280; AAA64977.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterobacteriaceae; Pantoea,
NCBI TaxID=549;
                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diphosphate synthase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Erwinia herbicola
                                                                                                                                                                                                                           301 AVS 303
                                                                                                                                                                                                                                                        AVS 302
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                                                                                                                                                                                                                                                                                                                                                               01-AUG-1991
                                                                                                                                                                                                                                                                                                                                  BRWHE
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-!- FUNCTION: Catalyzes the trans-addition of the three molecules of catalyzes the trans-addition of the three molecules of IPP onto DMAPP to form geranylgeranyl pyrophosphate.
-!- CATALYTIC ACTIVITY: Dimethylallyl diphosphate + isopentenyl diphosphate = diphosphate + geranyl diphosphate + isopentenyl diphosphate - diphosphate + trans, trans-farnesyl diphosphate.
-!- CATALYTIC ACTIVITY: Trans-farnesyl diphosphate + isopentenyl diphosphate + diphosphate + trans, trans-farnesyl diphosphate + isopentenyl diphosphate + geranylgeranyl diphosphate + isopentenyl diphosphate + geranylgeranyl diphosphate + isopentenyl by Trans-trans-farnesyl diphosphate + isopentenyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphosphate + geranylgeranyl diphospha
                                                                                                                                                           Capsicum annuum (Bell pepper).
Bukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; asterids;
Iamiids; Solamales, Solamacee, Capsicum.
                                                                                                                                                                                                                                              LDLACAVEMVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFGVIA
                                                                                                                                                                                                                                                                                                                                                                        137 EAEGLTPIAKTRAVSELSTAIGMQGLVQGQFKDLSEGDKPRSADAILLTNQFKTSTLFCA
                                                                                                                                                                                                                                                                                                                                                                                                                197 STQMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTDTGKDINQDAGKSTLVNLL
                                                                                                                          17 BOLLADIDSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Geranylgeranyl pyrophosphate synthetase, chloroplast precursor (GGPP synthetase) (GGPS) [Includes: Dimethylallyltransferase (BC 2.5.1.1); Geranyltranstransferase (BC 2.5.1.10);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kuntz M., Roemer S., Suire C., Hugueney P., Weil J.H., Schantz R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of a cDNA for the plastid-located geranylgeranyl pyrophosphate synthase from Capsicum annum: correlative increase enzyme activity and transcript level during fruit ripening."; Plant J. 2:25-34(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Badillo A., Steppuhn J., Deruere J., Camara B., Kuntz M.;
"Structure of a functional geranylgeranyl pyrophosphate synthase
from Capsicum annuum.";
                                                                  ä
Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Chloroplast.
SIMILARITY: Belongs to the FPP/GGPP synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSGAVERRIROHIRLASEHISAACONGHSTTOLFIQAMFDKKLA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                              84;
   DB 1;
   50.0%; Score 762.5; DB 1
56.0%; Pred. No. 2.4e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                  40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in plant terpenoid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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MEDLINE=95195169; PubMed=7888631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Lamuyo; TISSUE=Fruit;
MEDLINE=93272043; PubMed=1303794;
   Query Match
Best Local Similarity 56.0
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: Monomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4072;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 VEMVHAASLILLDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAF-GVIARAEGL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 TPIAKTRAVSELSTAIGMQGLVQGQPKDLS-EGDKPRSADAILLTNQPKTSTLFCASTQM 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 TPSRIVGAVABLAKSIGTEGLVAGOVADIKCTGNASVSLETLEFIHVHKTAALLESSVVL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTDTGXDINQDAGKSTLVN---- 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 IDSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGGLLDLACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    934802, 033201,
01-FEB-1994 (Rel. 28, Created)
16-OCT-2001 (Rel. 42, Last sequence update)
Geranylgeranyl pyrophosphate synthetase, chloroplast precursor (GGPP synthetase) (GGPS) [includes: Dimethylallyltransferase (EC 2.5.1.1);
Geranyltranstransferase (EC 2.5.1.10); Farnesyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GERANYLGERANYL PYROPHOSPHATE SYNTHETASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Buka-yota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of an Arabidopsis cDNA for geranylgeranyl
                                                                                                                                                                                                                                                                                                                                         Pfam, PF00348; polyprenyl synt, 1.
PROSITE, PS00444; POLYPRENYL SYNTHET 2; 1.
PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.
Transferase; Isoprene blosynthesis; Carotenoid blosynthesis; Chloroplast; Transit peptide.
7 CHLOROPLAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255 LIGSGAVEERLROHLRLASEHILSAACONGHSTTQLFIQAWFDKKLAA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325 ILGLBKAKEFAAELNREAKQQLEG--------PDSRKAA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2D527F5E43A29C6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 372; DB 1;
Pred. No. 9.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHLOROPLAST.
                                                                                                                                                                                                                      EMBL; X80267; CAAS6554.1; -.
PIR; S53722; S53722.
InterPro; IPR00092; Polyprenyl synt,
InterPro; IPR008949; Terpenoid synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pyrophosphate synthase.";
Plant Physiol. 104:1469-1470(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94286754; PubMed=8016276;
Scolnik P.A., Bartley G.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40173 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGPS1 OR AT4G36810
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NCBL TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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SPP ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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STANIN=CV. Columbia;

RM MEDLINE-200834819. Pubbed=10617198;

RM MEDLINE-200834819. Pubbed=10617198;

RM MEDLINE-200834819. Pubbed=10617198;

RM POBLY. T. Dusetrenteeft A., Stiekema W., Entian R.-D., Terryn N., Harris B., Amsorge W., Brandt D., Grivell L., Rieger M., Mueller M., Reicher B., Macher B., Mueller M., Reicher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Macher B., Warland B., Macher B., Warland B., Macher B., Brandt A., Peters S., Van Staveren M., Dirkew W., Macher B., Barrister S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., Barrister B., Hempel S., Feldpausch M., Lennard N., Mallarrol R., De Clark D., Wan Montagu M., Ragers J., Cronin A., Oniall M.A., Beray-Allen S., Clark L., Doggett J., Cronin A., Oniall M.A., Beray-Allen S., Macher A., Banderder M., Macher T.-H., Scharfe M., Grimm M., Loenhert T.-H., Scharfe M., Grimm M., Loenhert T.-H., Scharfe M., Grimm M., Loenhert B., Theopel C., Runk M., Macher B., Scharfe M., Macher B., Starke M., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Macher B., Stake B., Stake B., Macher B., Stake B., Macher B., Stak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diphosphate = diphosphate + geranylgeranyl diphosphate.
-!- PATHWAY: First committed step in carotenoid biosynthesis. Key enzyme in plant terpenoid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBDATT: Monomer.
-!- SUBCELLULAR LOCATION: Chloroplast.
-!- SIMILARITY: Belongs to the PPP/GGPP synthetase family.
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EMBL; AL161590; CAB80347.1; EMBL; L25813; AAA32797.1; -. EMBL; Z99708; CAB16803.1; -.

EMBL;

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SUBCELLULAR LOCATION: Chloroplast stroma; chromoplast (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ? 366 GERANYLGERANYL PYRO
366 AA; 39432 MW; 1EADBFD9C4CF4F77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.9%; Score 364.5; DB 1
39.5%; Pred. No. 3.8e-22;
iive 42; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUTAGENESIS OF CYSTEINE RESIDUES
                                                                                                                                                                                                                                                        EMBL; X98795; CAA67330.1; -. PIR; T10452; T10452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 39.5
les 96, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 NLL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 VVSPVRVVRAVGELAKAIGTEGLVAGGVVDISSEGLDLNDVGLEHLEFIHLHKTAALLEA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 STQMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTDTGKDINQDAGKSTLVNLL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ::| | ::| | ::| | ::| | SAVLGAIVGGGSDDEIBRLRKFPARCIGLLFQVVDDILD-VTKSSKELGKTAGKDLIADKL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jacohem. 247:942-950(1997).

J. Blochem. 247:942-950(1997).

J. Blochem. 247:942-950(1997).

J. Blochem. 247:942-950 (1997).

J. Blochem. 247:942-950 (1997).

J. Blochem. 247:942-950 (1997).

CATALYTIC ACTIVITY: Dimethylallyl diphosphate.

CATALYTIC ACTIVITY: Geranyl diphosphate.

CATALYTIC ACTIVITY: Geranyl diphosphate.

Alphosphate + trans.trans-farnesyl diphosphate.

CATALYTIC ACTIVITY: Trans-trans-farnesyl diphosphate.

CATALYTIC ACTIVITY: Trans-trans-farnesyl diphosphate.

CATALYTIC ACTIVITY: Trans-trans-farnesyl diphosphate.

PATHWAY: First committed step in carotenoid biosynthesis. Key enzyme in plant terpenoid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 VNKALDSAVPLR-EPLKIHEAMRYSLLAGGKRVRPVLCIAACELVGGEESTA--MPAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 GLTPIAKTRAVSELSTALGMQGLVQGQFKDL-SEGDKPRSA--DAILLTNQFKTSTLFCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 IDSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGGLLDLACA
                                                                                                                                                                                                                GERANYLGERANYL PYROPHOSPHATE SYNTHETASE
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGPP seranylgeranyl pyrophosphate synthetase, chloroplast precursor (GGPP synthetase) {GGPS} [Includes: Dimethylallyltransferase (BC 2.5.1.1); GEC 2.5.1.29)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sinapis alba (White mustard) (Brassica hirta).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Sinapis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.
MEDLINE=97433278; PubMed=9288918;
BOLLINE=97433278; PubMed=9288918;
Hobeika E., Hoffmann B., von Lintig J., Schledz M., Al-Babili S.,
Hobeika E., Kleinig H., Beyer P.,
"Chloroplast import of four carotenoid biosynthetic enzymes in vitro reveals differential fates prior to membrane binding and oligomeric
                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                  Pfam, PRO348; polypenyl synth.
PROSITE; PS0044; POLYPRENYL SYNTHET 2; 1.
PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.
Transferase; Isoprene blosynthesis; Carotenoid blosynthesis; Chloroplast; Transfer peptide.
TRANSIT
                                                                                                                                                                                                                                                                                                                                                          Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                     91; Indels
                                                                                                                                                                                                                                    108 R -> S (IN REP. 1).
141 A -> R (IN RRP. 1).
192 A -> S (IN RRP. 1).
40174 MW, EPA808BA75B6A005 CRC64;
                                                                                                                                                                                                                                                                                                                                                       24.2%; Score 369; DB 1;
ilarity 38.8%; Pred, No. 1.7e-22;
Conservative 46; Mismatches 91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Synthetase] (GGPS) [Includes: Dimethylallyltr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       366 AA
                    InterPro; IPR00092; Polyprenyl synt.
InterPro; IPR008949; Terpenoid synth.
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108
141
192
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                                                                                                                                                                                                                                                                                                          371 AA;
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                    108
141
192
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CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 LEASAVLGGIIGGGSDEBIBRLRKFARCIGLLFQVVDDILD-VTKSSQBLGKTAGKDLIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 ARCAVEMIHTMSLIHDDLPCMDNDDLRRGKPTMHKVYGEDVAVLAGDALLSFAFEHLASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 EG--LIPIAKTRAVSELSTAIGMQGLVQGQFKDL-SEGDKPRSA--DAILLINQFKTSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 FCASTQMASIAANASCEARENLHRPSLDLGQAFQLLDDLTDGMTDTGKDINQDAGKSTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 -- CAVENVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFGVIABA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 TSSEVSPARVVRAVGELAKAIGTEGLVAGOVVDISSEGLDLNNVGLEHLKFIHLHKTAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 IDSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGGLLDLA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GERANYLGERANYL PYROPHOSPHATE SYNTHETASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000092; Polyprenyl_synt.
InterPro; IPR008949; Terpenoid synth.
Para; PF00348; Polyprenyl_synt; 1.
PROSITE; PS00444; POLYPRENYL_SYNTHET 1; 1.
PROSITE; PS00444; POLYPRENYL_SYNTHET 2; 1.
Chloroplast; Transit peptide.
Chloroplast; Transit peptide.
TRANSIT.
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008291; Q53435; Q53437; Q53438;
01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Geranyltranstransferase (BC 2.5.1.10) (Farnesyl-diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FPP synthase).
Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
-!- SIMILARITY: Belongs to the FPP/GGPP synthetase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=ATCC 10149;
MEDLINE=93252758; PubMed=8486607;
MSDAINE=7. Obata 7., Cababe M., Takeshita A., Yokoyama K., Uchida M., Nishino T., Ogura K.;
"Thermostable farnesyl diphosphate synthase of Bacillus
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Best Local Similarity
Matches 91; Conserv
                                                                                                                       sporulation genes."
                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 AISHGGLLDLACAVEWHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 DPAVG--LPVACAIEKIHTYSLIHDDLPSMDNDDLRRGKPTNHKVFGBAWAILAGDGLLT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 KAFGVIAEA--EGLIPIAKIRAVSELSTAIGMQGLVQGQFKDLSEGDKPRSADAILLINQ 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 YAFQLITEIDDERIPPSVRLRLIERLAKAAGPEGMVAGQAADMEGEGKTLTLSELEYIHR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FKTSTLFCASTQMASIAANASCEARENLHRFSLDLGQAFQLLDDLTD---GWTDTGKDIN 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 HKTGKWLQYSVHAGALIGGADARQTRELDEFAAHLGLAFOIRDDILDIEGAEEKIGKPVG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 ISAEQLIADIDSRLDQLLPVQGER----DCVGAAMREGTLAPGKRIRPMLLLLTARDLGC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koyama T., Obata S., Saito K., Takeshita-Koike A., Ogura K.; "Structural and functional roles of the cysteine residues of Bacillus stearchermophilus farnesy! diphosphate synthase."; Blochemistry 33:12644-12648 (1994).
-!- CATALYTIC ACTIVITY: Geranyl diphosphate + isopentenyl diphosphate - adiphosphate + krans.trans-farnesyl diphosphate.
-!- SUBCELLULAR LOGATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the PPP/GGPP synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-007-1996 (Rel. 34, Created)
01-007-1996 (Rel. 34, Last sequence update)
10-007-2003 (Rel. 42, Last annotation update)
Geramyltransfransferase (EC 2.5.1.10) (Farnesyl-diphosphate synthase)
YQID OR BSU24280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Mismatches 129; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C->F,S: NO LOSS OF ACTIVITY.
C->F,S: NO LOSS OF ACTIVITY.
; 0F921C3F029EEBB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bācillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 QDA--GKSTLVNLLGSGAVBERLRQHLRLASEHLSAACQNG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 SDOSNNKATYPALLSLAGAKÉKLAFHIBAAORHIRNADVDG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.6%; Score 360.5; DB 1 34.9%; Pred. No. 6.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00348; polyprenyl synt; 1.
PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.
PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.
Transferase; Isoprene biosynthesis; NO LO
MURAGEN
73 73 72 LO
                                                                                                                                                                                                                                                                                                                                                                                                         PIR; JX0257; JX0257.
InterPro; IPR000092; Polyprenyl synt.
InterPro; IPR008949; Terpenoid synth.
                                                                                                                                                                                                                                                                                                                  EMBL; D12293; BAA02551.1; -...
EMBL; S72629; AAB32272.1; -...
EMBL; S72630; AAB32273.2; ALT_SEQ.
EMBL; S72633; AAB32274.1; -...
EMBL; S73635; AAB32275.2; ALT_SEQ.
PIR; JX0257; JX0257.
 MEDLINE=95001990; PubMed=7918490;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cuery Match
Best Local Similarity 34.99
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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SEQUENCE
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SPA BACSU
D ISPA BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RA Kunst F., Ogssawara N., Mosser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursler L., Brana A., Brann M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoff A., Erlich S.D., Emmerson P.T.,
RA Brian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga X., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Korita K., Lapidus A., Liu H., Masula S., Manano M.,
RA Korita K., Lapidus A., Liu H., Masula S., Manalo M., None E. S.M., Levine A., Liu H., Masula S., Manalo G., RA,
RA Medina N., Mellado R.P., Mizuno M., Moseti D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Satoro D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Roche B., Scoffone F.,
RA Satoro D., O'Reilly M., Ogawa R., Scofe B., Rose M., Sadale Y.,
RA Satoro D., O'Reilly M., Osawa R., Score B., Rose M., Sadale Y.,
RA Satoro J., Rocha B., Roche B., Rose M., Sadale Y.,
RA Satoro J., Schleich S., Schoeler P., Vassarotti A.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Takahashi H., Takemaru K.,
RA Tosaco V., Uchiyama S., Vandeler B., Wenler R., Vassarotti A.,
RA Winters P., Wambutt R., Wedler H., Weitzenegger T.,
RA Winters P., Wambutter R., Wedler H., Watersenegger T.,
RA Winters P., Wambutter R., Wedler H., Yamane K., Yastumoto K., Yatu K.,
RA The complete genome sequence of the Gram-positive bacterium Bacillus
STRAIN=168 / JH642;
MEDLINE=97124195; PubMed=8959508;
Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
Robayashi Y.;
                                                                                                                                                            "systematic sequencing of the 283 kb 210 degrees-232 degrees region of
the Bacillus subtilis genome containing the skin element and many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 390:249-256(1997).

-!- CATALYTIC ACTIVITY: Geranyl diphosphate + isopentenyl diphosphate = diphosphate + trans, trans-farnesyl diphosphate.

-!- SUBCELUTAR LOCATION: Cytoplasmic.

-!- SIMILARITY: Belongs to the PPP/GGPP synthetase family.
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PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.
PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.
Transferase; Isoprene biosynthesis; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.7%; Score 346.5; DB 1;
34.0%; Pred. No. 7.6e-21;
ive 52; Mismatches 108;
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InterPro; IPR008949; Terpenoid_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
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                                                                                                                                                                                                                                                                                                              crobiology 142:3103-3111 (1996)
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EMBL; Z99116; CAB14359.1; -.
PIR; A69961; A69961.
Subtilist; BG11714; YqiD.
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                                                        135
                                                                         127 TSHVSDEVSAEKRLRLVNELISAAGTEGMVGGQVADWBAGNRQVTLEELESIHERKTSKL 186
                                                                                                                                                                          --FCASTQMASIAANASCEARENLARFSLDLGQAFQLLDDLTD---GMTDTGKDINQDA- 247
                                                                                                                                                                                                      187 LGFCVIA--GAILADAPEEDIETLRTFSSHIGIGFQIRDDILDLEGSEEKIGKRVGSDTT 244
75
                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
lamiids, Gentianales, Apocynaceae, Rauvolfioideae, Vinceae,
LADIDSRLDQLLPVQGER----DCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGG
               AE - - AEGLTPIAKTRAVSELSTAIGMOGLVOGOPKDLSEGDKPRSADAILLITNOPKTSTL
                                                        LLDLACAVENVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFGVI
                                                                                                                                                                                                                                                                                                                                                                                                          Geranylgeranyl pyrophosphate synthetase, chloroplast precursor (GGPP synthetase) (GGPS) [includes: Dimethylallyltransferase (BC 2.5.1.1); Geranyltranstransferase (EC 2.5.1.10); Farnesyltranstransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: Catalyzes the trans-addition of the three molecules of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=cv. G. Don c20;
Bantignies B., Liboz T., Ambid C.;
"Nucleotide sequence a Catharanthus roseus geranylgeranyl pyrophosphate synthase gene.";
(In) Plant Gene Register PGR95-119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SIMILARITY: Belongs to the FPP/GGPP synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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PIR, T09966, T09966.
InterPro; IPR000092; Polyprenyl synt.
InterPro; IPR008949; Terpenoid synt.
Pfan; PP00348; polyprenyl synt; 1.
PROSITE; PS00723; POLYPRENYL SYNTHET_1; 1.
                                                                                                                                                                                                                                   -GKSTLVNLLGSGAVEERLRQHLRLASE 274
                                                                                                                                                                                                                                                      245 NDKSTYPSLLSLEGAKHKLDVHIKEAND 272
                                                                                                                                                                                                                                                                                                                                       357
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NCBI TaxID=4058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGPS1 OR GGC1
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 20
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042698;
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-!-CAPALYITIC ACTIVITY: Geranyl diphosphate + isopentenyl diphosphate + diphosphate + trans, trans-farnesyl diphosphate.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                   43 AMREGILAPGKRIRPMLLLITARDIGCAISHGGILDLACAVEMVHAASLILDDAMPCMDDA
                                                                                                                                                                                                                                                                                                                                                                                                       162 IVQGQFKDL-SEGDKPRSADAILLTNQFKTSTLFCASTQMASIAANASCEARENLHRFSL
                                                                                                                                                                                                                                                                         96 SMRYSILAGGKRVRPMLCIAACELFGGTESVA--MPSACAVEMIHTMSLMHDDLPCMDND
                                                                                                                                                                                                                                                                                                                                                 214 IVAGQVVDVCSEGIADVGLEHIEFIHIHKTAALLEGSVVLGAIVGGANDEQISKLRKFAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 DLGQAFQLLDDLTDGWTDTGKDINQDAGKS-----TLVNLLGSGAVBERLRQHLRLASE
                                                                                                                                                                                                                                                                                                                      103 QMRRGRPTIHTQYGEHVAILAAVALLSKAFGVIABA-EGLTPIAKTRAVSELSTAIGMQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Geranyltranstransferase (EC 2.5.1.10) (Farnesyl-diphosphate synthase)
                                                                                                                                                                                             Gaps
                                                                                 41 357 GERANYLGERANYL PYROPHOSPHATE SYNTHETASE
357 AA; 38786 MW; 81C52FDEALE06FA8 CRC64;
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MEDINE=97426617; PubMed=9278503;
MEDINE=97426617; Punkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Rirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-91210228, PubMed-2089044; Mediuchi K., Nishino T., Pujisaki S., Hara H., Nishimura Y., Horiuchi K., Nishino T., Fujisaki S., Hara H., Nishimura Y., Horiuchi and mucleotide sequence of the ispA gene responsible for farnesyl diphosphate synthase activity in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                          11;
                                                                                                                                                    DB 1; Length 357;
PROSITE; PSO0444; POLYPRENYL_SYNTHET_2; 1.
Chanaferase; Isoprene blosynthesis; Carotenoid biosynthesis;
Chloroplast; Transit peptide.
TRANSIT (POTENTIAL).
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                                                                                                                                                                                             Indels
                                                                                                                                                                                             40; Mismatches 100;
                                                                                                                                                  Query Match 22.6%; Score 345.5; DB 1
Best Local Similarity 37.9%; Pred. No. 1.3e-20;
Matches 92; Conservative 40; Mismatches 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275 HLS 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FPP synthase).
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    SUBCELLULAR LOCATION: Cytoplasmic (Potential).
    SIMILARITY: Belongs to the PPP/GGPP synthetase family.

                                                                                                                                                                                                   PIR; T10875; T10875.
InterPro; IPR00092; Polyprenyl synt.
InterPro; IPR008949; Terpenoid synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-USDA 110;
MEDLINE-98322110; PubMed-9655913;
                                                                                                                                                                                    EMBL; AE000082; AAB91752.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                             Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bradyrhizobium japonicum.
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                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 RSADAILLINQFKTSTLFCASTQMASIAA-NASCEARENLHRFSLDIGQAFQLLDDLTDG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 VPLDALERIHRHKTGALIRAAVRLGALSAGDKGRRALPVLDKYAESIGLAFQVQDDILDV 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LIVCAKKHVHLTGISAEQLLADIDSRLDQLLPVQGBRDCVGAAMREGTLAPGKRIRPMLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LLTARDLGCAISHGGLLDLACAVEMVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILAAVALLSKAFGVIAEAEGLTPIAKTR----AVSELSTAIGMQGLVQGQFKDLSEGDKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 387:394-401,[1997].
-!- CATALYTIC ACTIVITY:
= diphosphate + isopentenyl diphosphate
= diphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-COT-2003 (Rel. 42, Last annotation update)
Probable geranyltranstransferase (EC 2.5.1.10) (Farnesyl-diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  28;
                                                                                                                                                                                                                                                                                                                                                                                                                21.8%; Score 332; DB 1; Length 299; 33.8%; Pred. No. 1.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhizobiales;
SIMILARITY: Belongs to the FPP/GGPP synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 124; Indels
                                                                                                                                                                                                                                                                                           Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Alphaproteobacteria;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  46; Mismatches
                                                                                                                                                                                   EMBL; AE000148; AAC73524.1; -
EMBL; U82654; AAB40177.1; -
EMBL; U02065; U02065.
SWISS-2DPAGE; P22939; COLI.
ECOGene; EG10508; ispA.
InterPro; IPR000092; Polyprenyl synt.
InterPro; IPR08949; Parpenoid synt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97305956; PubMed=9163424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (strain NGR234)
                                                                                                                                                                      EMBL; D00694; BAA00599.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FPP synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pNGR234a.
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 101; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhizobium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid sym
                                                                                                                                                                                                                                                                                                                                                                                                                                                  101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISPA RHISN
P55539;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 VBQALARLICAEDHGETBLM-AAMRYATIHGGKRTR-ALLCLAAGALADTPAH-ILDDVG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 CAVEMYHAASLILDDDMPCMDDAQMRRGRPTIHTQYGBHVAILAAVALLSKAFGVIA--EA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGLTPIAKTRAVSELSTAIGMOGLVQGOFKDLSEGDKPRSADAILLINQFKTSTLFCAST 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 AAIEMMHACTLVHDDLPAMDDDVLRRGLPTVHVKFGRATAILVGDALQAHAFLTLASLDA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QMASIAANASCEARENLH----RFSLDLGQAFQLLDDLTDGMTDT---GKDINQDAG--K 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 PGDNRIALVR---ELAQAVSAEGAAGGQAMDLSLVGKHVELDRIVAMHRMKCGALVRASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 IDSRLDQLLPVQ--GERDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGGLLDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 STIVNLLGSGAVE--------BRURGHLRLASEHL 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 PICASIMGLOAAROFALDLLCEAGEAIAPIGPRAERLAOMLORASAYL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=USDA 110;
Tully R.E., Keister D.L.;
"Cloning and mutagenesis of a cytochrome P-450 locus from "cloning and mutagenesis of a cytochrome P-450 locus from Bradyrhizobium japonicum that is expressed anaerobically and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Protecobacteria; Alphaprotecobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00348; polyprenyl synt; 1.
PROSITE: PS00444; POLYPRENYL SYNTHET 2; 1.
PROSITE: PS00723; POLYPRENYL SYNTHET 1; 1.
Transferase; Isoprene biosynthesis; Plasmid.
SEQUENCE 332 AA; 34688 MW; EE68C1547449AA87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tully R.E., van Berkum P., Lovins K.W., Keister D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 1.3e-18; 40; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.0%; Score 320; DB 1; 35.4%; Pred. No. 1.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
synthase) (FPP synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59:4136-4142(1993)
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139
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SOUND DEPORT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMES outstation the Buropean Bioinformatics Institute are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SACFGLALOVIDDILDVITADÍTAALGKTPGKDAAAOKPÍCASIMGLQBARQFALDLLRDAG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGILAPGKRIRPMLLLITARDLGCAISHGGLLDLACAVEMVHAASLILDDMRCMDDAQM 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 VQGQFKDLSEGDKPRSADAILLINQFKTSTLFCASTQMASIAA---NASCEARE-NLHRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLDLGQAFQLLDDLTDGMTDT---GKDINQDAG--KSTLVNLLGSGAVERLRQHLRLAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 AGGGAIDLSLVGKHYELDRIVAMHRWKSGALVRASVRMGALCAVGVNAAHAALYCALDHY
                                                                                                                                                                                                                                                                                                        Bradyrhizobium japonicum USDA110.";
DNA Res. 9:180-197(2002).
-!- CATALYTIC ACTIVITY: Geranyl diphosphate + isopentenyl diphosphate
= diphosphate + trans, trans-farnesyl diphosphate.
-!- SUBCELULAR LOCATION: Cycoplasmic (Potential).
-!- SIMILARITY: Belongs to the FPP/GGPP synthetase family.
sequencing of a cytochrome P450 gene cluster from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40; Gaps
                                                                                                                          STRAIN=USDA 110;
MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsurucka H., Wada T., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 20.7%; Score 316; DB 1; Length 33 Best Local Similarity 33.4%; Pred. No. 2.8e-18; Matches 107; Conservative 45; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47644FAF0220CE4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00348; polyprenyl synt; 1.
PR051TE; PS00444; POLYPRBNYL SYNTHET 2; 1.
PR051TE; PS0073; POLYPRBNYL SYNTHET 1; 1.
Transferaes; Isoprene biosyntheeis; Complete proteome.
SEQUENCE 332 AA; 34638 MW; 47644FAF0220CE4C CRC64;
                             adyrhizobium japonicum.";
ochim. Biophys. Acta 1398:243-255(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AP005942, BAC47413.1, ALT_INIT.
PIR, 140213; 140213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR000092, Polyprenyl_synt.
InterPro, IPR008949; Terpenoid_synth.
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                                                                                                                                                                                                                                                                                     "Complete genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U12678; AAC28894.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105
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(Rel. 33, Created)
(Rel. 33, Last sequence update)

STANDARD;

CRTE CYAPA P48368; 01-FEB-1996 01-FEB-1996

RESULT 12 CRTE CYADA ID CRTE CY AC P48368; OT 01-FEB-OT 01-FEB-

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC ACTIVITY: Trans-trans-farnesyl diphosphate + isopentenyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 TOMASIAANASCEARENLHRPSLDLGQAFQLLDDLTDGMT---DTGKDINQD--AGKSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 ACAVEMVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFGVIA-EA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGLTPIAKTRAVSELSTAIGMOGLVOGOFKDL-SEGDKPRSADAILLTNOPKTSTLFCAS
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SECURICE PROM N.A.

IOEffelhardt M., Stirewalt V.L., Michalowski C.B., Annarella M.,
Parley J.Y., Schluchter M.M., Chung S., Newmann-Spallart C.,
Steiner J.M., Jakovattsch J., Bohnert H.J., Bryant D.A.;
"The complete sequence of the cyanelle genome of Cyanophora paradoxa:
the genetic complexity of a primitive plastid.";
(In) Schenk H.B.A., Herrmann R., Jeon K.W., Mueller N.B.,
Schwemmler W. (eds.);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 IDSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGGL---LDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Mucleotide sequence of the cyanelle DNA from Cyanophora paradoxa.";
Plant Mol. Biol. Rep. 13:327-332(1995).
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PIR, T06569; T06569.
InterPro, IPRO00092; Polyprenyl synt.
InterPro, IPRO00949; Terpenoid Synt.
InterPro, IPRO08499; Terpenoid Synt.
PROSTIE; PS00444; POLYPRENYL SYNTHET 2; I.
PROSTIE; PS00723; POLYPRENYL SYNTHET 1; I.
PROSTIE; PS00723; Tenceral Biosynthesis; Carotenoid biosynthesis; Experience biosynthesis; Transferase; Cyanelle.
ESQUENCE 300 AA; 33008 MW; 05950D0E3BA04934 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     STRAIN-UTEX LB 555 / Pringsheim;
Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg
10-OCT-2003 (Rel. 42, Last annotation update)
Geranylgeranyl pyrophosphate synthetase homolog (EC 2.5.1.29)
Synthetase) (Farnesyltranstransferase).
CRIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diphosphate = diphosphate + geranylgeranyl diphosphate.
-!- PATHWAY: Carotenoid and chlorophyll biosynthesis.
-!- SINILARITY: Belongs to the PPP/GGPP synthetase family.
                                                                                                                                                                                                                                               Būkaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 20.5%; Score 313.5; DB 1
1 Similarity 33.2%; Pred. No. 3.9e-18;
87; Conservative 54; Mismatches 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 VNLLGSGAVEERLROHLRLASE 274
                                                                                                                                                                             Cyanophora paradoxa
Cyanelle.
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                                                                                                                                                                                                                                                                                    NCBI TaxID=2762;
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NCBI_TaxID=1063;
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                                임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 VIAEREGLTPIAKTRAVSELSTAIGMOGLVOGOFKOLSEGDKPRSADAILLTNOFKTSTL 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 LADIDSRLDQLLPVQGE-----RDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHG 74
                                                                                                                                                                                                                                                                                                                                                       PERINEAL KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

MEDLINE=95350630; PubMed=7542800;

MEDLINE=95350630; PubMed=7542800;

MERLINE=95350630; PubMed=7542800;

MERLINE C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

MCKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.J., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Venter J.C.,

Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: Geranyl diphosphate + isopentenyl diphosphate
= diphosphate + trans,trans-farnesyl diphosphate.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Geranyltranstransferase (BC 2.5.1.10) (Farnesyl-diphosphate synthase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the FPP/GGPP synthetase family.
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PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.
PROSITE; PS0043; POLYPRENYL SYNTHET 1; 1.
Transferase; Isoprene blosynthesis; Complete proteome.
SEQUENCE 295 AA; 32407 MM; A64DE650266E670F CRC64;
                                                                                          295 AA
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InterPro; IPR008949; Terpenoid_synth.
255 PSFWG---VERSIKQAELLVEE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, U32822; AAC23087.1; -. PIR; C64123; C64123.
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Conservative 4
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                                                                                          STANDARD;
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Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       NCBI_TaxID=727;
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TIGR; H11438;
                                                                                                                                                                                                            synthase)
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                                                                                        ISPA HAEIN
P45204;
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194 FCASTQWASIAANASCEAR--ENLHRFSLDLGQAFQLLDDLTD----GWTDTGKDI--NQD 246
                                The sequence analysis of the photosynthesis region of Rhodobacter (Choudhary M., Kaplan S.;

"DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2.4.1."

"Nucleic Acids Res. 28:862-867(2000).

-! - CATALYTIC ACTIVITY: Trans-trans-farnesyl diphosphate + isopentenyl diphosphate = diphosphate + geranyl diphosphate.

-! - PATHMAY: Carotenoid and chlorophyll biosynthesis.

-! - SIMILARITY: Belongs to the FPP/GGPP synthetase family.
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PIR; T50750; T50750.
InterPro; IPRO00059; Polyprenyl_synt.
InterPro; IPRO008949; Terpenoid_synth.
Pfam; PF00348; polyprenyl_synt; IPROSITE; PS00444; POLYPRENYL_SYNTHET_2; 1.
PROSITE; PS00474; POLYPRENYL_SYNTHET_2; 1.
PROSITE; PS00474; PolyPRENYL_SYNTHET_1; 1.
PROSITE; PS00712; Calorophyll_Diosynthesis; Carotenoid biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
MEDINE=55238278; PubMed=7721699;
Lang H.P., Cogdell R.J., Takaichi S., Hunter C.N.;
"Complete DNA sequence, specific Tn5 insertion map, and gene assignment of the carotenoid biosynthesis pathway of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
                                                                                                                                                                                                                                                                                                                                       CRTE_RHOSH STANDARD; PRT; 288 AA.
P54976; Q9RFC5;
01-CCT-1996 (Rel. 34, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Geranylgeranyl pyrophosphate synthetase (BC 2.5.1.29)
synthetase) (Farnesyltranstransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAINEATCC 17023 / 2.4.1 / NCIB 8253 / DSM 159;
MEDLINE=20115911; PubMed=10648776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase.
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                                                                                                                            247 AGKSTLVNLLG-SGAVEE 263
                                                                                                                                                             245 LDKSTYPKLLGLSGAKQK 262
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60
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244
264
274
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 YEAFPWEEL---GARIGEAFQVADDLRDALCDAETLGKPAGQDEIHARPNAVREYGVEGA 244
                                                                                                                                                                                                                                                                                                        88 AASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFGVIAEABGLTPIAKT 147
                                                                                                                                                                                                                                                                                                                                                                                                                               148 RAVSELSTAIGM-QGLVQGQFKDLSEGDKPRSADAILLTNQPKTSTLFCASTQMASJAAN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 CASLVHDOLPCFDDAEIRRGKPIVHRAYSBPLAILIGDSLIVMGFEVLARAAADQPQRAL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 ASCEARENLHRFSLDLGQAFQLLDDLTDGMTDT---GKDINQDA--GKSTLVNLLGSGAV 261
                                                                                                                                                                                  ----GKRIRPMILLLTARDLGCAISHGGLLDLAC-AVEMVH 87
                                                                                                                                                                                                                         16 ARGQGSEAPSKLATALDYAVTPGGARIRPTLLLSVA--TACGDDRPVLSDAAAVALELIH 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98175686; PubMed=9515931;
Shimizu N., Koyama T., Ogura K.;
Publecular Clohing, expression, and characterization of the genes
encoding the two essential protein components of Micrococcus luteus
B-P 26 hexaprenyl diphosphate synthase.;
J. Bacteriol. 180:1578-1581(1998).
-!- CATALYTIC ACTIVITY: Geranyl diphosphate + isopentenyl diphosphate.
= diphosphate + trans.trans-farnesyl diphosphate.
-!- SUBCELLUIAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: Belongs to the FPP/GGPP synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Geranyltranstransferase (EC 2.5.1.10) (Parnesyl-diphosphate synthase)
                                                                                                                             Gaps
                                                                                                                          32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Micrococcus luteus (Micrococcus lysodeikticus).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Micrococcaceae; Micrococcus.
                                                           Length 288;
                                                                                                                      96; Indels
30256 MW; SA7BD5BC41811A36 CRC64;
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                                                           ch 20.1%; Score 307; DB 1; Similarity 35.5%; Pred. No. 1.3e-17; 88; Conservative 32; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 AA
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InterPro; IPR00092; Polyprenyl_synt.
InterPro; IPR008949; Terpenoid_synth.
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MEDLINE=98175686; PubMed=9515931;
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288 AA;
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O66126;
SEQUENCE
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Best Local
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Length 291;

DB 1;

20.0%; Score 304.5;

Query Match

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                                                                                                         84 EMVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAPGVIARARGETP 143
                                                                                                                                                                                                                                                 83
                                                                           72
                                              24 DSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGGLLDLACAV
                                                                144 IAKTRAVSELSTAIGMOGLVQGQFKDLSEGDKPRSADAILLITNQFKTSTLFCASTQMASI
                                                                                                                                                                                                                                 204 AANASCEARENLHRFSLDLGQAFQLLDDLTD-----GMTDTGKDINQDAGKSTLVNL
                  17; Gaps
36.2%; Pred. No. 2e-17; rative 36; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                         completed: February 29, 2004, 14:45:03
                                                                                                                                                                                                                                                                                              256 LGSGAVERRLRQHL 269
                Conservative
                                                                                                                                                                                                                                                                                                                time : 6.10674 secs
                  92.
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(without alignments)
3180.293 Million cell updates/sec
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1526
1 LIVCAKKHVHLTGISABQLE....HSTTQLFIQAWFDKKLAAVS 303
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1. /cgm2_6/prodata/2/pubpaa/US07_PUBCOMB.pep:*
2. /cgm2_6/prodata/2/pubpaa/PCT_NEW PUB.pep:*
3. /cgm2_6/prodata/2/pubpaa/NCT_NEW PUB.pep:*
4. /cgm2_6/prodata/2/pubpaa/US06_PUBCOMB.pep:*
5. /cgm2_6/prodata/2/pubpaa/US06_PUBCOMB.pep:*
6. /cgm2_6/prodata/2/pubpaa/US07_NEW PUB.pep:*
7. /cgm2_6/prodata/2/pubpaa/US08_NEW PUB.pep:*
8. /cgm2_6/prodata/2/pubpaa/US08_PUBCOMB.pep:*
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12. /cgm2_6/prodata/2/pubpaa/US09B_PUBCOMB.pep:*
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15. /cgm2_6/prodata/2/pubpaa/US00B_PUBCOMB.pep:*
16. /cgm2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep:*
17. /cgm2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep:*
18. /cgm2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep:*
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18. /cgm2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  809742 segs, 211153259 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                              1 protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 26, Appl	Sequence 2, Appli	Sequence 185, App	Sequence 1, Appli	Sequence 2, Appli	Sequence 17358, A	Sequence 10617, A	Sequence 18, Appl	Sequence 18010, A	Sequence 8506, Ap	Sequence 64, Appl	Sequence 64, Appl	Sequence 12583, A	Sequence 37, Appl	Sequence 5239, Ap
	ID	US-09-941-947A-26	US-10-218-118-2	US-10-166-225A-185	US-09-547-267-1	US-09-920-923-2	US-10-369-493-17358	US-10-369-493-10617	US-10-108-915-18	US-10-369-493-18010	US-10-369-493-8506	US-09-925-637-64	US-10-084-205-64	US-09-815-242-12583	US-09-920-923-37	US-09-815-242-5239
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	Query Match Length DB	303	303	295	295	295	294	292	369	294	291	287	287	293	293	288
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	Score	1526	1526	427	425	425	412.5	394.5	388	381.5	380.5	376.5	376.5	375.5	375.5	368.5
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222 229 220 24		9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	1 W W 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

ALIGNMENTS

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1 LIVCAKKHVHLIGISARQLLADIDSRLDQLLPVQGBRDCVGAAMREGILAPGKRIRPMLL 60
                                                                                                                                   APPLICANT: Cheng, Garden, actions a APPLICANT: Cheng, Garden, Deana J. APPLICANT: Cheng, Obena J. APPLICANT: Dicosimo, Deana J. APPLICANT: Dicosimo, Deana J. APPLICANT: Miler: Edward S. Jr. APPLICANT: Miler: Edward S. Jr. APPLICANT: Miler: Edward S. Jr. APPLICANT: Miler: Edward S. Jr. APPLICANT: Picateggio, Steve APPLICANT: Picateggio, Steve APPLICANT: Picateggio, Steve APPLICANT: Rouviere, Pierre B. TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE PRICE REPEACH. C. 11903 US NA CURRENT FILING DATE: 2001-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR FILING DATE: 2000-09-01
SOFTWARE: Microsoft Office 97
SOFTWARE: Microsoft Office 97
LENGTH: 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LTYCAKKHYHLTGISAEQILADIDSRLDQILEVQGBRDCVGAAMREGTLAPGKRIRPMLL
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llarity 100.0%; Pred. No. 2.3e-150;
Conservative 0; Mismatches 0; 1
                                              Sequence 26, Application US/09941947A Publication No. US20030003528A1 GENERAL INFORMATION:
                                                                                                                           APPLICANT: Brzostowicz, Patricia C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Pantoea stewartii
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                              -09-941-947A-26
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US-09-941-947A-26
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Best Local S
RESULT 1
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                                                                        181 AILLINGFKISTLFCASTQMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGWIDIG 240
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                                                    121 ILAAVALLSKAFGVIAEAEGLTPIAKTRAVSELSTAIGMQGLVQGQFKDLSEGDKPRSAD 180
                                                                                                                                                                                       KDINQDAGKSTLVNLLGSGAVEERLRQHLRLASEHLSAACQNGHSTTQLFIQAWFDKKLA 300
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                                                                                                                                                                                                                                                                                                                                                                       Publication US/10218118
Publication No. US20030148319A1
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Pleacagaio, Stephen
APPLICANT:
Cheag, Qiong
TITLE OF INVENTION: Genes Encoding Carotenoid Compounds
FILE REFERENCE: Class of US
CURRENT FILING DATE: 2002-08-13
PRIOR PLING DATE: 2002-08-13
PRIOR PLING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 14
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Matches 303; Conserv
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; ORGANISM: Pantoea
JS-10-218-118-2
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IS-10-218-118-2
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RESULT 3

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64 AWVDAACAVEMVHAASLIFDDMPCMDDARTRRGQPATHVAHGBGRAVLAGIALITBAMRI 123
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28.0%; Score 427; DB 14; Length 295;
Best Local Similarity 39.6%; Pred. No. 6.8e-36;
Matches 111; Conservative 37; Mismatches 102; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hohmann, Hans-Peter
APPLICANT: Pasamontes, Luis
APPLICANT: Fessier, Michel
APPLICANT: van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SOUTHERS: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 TLVNLLGSGAVEERLROHLRLASEHLSAACQNGHSTTQLF 290
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STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
COUNTRY: USA
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,267
FILING DATE:
                                                                  APPLICANT: BEREY, Alan APPLICANT: BRETZEL, Werner APPLICANT: BRETZEL, Werner APPLICANT: BRETZEL, Warner; APPLICANT: LOPEZ-UJIBAREI, Rual APPLICANT: LOPEZ-UJIBAREI, Rual APPLICANT: MYER, Anne F. APPLICANT: WILISEEV, Alexei A. TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION FILE REFERENCE: C38435/121966
CURRENT FILING DATE: 2002-06-05
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin version 3.1
SEQ ID NO 185
LENGTH: 295
Application US/10166225A o. US20030148416A1
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// Patent No. US20020147371A1
// GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Paracoccus sp. R1534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-166-225A-185
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; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-10-369-493-17358
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US-10-369-493-17358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 VAGLEMISIIKGLDKAETEQIMAFGRQIĞRVFQSYDDLIDVIGDKASFGKDTARDTAAFG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 -LLDLACAVEMVHAASLILDDMPCMDDAQMRGRPTIHTQYGEHVAILAAVALLSKAFGV 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAEAEGLTPIAKTRAVSELSTAIGMOGLVOGORKDLSEGDKPRSADAILLTNOFKTSTLF 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 IDSRLDQLLPVQGERDCV----GAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09920923
Publication No. US20030022273A1
GRARAL INFORMATION
APPLICANT: Pasamontes, Luis
APPLICANT: Pasamontes, Luis
APPLICANT: Tsygankov, Yuri
TITLE OF INVENTION: Improved Fermentive Carotenoid
FILE REFRENCE: Improved Fermentive Carotenoid
CURRENT FILING DATE: 2001-08-02
PRIOR PPLICATION NUMBER: 08/990,923
CURRENT FILING DATE: 1997-12-01
REIOR PLING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
27.9%; Score 425; DB 9; Length 295;
Best Local Similarity 39.6%; Pred. No. 1.1e-35;
Matches 111; Conservative 37; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 TLVNLLGSGAVEERLRQHLRLASEHLSAACQNGHSTTQLF 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: POKIAS, Bruce A.
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMNUMICATION INFORMATION:
TELEPHONE: (201) 235-5801
TELEPHONE: (201) 235-2363
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Flavobacterium sp. R1534 S-09-920-923-2
CLASSIFICATION:
PRIOR APPLICATION DATA:
PPLICATION NUMBER: 08/660,645
FILING DATE:
                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                LENGTH: 295 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Sequence 17358, Application US/10369493
; Sequence 17358, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INPORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Starer, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF; TITLE OF INVENTION: BARNS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: BANDER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NOS: 47374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 CASTOMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTD---TGKDINQD-AGKS 250
                               64 ANYDAACAVEMVHAASLIFDDMPCMDDARTRRGQPATHVAHGBGRAVLAGIALITEAMRI 123
                                                                                                               135 IAEAEGLIPIAKTRAVSELSTAIGMOGLVQGQFKDLSEGDKPRSADAILLTWQFKTSTLF 194
                                                                                                                                                                            124 LGEARGATPDQRARLVASMSRAMGPVGLCAGQDLDL---HAPKDAAGIEREQDLKTGVLF 180
-LIDLACAVENVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFGV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 QPLDBIXDIIBBRAMPAHIERLNSPDMLXNSMLYSLKAGGKRIRPALLLATWKSFQKDISQ
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es 113; Indels
                                                                                                                                                                                                                                                                                                                                                            251 TLVNLLGSGAVERRIRQHIRLASEHLSAACQNGHSTTQLF 290
                                                                                                                                                                                                                                                                                                                                                                                               27.0%; Score 412.5; DB 15; 37.6%; Pred. No. 2.2e-34;
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION NUMBER: US, 10,10,369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 18010
LENGTH 294
                                                                                                                                               142 TPIAKTRAVSELSTAIGMOGLVOGOPKDL-SEGDKPRSADAILLINOFKTSTLFCASTOM 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 GVIA-EAEGLTPIAKTRAVSELSTAIGMOGLVQGOFKDLSEGDKPRSADAILLT--NOFK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSTLFCASTOMASIAANASCEARENLHRFSLDIGQAFQLLDDLTDGMTD---TGKDINQD 246
                                                                                              146 VEMIHTMSLIHDDLPCMDNDDLRRGKPTNHKVYGEDVAVLAGDALLAFAFEHVAASTEGV 205
                                                                                                                                                                                                                                        201 ASIAANASCEARENIHRFSLDIGOAFOLLDDLTDGMTDTGKDINQDAGKS-----TLVN 254
                                                                                                                                                                                                                                                                       89 VNQALDAAIALRDPHK-IHQAMRYSLLAGGKRVRPVLCIAACELVGG--TBATAIPAACA 145
                                                                                                                                                                                  18 QLIADIDSRLDQLLPVQGB-RDCVGAAMREGTLAPGKRIRPMLLLLTAR----DLGCAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 HGGLLDLACAVEMVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAF
                                                     83 VEMVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAF-GVIAEAEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 25.0%; Score 381.5; DB 15; Best Local Similarity 36.9%; Pred. No. 3.7e-31; Matches 101; Conservative 42; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --AGKSTLVNLLGSGAVEERLROHLRLASEHLSA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 18010, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             325 ILGIDKSKEFAQELLKDAKEQLS 347
                                                                                                                                                                                                                                                                                                                                              255 LLGSGAVEERLROHLRLASEHLS 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: SPHINGOMONAS US-10-369-493-18010
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            APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Coldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTBINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(5205.2)
FILE REFERENCE: 38-10(5205.2)
CURRENT PILING DATE: 2003-02-28
PRIOR PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10617
LENGTH: 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 CAVENVHAASLILDDMPCMDDAOMRRGRPTIHTOYGEHVAILAAVALLSKAFGVIAE-AE 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 GLTPIAKTRAVSELSTAIGMOGLVQGOFKDLSEGDKPRSADAILLTNOFKTSTLFCASTO 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 MASIAANASCEARENLHRPSLDIAGQAFQLLDDLTDGMTD---TGKDINQDA--GKSTLVN 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Publication No. US20020177204A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
FULL APPLICANT: Cahoon, Rebeca E.
APPLICANT: Shen, Jennie
APPLICANT: Williams, Mark
TITLE OF INVENTION: Geranylgeranyl Pyrophosphate Synthases
FILE REFERBNCE: BB1286 US NA
CURRENT PELLON NUMBER: BALIER APPLICATION NUMBER: 09/452,238
PRIOR PLILING DATE: EARLIER APPLICATION NUMBER: 09/452,238
PRIOR PLILING DATE: EARLIER FILING DATE: 1999-12-01
PRIOR FILING DATE: EARLIER FILING DATE: 1999-December-02
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Microsoft Office 97
SEQ ID NO S: 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.9%; Score 394.5; DB 15; 36.0%; Pred. No. 1.6e-32; tive 45; Mismarches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLGSGAVEERLRQHLRLASEHLSA 278
                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Sphingomonas aromaticivorans
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hes 95; Conservative
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US-10-108-915-18
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Best Loca Matches

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Length 294; Indels 69

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LLSKAFGVIABAEGLTPIAKTRAVSELSTAIGMOGLVQGQFKDLSEGDKPRSADAILLTN 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 INTEYELG--MKSAIALEMIHTYSLIHDDLPAMDNDDYRRGKLTNHKVYGEWTAILAGDA 114
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| Jo-084-205-64
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US-09-815-242-12583
US-09-815-242-12583
; Sequence 12583, Application US/09815242
; Patent No. US20020061565A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Staphylococcus aureus
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LENGTH: 287
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"FELICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
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TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Polypeptides
FILE REFERENCE: PB560
CURRENT APPLICATION NUMBER: US/09/925,637
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: PCT/0S00/23773
PRIOR APPLICATION NUMBER: PCT/0S00/23773
PRIOR PILING DATE: 1099-09-01
PRIOR PILING DATE: 1099-09-01
PRIOR PPLICATION NUMBER: US 08/181,986
PRIOR PPLICATION NUMBER: US 08/956,171
PRIOR APPLICATION NUMBER: US 08/956,171
PRIOR APPLICATION NUMBER: US 60/009,861
PRIOR FILING DATE: 1997-10-20
PRIOR FILING DATE: 1996-01-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PATENTIN VOTE: 2.0
SEQ ID NO 64
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Patent No. US20020103338Al
GENERAL INFORMATION:
APPLICANT: Choi
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98; Conservative
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3-09-925-637-64
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Best Local S
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ORGANISM:
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Matches
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APPLI CANT APPLICANT

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Pred. No. 8.1e-30;
41; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5239, Application US/09815242
Patent No. US20020061569A1
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36.2%;
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APPLICANT: Syskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
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Best Local Similarity 36.2
Matches 97, Conservative
                                                                                                                                                                                                                                                                                       Query Match 24.6%
Best Local Similarity 38.3%
Matches 90; Conservative
SOFTWARE: PatentIn Ver. 2.1
                                                                                             TYPE: PRT
ORGANISM: B-396
PEATURE:
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US-09-815-242-5239
                           SEQ ID NO 37
LENGTH: 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 LLSKAPGVIAEABGLTPIAKTRAVSELSTAIGMOGLVQGQPKDLSEGDKPRSADAILLTN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 KTKTGALLTFAVMSAADIANVDDATKEHLESYSYHLGMKFQIKDDLLDCYGDEAKLGKKV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 INTEYELG--WKSAIALEMIHTYSLIHDDLPAMDNDDYRRGKLTNHKVYGEWTAILAGDA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 QPKTSTLFCASTQMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTD---TGKDI 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 LTGISABQLLADIDSRLDQLLPVQGERDCVGAAMREGTL----APGKRIRPMLLLLTARD 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MTNLPMNKLIDBVNNELS----VAINKSVMDTQLEESMLYSLNAGGKRIRPVLLLLTLDS 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.6%; Score 375.5; DB 9; Length 293; ilarity 35.6%; Pred. No. 1.6e-30; Conservative 43; Mismatches 119; Indels 15;
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APPLICANT: Pasamontes, Luis
APPLICANT: Pasamontes, Yuri
TITLES OF INVENTION: Improved Fermentative Carotenoid Production
FILE REFERENCE: Improved Fermentive Carotenoid
CURRENT APPLICATION NUMBER: US/09/920,923
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 08/980,832
PRIOR FILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
                                                                                                                     APPLICANT: TRANSC, JOHN D.
APPLICANT: Cart, Grant J.
APPLICANT: Cart, Grant J.
APPLICANT: Yamamoco, Robert T.
APPLICANT: Yamamoco, Robert T.
APPLICANT: Yamamoco, Robert T.
APPLICANT: Yamamoco, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA,011A
CURRENT APPLICATION NUMBER: 00/99/815,242
PRIOR APPLICATION NUMBER: 00/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-22
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-010-23
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
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Publication No. US20030022273A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Staphylococcus aureus
JS-09-815-242-12583
      Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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Matches 98; Conserv
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Query Match

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76 ILDLACAVEMVHAASLILDDAMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAPGVI 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
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                                                                                                                                                   Length 293;
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APPLICANT: Trawarch, Robert T.
APPLICANT: Yamamoco, Robert T.
APPLICANT: Yamamoco, Robert T.
APPLICANT: Yamamoco, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Dentification of Essential Genes in TITLE OF INVENTION: Dentification of Essential Genes in TITLE OF INVENTION: Dentification of Essential Genes in TITLE OF INVENTION: Dentification of Essential Genes in TITLE OF INVENTION: Dentify 0.3-21
PRICA PAPLICATION NUMBER: 60/19, 078
PRICA PAPLICATION NUMBER: 60/206, 848
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PRICA PAPLICATION NUMBER: 60/207, 737
PRICA PALING DATE: 2000-10-23
PRICA APPLICATION NUMBER: 60/257, 931
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PRICA PAPLICATION NUMBER: 60/269, 308
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PRICA PAPLICATION NUMBER: 60/
                                                                                                                                         24.6%; Score 375.5; DB 10; Length 38.3%; Pred. No. 1.6e-30; tive 38; Mismatches 86; Indels
CTHER INFORMATION: Description of Unknown Organism: Unkown US-09-920-923-37
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5.

sarch completed: February 29, 2004, 15:27:54
)b time : 22.1175 secs

¹³⁴ VIABABGLIFPIAKTRAVSELSTAIGMQGLVQGQFKDLSBGDKRRSADAILLINQFKTSTL 193
117 LISSDDRLTDEVKIKVLQRLSIASGHVGKVGGMLDMQSBGQPIDLETLEMIHKTKTGAL 176

¹⁹⁴ FCASTQMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGWTD---TGKDINQDA--G 248
177 LTFAUMSAADIANVDDATKEHLESYSYHLGMWFQIKDDLLDCYGDEAKLGKKVGSDLENN 236

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TELEPHONE: 212-246-5959; TELEFAX: 212-246-5959; INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 302 amino acids: TYPE: AMINO ACID TOPOLOGY: linear MOLECULE TYPE: protein US-07-783-705A-1
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                                                                                 February 29, 2004, 14:35:44; Search time 9.20761 Seconds (without alignments) 1698.885 Million cell updates/sec
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Sequence 37
Sequence 2,
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Seguence 4,
Seguence 4,
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Sequence 2,
Sequence 2,
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Sequence 1
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Sequence
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-095-726-4

US-08-095-724-4

US-08-095-724-4

US-08-095-724-2

US-08-095-726-2

US-08-095-726-2

US-08-095-726-2

US-08-095-623A-2

US-08-096-623A-2

US-08-096-623A-2

US-08-096-645A-1

US-08-096-645A-1

US-09-228-718-1

US-09-547-26-1

US-09-547-267-1

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US-09-920-928-910B-9

US-09-920-928-910B-7
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Maximum Match 100%
Listing first 45 summaries
                                                        using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                           US-09-941-947A-26
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Match Length DB
                                                        4 protein - protein search,
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Length 302;

88.1%; Score 1344.5; DB 1;

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USA
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                                                                                                                                                                                                                                      181 AILLINQFKTSTLFCASTQMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTDTG 240
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                Gaps
                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ausich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Mukharji, Indrani
APPLICANT: Morffitt, John H
APPLICANT: Yarger, James G
APPLICANT: Yen, Huei-Che B
TITLE OF INVENTION: Beca-Carotene Biosynthesis in
TITLE OF INVENTION: Genetically Engineered Hosts
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 200 E Randolph St CITY: Chicago
88.4%; Pred. No. 1.3e-146;
tive 16; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,726
FILING DATE: 21-UTL-1993
CLASSIFICATION ATA:
APPLICATION TOWNER: US 07/785,566
FILING DATE: 3C-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5530188val B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08095726
Patent No. 5530188
GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPAX: 3128564972
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                     Matches 268; Conservative
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MEDIUM TYPE: Floppy
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 60680-0703
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137 BAEGLIPIAKTRAVSELSTAIGMOGLVOGOFKDLSEGDKPRSADAILLINOFKISTLFCA 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 GSGAVEERLROHLRLASEHLSAACQNGHSTTQLFIQAWFDKKLA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ausich, Rodney L
APPLICANT: Ausich, Rodney L
APPLICANT: Mutharii, Indrani
APPLICANT: Mutharii, Indrani
APPLICANT: Proffitt, John H
APPLICANT: Yen, Huel-Che B
ITLE OF INVENTION: Lycopene Biosynthesis in
TITLE OF INVENTION: Lycopene Biosynthesis in
TITLE OF INVENTION: Lycopene Biosynthesis in
TITLE OF INVENTION: Lycopene Biosynthesis in
TITLE OF INVENTION: Lycopene Biosynthesis in
TITLE OF INVENTION: Lycopene Biosynthesis in
TITLE OF INVENTION: Lycopene Biosynthesis in
TITLE OF INVENTION: Lycopene Biosynthesis in
TITLE OF INVENTION: Benetically Engineered Hosts
NUMBER OF SEQUENCES: 70
CORRESSEE: Admic Amoco Corp., Patents and Licensing Dept
STATE: LL
CTIT: Chicago
STATE: IL
                                                  Indels
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     DB 1;
50.0%; Score 763.5; DB 1
56.0%; Pred. No. 1.5e-79;
cive 40; Mismatches 84
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SOCTUMENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,043
FILING DATE: 22-UUL-1993
CLASSIFICATION 1435
PRIOR APPLICATION WASER: US 07/785;568
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: GALLOWAY, NO. 5530189val B
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08096043
Patent No. 5530189
GENERAL INFORMATION:
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TYPE: amino acide
TYPE: amino acid
     Query Match
Best Local Similarity 56.0%
Matches 159; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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29,381
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REGISTRATION NUMBER: 29
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                         67 LDLACAVELTHTASLALDDMPCMDNAELRRGQPTTHKKFGESVALLASVGLLSKAFGLLA 126
                                                                                                                                                                                                                                          137 EAEGLIPIAKTRAVSELSTAIGMOGLVOGOFKDLSEGDKPRSADAILLTNOFKISTLFCA 196
                                                                                                                                                                                                                                                                 127 ATGDLPGERRAQAVNELSTAVGLQGLVLGQFRDLNDAALDRTPDAILSTWHLKTGILFSA 186
                                                                                                             99
                                                                                            197 ST@MASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTDTGKDINQDAGKSTLVNLL
                                                              17 EQLLADIDSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGGL
                           l; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             247 GADAARQKLREHIDSADKHLTFACPQGGAIRQ-FMHLWFGHHLA 289
                                                                                                                                                                                                                                                                                                                                                                                                                   257 GSGAVERLRQHLRLASEHLSAACQNGHSTTQLFIQAWFDKKLA 300
                       84; Indels
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: 200 E Randolph St
Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INCORMATION:

APPLICANT: Ausich, Rodney L

APPLICANT: Ausich, Rodney L

APPLICANT: Micharii, Tindrani

APPLICANT: Micharii, John H

APPLICANT: Yarger, James G

APPLICANT: Yarger, James G

APPLICANT: Yen, Huei-Che B

TITLE OF INVENTION: Phycoene Biosynthesis in

TITLE OF INVENTION: Genetically Engineered Hosts

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amoco Corp., Patents and Licensing Depu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 763.5; DB 1
56.0%; Pred. No. 1.5e-79;
tive 40; Mismatches 84
Best Local Similarity 56.0%; Pred. No. 1.5e-
Matches 159; Conservative 40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
WEDLUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
APPLICATION NUMBER: US O7/785,569
FILING DATE: 30-OCT-1991
ATTORNEY AGENT INFORMATION:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Galloway, No. 5545816val TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08093577
Patent No. 5545816
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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amino acid
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Sest Local Similarity 56.0
Aatches 159; Conservative
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MOLECULE TYPE: protein
-08-093-577-4
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of Zeaxanthin and Zeaxanthin in Genetically Engineered Hosts
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76
                                17 EQLLADIDSRIDQLIPVQGERDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGGL
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STREET: 120 S. Riverside Plaza, 22nd Floor
CITY: Chicago
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WEDIUM TYPE: FTORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BATCHTIN Release #1.0, Vers
SOFTWARE: Patentin Release #1.0, Vers
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,623A
FILING DATE: 22-UUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/805,061
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,921
FILING DATE: 28-FEB-1991
PRIOR APPLICATION NUMBER: US 07/562,674
FILING DATE: 01-AUG-1990
PRIOR APPLICATION NUMBER: US 07/525,551
FILING DATE: 18-WAY-1990
PRIOR APPLICATION NUMBER: US 07/525,551
FILING DATE: 18-WAY-1990
PRIOR APPLICATION NUMBER: US 07/525,551
FILING DATE: US WAR-1990
ATTORNEY/AGENT INFORMATION:
WANTEN CALLOND NUMBER: US 07/487,613
FILING DATE: US WAR-1990
ATTORNEY/AGENT INFORMATION:
WANTEN CALLOND NUMBER: US 07/487,613
FILING DATE: US WAR-1990
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 655-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ausich, Rodney L.
APPLICANT: Brinkhaus, Friedhelm L.
APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H.
APPLICANT: Yarger, James G.
APPLICANT: Yen, Huel-Che B.
TITLE OF INVENTION: Biosynthesis of
TITLE OF INVENTION: Glycosylated Ze
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08096623A
Patent No. 5684238
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                    , MOLECULE TYPE: protein US-08-095-726-2
                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.7 EAEGLTPIAKTRAVSELSTAIGMQGLVQGQFKDLSEGDKPRSADAILLTNQFKTSTLFCA 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 GADAARQKLREHIDSADKHLTFACPQGGAIRQ-FWHLWFGHHLA 289
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                                                                                                                                                                                                                                                              Indels
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APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Mukharji, Indrani
APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H
APPLICANT: Yarger, James G
APPLICANT: Yarger, James G
APPLICANT: Yer, Huei-Che B
INTILE OF INVENTION: Beta-Carotene Biosynthesis in
TITLE OF INVENTION: Genetically Engineered Hosts
NUMBER OF SEQUENCES:
ADDRESSED: Amoco Corp., Patents and Licensing Dept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Amoco Corp., Patents and Licensing Dept
200 E Randolph St
                                                                                                                                                                                                                                                           40; Mismatches
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COMPUTER: IBM PC compacible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PSTEM: PC-DOS/MS-DOS
SOFTWARE: PSTEM: Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,726
FILING DATE: 21-UUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/785,566
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5530188val B
TELECHONE: 312856180
TELECHONE: 312856180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08095726
Patent No. 5530188
TELEFAX: (312) 655-1501
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acids
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                              Matches 159; Conservative
                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5-08-095-726-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: STATE:
                                                                                                                                                                                                                    Query Match
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76 IDIACAVELTHIASIMLDDMPCMDNAEIRRGQPTTHKKFGESVAILASVGILASKGEIA 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 IDIACAVEMVHAASLIIDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFGVIA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 STQMASIAANASCEARENLHRPSLDLGQAFQLLDDLTDGWTDTGKDINQDAGKSTLVNLL 256
                                                                                                                                                                                                                                                                                                                                             75
                                                                                                                                                                                                                                                                                     16 EVWRQSIDDHLAGILPETDSQDIVSLAWREGWWAPGKRIRPLLMJAARDLRYQGSMPTL
                                                                                                                                                                                                                       17 EQLLADIDSRIDGILPVQGERDCVGAAMREGTLAPGKRIRPMILLLTARDLGCAISHGGL
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      DB 1; Length 307;
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200 E Randolph St
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APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Mukharii, Indrani
APPLICANT: Proffitt, John H
APPLICANT: Proffitt, John H
APPLICANT: Yarger, James G
APPLICANT: Yarger, James G
APPLICANT: Yen, Huei-Che B
TITLE OF INVENTION: Lycopene Biosynthesis in
TITLE OF INVENTION: Genetically Engineered Hosts
NUMBER OF SEQUENCES: 70
CORRESPONDENCE: 70
Query Match 50.0%; Score 763.5; DB 1
Best Local Similarity 56.0%; Pred. No. 1.6e-79;
Matches 159; Conservative 40; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IMP PC COMPACTIBLE
COMPUTER: IMP PC COMPACTIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION NUMBER: US/08/096,043
FILING DATE: 22-UUL-1993
CLASSIFFICATION: 435
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 07/785,568
FILING DATE: 30-OCT-1991
ATTORNEY/AGERT INFORMATION:
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TELECOMMUNICATION INFORMATION:
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Patent No. 5530189
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US-08-096-623A-2
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                                                                                                                                                                              50.0%; Score 763.5; DB 1; Length 307; 56.0%; Pred. No. 1.6e-79;
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STREET: 200 E Randolph St
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ausich, Rodney L.
APPLICANT: Brinkhaus, Friedhelm L.
APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H.
APPLICANT: Proffitt, John H.
APPLICANT: Proffitt, John H.
APPLICANT: Proffitt, John H.
APPLICANT: Proffitt, John H.
APPLICANT: Pen, Huei-Che B.
TITLE OF INVENTION: Phytoene Biosynthesis in
TITLE OF INVENTION: Genetically Engineered Hosts
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                               40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Batentin Release #1.24
CURRENT APPLICATION DATA:
RPELICATION NUMBER: US/08/093,577
FILING DATE: 19-UUL-1993
CLASSIPICATION ADAP:
APPLICATION NUMBER: US 07/785,569
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5545816val B
TELECHONNICATION INPORMATION:
TELECHONNICATION:
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Patent No. 5545816
GENERAL INFORMATION:
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INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid
TYPE: 307 amino acids TYPE: amino acid TOPOLOGY: 1:000 OLEOTH
                                                                                                                                                                                   Query Match
Best Local Similarity 56.08
Matches 159; Conservative
                                                                                                    MOLECULE TYPE: protein
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APPLICANT: Ausich, Rodney L.
APPLICANT: Ausich, Rodney L.
APPLICANT: Brinkhaus, Friedhelm L.
APPLICANT: Brinkhaus, Friedhelm L.
APPLICANT: Proffitt, John H.
APPLICANT: Yarger, James G.
APPLICANT: Yes, Hand-Che B.
APPLICANT: Yes, Hand-Che G.
APPLICANT: Yes, Hand-Che G.
APPLICANT: Yes, Hand-Che G.
APPLICANT: Yes, Hand-Che G.
APPLICANT: Yes, Hand-Che G.
APPLICANT: Yes, Hand-Che G.
APPLICANT: Yes, Hand-Che G.
APPLICANT: Yes, Hand-Che G.
APPLICANT: Yes, Hand-Che G.
APPLICANT: I. 120 S. Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 LDLACAVBLTHTASLMLDDWPCMDNAELRRGQPTTHKKFGBSVALLASVGLLSKAFGLIA 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 STOMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTDTGKDINQDAGKSTLVNLL 256
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                                                                                                                                                          Query Match 50.0%; Score 763.5; DB 1; Length 307; Best Local Similarity 56.0%; Pred. No. 1.6e-79; Matches 159; Conservative 40; Mismatches 84; Indels 1
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: The PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 22-JUL-1993
CLASS!FICATION NUMBER: US/08/096,623A
FILING DATE: 22-JUL-1993
PRIOR APPLICATION NUMBER: US 07/805,061
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,921
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,921
PRIOR APPLICATION DATA:
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FILING DATE: 18-MAY-1990
PRIOR APPLICATION DATA:
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; TOPOLOGY: Linear
; MOLECULE TYPE: protein
US-08-093-577-2
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APPLICANT: Pasamontes, Luis
APPLICANT: Pesaier, Michel
APPLICANT: van Loon, Adolphus
APPLICANT: van Loon, Adolphus
APPLICANT: van ERMENTRIVE CAROTENOID PRODUCTION
NUMBER OF SUCURNES: 47
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: BP 95108888.9
FILING DATE: 09-UN-1995
ATTORNEY/ACENT INFORMATION:
                                                               AMO-006.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08660645A
Patent No. 6087152
FILING DATE: 02-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 4MO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 655-1501
INFORMATION 122 655-1501
INFORMATION FROM 12: 5EQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acids
STRANDEDNESS:
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Best Local Similarity 56.0 Matches 159; Conservative
                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
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US-08-660-645A-1
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CASTOMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTD---TGKDINQD-AGKS 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 VEIRLAQ---ISGQFGVVSAPIGAAMSDAALSPGKRFRAVLMLMVAE-----SSGGVCD 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 IDSRLDQLLPVQGERDCV----GAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGG---
                                                                                                                                                                                                                                                                                                                                   27.9%; Score 425; DB 3; Length 295; 39.6%; Pred. No. 1.8e-40;
                                                                                                                                                                                                                                                                                                                                                                                 37; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09298718

Betent No. 6124113

GENERAL INFORMATION:
APPLICANT: Hohmann, Hans-Peter
APPLICANT: Tessier, Michel
APPLICANT: Van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 TLVNLLGSGAVEERIRQHIRLASEHLSAACQNGHSTTQLF 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 PKGGLMAVGQMGD-VAQHYRASRAQLDBLMR-----TRLF 274
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/298,718
REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMUNICATION INFORMATION:
TELEPRED (201) 235-5801
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 and and a cids
LENGTH: 295 and and a cids
TYPE: and a cid
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
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STREET: 340 Kingsland Street
CITY: Nutley
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               39.68;
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Best Local Similarity 39.6'
Matches 111; Conservative
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TELEPAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENCTH: 295 amino acids
                                                                                                                                                                                                                                                                                                                                                                       Query Match 27.9%;
Best Local Similarity 39.6%;
Matches 111; Conservative 3
                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-546-969-1
                                                                                                                                                                                                       single
                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
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LENGTH: 295
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APPLICANT: Pasamontes, Luis
APPLICANT: Pasamontes, Luis
APPLICANT: Tesier, Michal
APPLICANT: Tesier, Michal
APPLICANT: Tesier, Michal
APPLICANT: Tesier, Michal
APPLICANT: Tesier, Michal
APPLICANT: Tesier, Michal
APPLICANT: Tesier
CORRESCEDENCES: 47
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CORRESCEDENCES: ADRESCE: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: ADRESCES: AD
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39.6%; Pred. No. 1.8e-40;
Live 37; Mismatches 102; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,969
FILING DATE:
REPERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMMUNICATION INFORMATION:
TELEPAK: (201) 235-2363
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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REGISTATION NUMBER: 32,748
REPERENCE/DOCKET NUMBER: RAN 6002/170
FELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
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Patent No. 6207409
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                                                                                                                                                                                                   LENGTH: 295 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 27.9%
Best Local Similarity 39.6%
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
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124 LGEARGATPDORARLVASMSRAMGPVGLCAGODLDL---HAPKDAAGIEREQDLKTGVLF 180
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                                                                                                                                                                                                                                                     76 -LLDLACAVEMYHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFGV 134
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                                                                                                                     23 IDSRLDQLLPVQGERDCV----GAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGG---
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APPLICANT: Pasamontes, Luis
APPLICANT: Pasamontes, Luis
APPLICANT: Tygankov, Yulis
TITLE OF INVENTION: Improved Fermentative Carotenoid
FILE REPERENCE: Improved Fermentive Carotenoid
CURRENT APPLICATION NUMBER: US/08/980,832B
CURRENT PILING DATE: 1997-12-01
NUMBER OF SEQ. DD NOS: 66
SOFTWARE: PatentIn Ver. 2.1
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         Length 295;
; Score 425; DB 3; Length 29; Pred. No. 1.8e-40; 37; Mismatches 102; Indels
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; ORGANISM: Flavobacterium sp. R1534
US-08-980-832-2
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US-09-920-923B-2
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LENGTH: 295
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181 VAGLEMLSIIKGLDKAETEQLMAFGRQLGRVFQSYDDLLDVIGDKASTGKDTARDTAAPG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 -LLDLACAVEMVHAASLILDDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFGV 134
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                                                                                                                                                                                                                                                     APPLICANT: Pasamontes, Luis
APPLICANT: Tessier, Michel
APPLICANT: Tessier, Michel
APPLICANT: Van Loon, Adolphus
TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                     251 TLVNLLGSGAVERRIRQHLRLASEHLSAACQNGHSTTQLF 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,267
                                                                           241 PKGGLMAVGQMGD-VAQHYRASRAQLDELMR-----TRLF
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REGISTRATION NUMBER: 32,748
REFERENCE/DOCKET NUMBER: RAN 6002/170
TELECOMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,645
                                                                                                                                                                       Sequence 1, Application US/09547267
Patent No. 6613543
                                                                                                                                                                                                                                      APPLICANT: Hohmann, Hans-Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (201) 235-25801
TELEPAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 39.64
Matches 111; Conservative
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MOLECULE TYPE: protein
18-09-547-267-1
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: six
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IS-09-547-267-1
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64 AMVDAACAVEMVHAASLIFDDMPCMDDARTRRGQPATHVAHGBGRAVLAGIALITEAMRI 123
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                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Pasamontes, Luis
APPLICANT: Payamontes, Luis
FAPLICANT: Tsygamontes, Luis
TITLE OP INVENTION: Permentative Carotenoid Production
FILE REFERENCE: 15464 US (C38435/125944)
CURRENT APPLICATION NUMBER: US/09/920,923B
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 08/980,832
PRIOR AILING DATE: 1997-12-01
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin version 3.1
251 TLVNLLGSGAVEERLRQHLRLASEHLSAACQNGHSTTQLF 290
                                 241 PKGGLMAVGQMGD-VAQHYRASRAQLDELMR----TRLF 274
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US-09-920-93B-2
; Sequence 2, Application US/09920923B
~**ant No. 6677334
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Matches 111; Conservative
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Abp96685 Pantoea s
Aao16020 Pantoea s
Aav7463 Polypepti
Aaw82255 C. utilis
Aaw99098 Erwinia u
Aaw9009 Erwinia u
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(c) 1993 - 2004 Compugen Ltd
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Aau36990 Staphyloc Abu16439 Protein e Aag42844 Arabidops Aag42843 Arabidops Abp99379 Arabidops Abb93265 Herbicida Staphyloc Herbicida Flavobact Staphyloc Herbicida Staphyloc Arabidops Arabidops Arabidops Arabidops Arabidops Arabidops Herbicida Aau33743 8 Abb92493 B Aag42713 Aag42712 Aag07000 Aag42711 Aag06999 Abb91864 1 Aag07001 AAG07000 AAG42711 ABU16439 AAG42844 ABP99379 ABB93265 AAU33743 ABB92493 AAB23333 AAG07001 AAG06999 AAG42843 AAG42713 AAG42712 ABB91864 AAW69537

ALIGNMENTS

Carotenoid; isopentenyl pyrophosphate; antheraxanthin; astaxanthin; diet; anti-oxidant; steroid; flavour; fragrance; electro-optic application; aquaculture; enzyme; geranylgeranyl pyrophosphate synthase; CrtE. Pantoea stewartii geranylgeranyl pyrophosphate synthase (CrtE) enzyme. AAB22311 standard; protein; 303 AA. (first entry) Pantoea stewartii. 25-JUL-2002 AAB22311; RESULT 1 4AE2231

WO200218617-A2

07-MAR-2002

04-SEP-2001; 2001WO-US027420.

01-SEP-2000; 2000US-0229858P.

(DUPO) DU PONT DE NEMOURS & CO E I.

Koffas M, Miller Dicosimo DJ, Rouviere PB; ò Brzostowicz PC, Cheng Q, Odom JM, Picataggio SK,

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WPI; 2002-351711/38. N-PSDB; AAD35509.

by in Producing carotenoid compounds e.g. antheraxanthin and astaxanthin, by using microorganisms having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolize single carbon substrates.

Claim 15; Page 134-135; 156pp; English.

The invention relates to a method for producing carotenoid compounds. The method comprises a transformed metabolising host cell, comprising suitable levels of isopertenyl pyrophosphate and a nucleic acid molecule encoding an enzyme in the carotenoid biosynthetic pathway, under the control of regulatory sequences, and contacting the host cell with carbon substrate to produce a acrotenoid compound. The method is useful for producing carotenoid compounds such as antheraxanthin and astaxanthin, by using microorganism having a nucleic acid molecule encoding enzymes in

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the carotenoid biosynthetic pathway and which metabolise single carbon substrates. The carotenoids have potent anti-oxidant properties useful in diet, and aquaculture elements. The carotenoids are also useful as intermediates in the synthesis of teroids flavours and tragrances and compounds for potential electro-optic applications. The present sequence is Pantoea stewartii geranylgeranyl pyrophosphate synthase (CTLE) enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pantoea stewartii; carotenoid biosynthetic enzyme; crtB; crtX; crtY; crtI; crtB; crtZ; granylgeranyl pyrophosphate synthase; enzyme; phytoene; carotenoid.
                                                                                                                                                                     Gaps
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                                                                                                                                         Length 303;
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                                                                                                                                       Score 1526; DB 5;
Pred. No. 2.6e-152;
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100.0%; Pred. No. 2...
0; Mismatches
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                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 303; Conservative
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                                                                                   used in the invention
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                                                                                                              Sequence 303 AA;
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prophosphate synthase (crtB), zeaxanthin glucosyl transferase (crtX), phytopen desaturase (crtI), phytoene synthase (crtB), zeaxanthin glucosyl transferase (crtX), (crtB) and beta-carotene hydroxylase (crtZ) enzymes (see ABP96685 to ABP96690) encoded by ACC44759 to ACC44764. (I) can be used for regulating carotenoid biosynthesis in an organism, by over-expressing (!) in an organism. (I) and the genes encoding (I) are useful for converting phytoene to the carotenoids, for creating recombinant organism; that has a phytoene various carotenoid compounds, and also for enhancing or manipulating carotenoid compounds. (I) can also be used for producing gene products having enhanced or altered activity
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                                    present invention describes Pantoea stewartii carotenoid biosynthetic
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Pred. No. 2.6e-152;
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100.0%; Pred. No. ...
0, Mismatches
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           Claim 4; Page 57-58; 68pp; English
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Matches 303; Conservative
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(KIRI ) KIRIN BEER KK.
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                                                                                                                          The invention comprises the amino acid and coding sequence of a number of carotenoid (crt)-related proteins. The crt-related DNA and protein sequences of the invention are useful for engineering cells which are able to produce carotenoids. The present amino acid sequence represents a crt-related protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                               240
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                                                                                                                                                                                                                             Length 303;
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                                                                                                                                                                                                                                                  1; Indels
    Schroeder WA;
                                                                                                                                                                                                                          99.5%; Score 1518; DB 6;
99.3%; Pred. No. 1.8e-151;
live 1; Mismatches 1;
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                                                                                                          Claim 20; Page 61-62; 74pp; English
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90JP-00053255.
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    SR,
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Best Local Similarity 99.3
Matches 301; Conservative
      Kollmann
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                           WPI; 2003-075455/07.
N-PSDB; ABT14192.
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05-MAR-1990;
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    Souza ML,
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28-JAN-1991
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                                                                                                                                                                                Gene products are useful for the synthesis of carotenoids, useful as coloring, vitamin A precursor, and possibly in prevention of cancer. also AAQ06293-9. (Updated on 24-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                       DB 2; Length 302;
                                                                                        DNA sequences encoding enzymes for carotenoid biosynthesis of carotenoid cpds. e.g. beta-carotene, lycopene, phytoene,
                                                                                                                                                                                                                                                                                                     Query Match 88.1%; Score 1344.5; DB 2; Length Best Local Similarity 88.4%; Pred. No. 3.9e-133; Matches 268; Conservative 16; Mismatches 18; Indels
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Nakamura
                                                                                                                                                   Claim 1; Fig 1; 40pp; English
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Kobayashi K,
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                                    WPI; 1990-322212/43
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16-JUL-1999
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preparation of

WPI; 1998-560727/48

N-PSDB; AAV73179

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240
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241 KDSNQDAGKSTLVNLLGPRAVEERLRQHLQLASEHLSAACQHGHA-TQHFIQAMFDKKLA 299
                                                                                                     This invention describes a novel method for the preparation of carotenoids using genes and proteins isolated from Candida utilis. The invention specifically describes the isolation of a 3-hydroxy-3-methylglutaryl coenzyme A (HWG-COA) reductase protein. This sequence represents the Candida utilis crtE protein which is used in the method of the invention. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILAAVALLSKAFGVIABAEGLIPIAKTRAVSELSTAIGMOGLVQGQPKDLSEGDKPRSAD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AILLINQFKTSTLFCASTQMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTDTG 240
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                                                                                                                                                                                                                                                                                                                                                                       1 LIVCAKKHVHLIGISABQLLADIDSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLL
                                                                                                                                                                                                                                                                                                                                                                                             LLTARDLGCAISHGGLLDLACAVEWVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                1,
                                                                                                                                                                                                                                                                                            Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein encoded by the carotenoid biosynthesis gene crtB.
                                                                                                                                                                                                                                                                                                                                Indels
Gene useful for increase in carotenoid production - and carotenoid.
                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                     Score 1344.5; DB 2, Pred. No. 3.9e-133; 16; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą
                                                                   Example 2; Fig 5-7; 54pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW87888 standard; protein; 302
                                                                                                                                                                                                                                                                                            88.1%;
88.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97JP-00140460
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(first entry)
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Best Local Similarity 88.4
Matches 268; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KIRI ) KIRIN BREWERY KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pantoea ananatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVS 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVS 302
                                                                                                                                                                                                                                                       Sequence 302 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP10327865-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAY-1997;
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10-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301
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The present sequence represents a protein involved in carotenoid biosynthesis. The specification describes astaxanthin diglucosides and adonixanthin-3'-glucosides. The specification also describes a method for the preparation of a carotenoid glycoside, in which all, or part of, carotenoid biosynthesis genes crtE, crtB, crtI, crtY, crtZ, crtX or crtW are introduced to a microbe or plant and expressed. The transformed organism is cultured and astaxanthin diglucosides, adonixanthin-3'-glucosides, and/or astaxanthin monoglucoside are collected. The carotenoid glucosides are used as food additives. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLTARDLGCAISHGGLLDLACAVEMVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 KDINQDAGKSTLVNLLGSGAVEERLRQHLRLASEHLSAACQNGHSTTQLFIQAWFDKKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILAAVALLSKAFGVIAEAEGLTPIAKTRAVSELSTAIGMOGIVOGOFKDLSEGDKPRSAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 KDSNQDAGKSTLVMLLGPRAVEERLRQHLQLASEHLSAACQHGHA-TQHFIQAMFDKKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AILLINOFKTSTLFCASTOMASIAANASCBARENLHRFSLDLGQAFQLLDDLTDGMTDTG
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MIVCAKKGVHLIRDAARQLLADIDRRLDQLLFVEGERDVVGAAMREGALAPGKRIRPMLL
                                                                                                                                                                                                                                                                                                                                                                                                    1 LTVCAKKHVHLTGISABQLLADIDSRLDQLLPVQGBRDCVGAANREGTLAPGKRIRPMLL
                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta-carotene hydroxylase; crtY; crtB; crtI; xanthophyll;
                                                                                                                                                                                                                                                                                                                                          Length 302;
                                                                                                                                                                                                                                                                                                                                          88.1%; Score 1344.5; DB 2; Length
88.4%; Pred. No. 3.9e-133;
.ive 16; Mismatches 18; Indels
                                                                          New carotenoid glucoside(s) - used as food additives.
(KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brwinia uredovora crtE protein sequence
                                                                                                       Disclosure; Page 17-18; 26pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW99098 standard; protein; 302 AA
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                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 88.4
Matches 268; Conservative
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                             WPI; 1999-099030/09.
N-PSDB; AAV84080.
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                                                                                                                                                                                                                                                                                                                Sequence 302 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-0CT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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Best Local S
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240

299

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The present sequence is that of a recombinant Erwinia herbicola geranyl-

Geranyl pyrophosphate (GGPP) synthase. The N-terminal 13 residues of the
Cantive GGPP synthase (AAMOII19) are deleted and replaced by 4 extraneous
amino acids from pARC306, providing a more active enyzme. The most active
Co indicated in AAT40790. GGPP is a 20-carbon atom precursor of phytoene,
the first carotemoid in the carotemoid biosynthesis pathway. The phytoene
CC synthase (AAMOII21) participates in the pathway by providing phytoene
CF from GGPP. Production of total carotemoids in a plant can be increased by
CF transforming the plant with DNA encoding enzymes involved in the
CF biosynthesis pathway, in particular the lycopene cyclase gene (AAT40795).
CF biosynthesis prepared biosynthetically from phytoene through four
CF dehydrogenase (AAMOII23) in Erwinia sp. Beta- carotene is produced by
CF the tobacco ribulose bis-phosphate carboxylase-oxygenase gene (see
CF the tobacco ribulose bis-phosphate carboxylase-oxygenase gene (see
CF the tobacco ribulose bis-phosphate carboxylase-oxygenase gene (see
CF the tobacco ribulose bis-phosphate carboxylase-oxygenase gene (see
CF the tobacco ribulose bis-phosphate carboxylase-oxygenase gene (see
CF the tobacco ribulose bis-phosphate carboxylase-oxygenase gene (see
CF the tobacco ribulose bis-phosphate carboxylase-oxygenase gene (see
CF the tobacco ribulose bis-phosphate carboxylase-oxygenase gene (see
CF carotemoids in the chloroplast of transformed plants as compared to
CF aratway for biological synthesis of further C40 carotene is an
CF gettway for biological synthesis of further C40 carotene is an
CF carathin and zeaxanthin diglucoside (Updated on 25-MMR-2003 to correct
CF PR field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                               Increasing prodn. of total carotenoid(s) in a higher plant - by transforming with vector encoding chloroplast transit peptide operably linked to the Erwinia herbicola lycopene cyclase structural gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 MLQIVALASASSPSTRETLHAFALDFGQAFQLLDDLRDDHPETGKDRNKDAGKSTLVNRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 LDLACAVENVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFGVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STOMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTDTGKDINQDAGKSTLVNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 EQLIADIDSRIDQLIPVQGERDCVGAAMREGTLAPGKRIRPMLLLITARDLGCAISHGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>EAEGLTPIAKTRAVSELSTAIGWQGLVQGQFKDLSEGDKPRSADAILLTNQFKTSTLFCA</u>
                                                                                                                                                                                                                                                                                         Proffitt J, Mukharji I, Yarger J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0%; Score 763.5; DB 2; 56.0%; Pred. No. 9.4e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Fig 3; 99pp; English.
                                                                                                                                        90US-00525551.
90US-00562674.
91US-00662921.
91US-00785566.
                                                                              93US-00095726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 159; Conservative
                                                                                                                                                                                                                                                                                           Brinkhaus FL,
                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-308823/31
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Best Local Similarity
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                                                                                                                                                                                                                                                 (STAD ) AMOCO
                                                                              21-JUL-1993;
US5530188-A.
                                                                                                                                                              03-AUG-1990
28-FEB-1991
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                                                                                                                      02-MAR-1990
                                                                                                                                          18-MAY-1990
                                     25~JUN-1996
                                                                                                                                                                                                                                                                                                             RL;
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                                                                                                                                                                                                                                                                                         Yen HB,
                                                                                                                                                                                                                                                                                                               Ausich
셤
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                                                                                                                                                                                                                                              The present invention describes beta-carotin hydroxylase. Beta-carotene can be used in the preparation of xanthophylls and their metabolites. The present sequence represents an Brwinia uredovora crtE protein sequence from the present invention. (Updated on 17-0CT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AILLINOFKTSTLFCASTQMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTDTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AILWINHFKTSTLFCASMQMASIVANASSEARDCLHRPSLDLGQAFQLLDDLTDGMTDTG
                                                                                                                                 Beta-carotin hydroxylase - useful for preparation of xanthophylls and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LTVCAKKHVHLTGISAEQILADIDSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLTARDLGCAISHGGLLDLACAVEWVHAASLILDDMPCMDDAOMRRGRPTIHTOYGEHVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1LAAVALLSKAFGVIAEABGLTPIAKTRAVSBLSTAIGMOGLVOGOPKDLSEGDKPRSAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGPP synthase; lycopene cyclase; phytoene synthase; beta-carotene; phytoene dehydrogenase-4H; carotenoid; C40; zeaxanthin; diglucoside; pigment; food colourant; chropatet transit peptide; increase yield; tobacco ribulose bis-phosphate carboxylase-oxygenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant truncated geranylgeranyl pyrophosphate synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                    88.1%; Score 1344.5; DB 2
88.4%; Pred. No. 3.9e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Mismatches
                                                                                                                                                                                                      Disclosure; Page 12-13; 17pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .4
Anote= "heterologous
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97JP-00213648
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 88.49
Matches 268; Conservative
                                     (KIRI ) KIRIN BREWERY KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
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                                                                                WPI; 1999-208113/18.
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                                                                                                                                                                their metabolites
                                                                                                  N-PSDB; AAX19118
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07-AUG-1997;
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10-DEC-1996
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Peptide
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126 136

92 99

Gaps

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84; Indels

Length 298;

196

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E. herbicola, geranylgeranyl pyrophosphate synthase; pARC376; GGPP synthase; biosynthesis; carotenoid; lycopene; farnesyl pyrophosphate; phytoene; PPP; isopentyl pyrophosphate; IPP; tail to tail dimerisation; phytoene synthase; phytoene dehydrogenase-4H; food colourant; herbicide; norflurazon.
                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding Erwinia herbicola phytoene dehydrogenase-4H - used prodn. of lycopene, and to produce transgenic plants resistant norflurazon.
                                                                                                                                       terminallly modified geranylgeranyl pyrophosphate synthase
         247 GADAARQKIREHIDSADKHLTPACPQGGAIRQ-FMHWFGHHLA 289
257 GSGAVEERIROHIRIASEHISAACONGHSTTQLFIQAWFDKKLA 300
                                                                                                                                                                                                                                                                                                                                                                  Proffitt J, Mukharji I,
                                                                AAW00171 standard, protein; 298 AA
                                                                                                                                                                                                                                                                                        90US-00487613.
90US-00525551.
90US-00562674.
91US-00662921.
91US-00785568.
                                                                                                                                                                                                                                                                        93US-00096043
                                                                                                   (revised)
(revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-308824/31.
                                                                                                                                                                                                                   Pantoea agglomerans
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03-AUG-1990;
28-FEB-1991;
30-OCT-1991;
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25-MAR-2003
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Ausich RL;
                                                                                  AAW00171;
                                              MESULT 9
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This sequence represents Erwinia herbicola geranylgeranyl pyrophosphate (GGPP) synthase encoded by DNA derived from the plasmid pARC489B. The enzyme encoded by this sequence differs from the wild type synthase in that 13 amino terminal trins are deleted and replaced by four extraneous amino acids. This causes the GGPP synthase to be more active. Certaninal truncation of the enzyme was found to further improve the citivity. GGPP synthase is an enzyme which is involved in the biosynthesis of carotenoids, esp. lycopene, from the ubiquitous precursor, farnesyl pyrophosphate. In E. herbicola, pytroene has been tound to be formed biosynthetically in a two-step process. The initial step is the condensation of farnesyl pyrophosphate (FPP) and isopentyl synthase. In this reaction is catalysed by GSPP pyrophosphate (FPP) and isopentyl pyrophosphate (FPP) and isopentyl pyrophosphate (FPP) and isopentyl pyrophosphate (FPP) and isopentyl pyrophosphate (FPP) and isopentyl pyrophosphate (FPP) and isopentyl pyrophosphate (FPP) and isopentyl pyrophosphate (FPP) and isopentyl pyrophosphate (FPP) and isopentyl pyrophosphate (FPP) and isopentyl pyrophosphate (FPP) and isopentyl pyrophosphate (FPP) and isopentyl pyrophosphate (FPP) and isopentyl pyrophosphate (FPP) and isopentyl pyrophosphate (FPP) and isopentyl pyrophosphate (FPP) and isopentyl pyrophosphate (FPP) and isopente (FPP) and isopentyl pyrophosphate which is used as a food colourant.

Commercial production of lycopene which is used as a food colourant by protected from the herbiciale norflurazon. (Updated on 25-MRA-2003 to correct PF field.) (Updated on 16-OCT-2003 to standardise OS field) Example 1; Fig 3; 87pp; English.

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                                                                                                                                               126
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                                                                                           99
                                                                                                                                    127 ATGDLPGERRAQAVNELSTAVGLQGLVLGQFRDLNDAALDRTPDAILSTWHLKTGILFSA
                                                                   17 BOLLADIDSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGGL
                                                                                                                      77 LDLACAVENVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFGVIA
                                                                                                                                                                       137 EAEGLIPIAKTRAVSELSTALGMOGLVOGOFKOLSEGDKPRSADAILLITWOFKTSTLFCA
                                                                                                                                                                                                                       197 STOMASIAANASCEARENLHRRSLDLGQAFQLLDDLTDGMTDTGKDINQDAGKSTLVNLL
                                                                                  The sequences given in AAW00341-42 represent the wild type and an N-terminally truncated form of geranylgeranyl pyrophosphate (GGPP)
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wild type; N-terminally truncated; geranylgeranyl pyrophosphate; (
GGPP synthase; phytoene synthase; carotenoid; phytoene; pARC306A;
pARC489D; transit peptide; tobacco; chloroplast; skin disorder.
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                     Length 298;
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                                                                                                                                                                                                                                                                                            247 GADAARQKEREHIDSADKHLTFACPQGGAIRQ-FWHLWFGHHLA 289
                                             Indels
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                     DB 2;
                     50.0%; Score 763.5; DB 2
56.0%; Pred. No. 9.4e-72;
ive 40; Mismatches 84
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90US-00562674.
91US-00662921.
91US-00785569.
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(first entry)
                                                Conservative
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                                 Best Local Similarity
Matches 159; Conserv
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Sequence 298 AA;
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03-AUG-1990;
28-FEB-1991;
30-OCT-1991;
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Ausich RL;
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                         Query Match
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Yarger J;

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synthase. GGPP synthase is a enzyme which, along with phytoene synthase (see also AMW00343), catalyse the formation of carotenoids, particularly phytoene. The N-terminally truncated form of GGPP synthase has the first thirteen amino acids replaced by four heterologous amino acids derived from the plasmid pARC306A. This enzyme is about twice as active as the wild type enzyme. A C-terminal truncated protein was found to have even higher activity and was cloned into plasmid pARC489D. The GGPP synthase coding sequences may be attached to the transit peptide sequence given in AAW00344, for transport into tobacco chloroplasts. This allows the tobacco plants to produce high levels of phytoene for use in the treatment of skin disorders. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 16-OCT-2003 to standardise OS field)
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Sequence 298 AA;

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136
                                                                                                                                                                                                                                      67 LDLACAVELTHTASLMLDDMPCMDNAELRRGQPTTHKKFGESVAILASVGLLSKAFGLIA 126
                                                                                                                                                                                                                                                                                                                137 EAEGLTPIAKTRAVSELSTAIGMOGLVQGQFKDLSEGDKPRSADAILLTNQFKTSTLFCA 196
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                                                                                                                                                                                                          77 LDLACAVEMVHAASLIILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSXAFGVIA
                                                                                                                                      17 BOLLADIDSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLLLLFARDLGCAISHGGL
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  Length 298;
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hery Match 50.0%; Score 763.5; DB 2; Length sest Local Similarity 56.0%; Pred. No. 9.4e-72; Atches 159; Conservative 40; Mismatches 84; Indels
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AAW32470 standard; protein; 298
                                                                              (revised)
                                                   AAW32470;
SULT 11
            432470
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(revised)
(first entry) 17-0CT-2003 25-MAR-2003 15-JAN-1998 Erwinia herbicola geranylgeranyl pyrophosphate synthase.

Geranylgeranyl pyrophosphate synthase; Erwinia herbicola; GGPP; lycopene cyclase; recombinant enzyme; transgenic organism; beta-carotene; yeast; plant; vitamin A; cancer.

Pantoea agglomerans

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/note= "Encoded by ACC"
Location/Qualifiers
   Key
Misc-difference
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JS5656472-A 12-AUG-1997 95US-00473512.

07-JUN-1995;

90US-00487613. 90US-00525551. 90US-00562674. 91US-00662921. 93US-00095726. 02-MAR-1990; 18-MAY-1990; 03-AUG-1990; 28-FEB-1991; 21-JUL-1993;

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Inverse true marketime mass been accorded mixing encourses and anywhintal metricolar molecule comprises at least 1125 bp and is present in the plasmids molecule comprises at least 1125 bp and is present in the plasmids parciaty, parcisty, parcisty and parciator. The present sequence represents the amino acid sequence corresponding to the preferred heterologous structural gene of Erwinia herbicola geranylgeranyl pyrophosphate (GGPP) synthase. The new DNA molecule can be used to produce the recombinant enzyme and transgenic organisms, e.g. yeasts or plants, with increased beta-carotene levels. Beta-carotene is used as a colourant in margarine and butter and as an intermediate for vitamin A, and may prevent cancer. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                      DNA encoding Erwinia herbicola lycopene cyclase - for producing recombinant enzyme, and transgenic organisms with increased beta-carotene
                                                                                                                                                                                                                                                                                               molecule has been isolated which encodes an Brwinia herbicola
                                                   HB
                                                      Yen
                                                      ٦,
                                                        Yarger
                                                      RI,
                                                      Ausich
                                                                                                                                                                                                                                                             Example 2; Fig 3; 102pp; English
                                                        Proffitt J,
                 (STAD ) AMOCO CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 298 AA;
                                                                                                                  WPI; 1997-414592
N-PSDB; AAT91542
                                                                           Brinkhaus
                                                        Mukharji
                                                                                                                                                                                                                        levels.
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196 186 77 LDLACAVEMVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFGVIA 136 99 137 BARGLTPIAKTRAVSELSTAIGMOGLVOGOFKDLSEGDKPRSADAILLTNOFKTSTLFCA ROLLADIDSRIDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGGL 7 EVMRQSIDDHLAGILPETDSQDIVSLAMREGVMAPGKRIRPLIMLLAARDLRYQGSMPTL STOMASIAANASCEARENLHRRSIDLGQAFQLLDDLTDGWTDTGKDINQDAGKSTLVNLL 1; Length 298; GSGAVEBRIRQHIRLASZHISAACQNGHSTTQLFIQAWFDKKLA 300 247 GADAARQKLREHIDSADKHLTFACPQGGAIRQ-FMHLWFGHHLA 84; ä 50.0%; Score 763.5; DB 2 56.0%; Pred. No. 9.4e-72; iive 40; Mismatches 84 Local Similarity 56.0% nes 159; Conservative 197 17 Query Match Best Loca Matches d В ठ g Š 셤 ઠે 셤 Š Š

Geranylgeranyl pyrophosphate synthase. AAW01119 standard; protein; 307 (first entry) (revised) (revised) 16-0CT-2003 25-MAR-2003 10-DEC-1996 AAW01119; RESULT 12 AAW01119

GGPP synthase; lycopene cyclase; phytoene synthase; beta-carotene; phytoene dehydrogenase-4H; carotenoid, C40; zeaxanthin; diglucoside; pigment; food colourant; chloroplast transit peptide; increase yield; tobacco ribulose bis-phosphate carboxylase-oxygenase.

Pantoea agglomerans

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17 EQLIADIDSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGGL 76
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Matches 159; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is that of the Erwinia herbicola geranylgeranyl. pyrophosphate (GGPP) synthase. GGPP is a 20-carbon atom precursor of phytoches, the first carctenoid in the carctenoid biosynthesis pathway. The phytoche synthase (AAW01121) participates in the pathway by providing phytoche from GGPP. Production of total carotenoids in a plant can be increased by transforming the plant with DNA encoding enzymes involved in the biosynthesis pathway, in particular the lycopene cyclase gene (AAT40795). Lycopene is prepared biosynthetically from phytoene through four sequential dehydrogenation reactions which can be carried out by a single dehydrogenase (AAW01123) in Erwinia sp.. Beta-carotene is produced by the action of lycopene cyclase on lycopene. A chloroplast transit peptide of the tobacco ribulose bis-phosphate carboxylase- oxygenase gene (see ANT40794) is operatively linked in frame to the 5' end of the total caroteural gene. This leads to increased production of total carotenoids in the chloroplast of transformed plants as compared to total carotenoids in the chloroplast of transformed plants as compared to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 native, non-transformed plants of the same type. Beta- carotene is an effective and apparently harmless food colourant and is also in the pathway for blological synthesis of further C40 carotenoids such as zeazanthin and zeazanthin dilucoside. (Updated on 25-MAR-2003 to correct pf field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 LDLACAVELTHTASLALDDMPCMDNAELRRGQPTTHKKFGSSVALLASVGLLSKAFGLIA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 ATGDLPGERRAQAVNELSTAVGLQGEVLQQPRDLNDAALDRTPDAILSTNHLKTGILFSA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDLACAVEMYHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFGVIA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 EAEGLTPIAKTRAVSELSTAIGMQGLVQGQFKDLSEGDKPRSADAILLTNQFKTSTLFCA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 STQMASIAANASCEARENLHRFSLDIGQAFQLLDDLTDGWTDTGKDINQDAGKSTLVNLL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 EQLIADIDSRIDQLIPVQGERDCVGAAMREGTLAPGKRIRPMLLLITARDLGCAISHGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                             Proffitt J, Mukharji I, Yarger J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSGAVEERLROHLRLASEHLSAACONGHSTTOLFIQAWFDKKLA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Fig 2; 99pp; English.
                                                                                                                                                                                                      90US-00525551.
90US-00562674.
91US-00662921.
91US-00785566.
                                                                                                                93US-00095726
                                                                                                                                                                            90US-00487613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity 56.0
159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             Brinkhaus FL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-308823/31.
                                                                                                                                                                                                                                                                                                                                                              (STAD ) AMOCO CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT40789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 307 AA;
                                                                                                                   21-JUL-1993;
                                                                                                                                                                                                                                                                                                      30-OCT-1991;
US5530188-A.
                                                                                                                                                                                                         18-MAY-1990;
03-AUG-1990;
                                                        25-JUN-1996
                                                                                                                                                                                                                                                                        28-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ausich RL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                             Yen HB,
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This sequence represents Erwinia herbicola geranylgeranyl pyrophosphate (GGPP) synthase encoded by DNA derived from the plasmid pARC376. GGPP synthase is an enzyme which is involved in the biosynthesis of carotenoids, esp. lycopene, from the ubiquitous precursor, farnesyl pyrophosphate. In B. herbicola, phytoene has been found to be formed biosynthetically in a two-step process. The initial step is the condensation of farnesyl pyrophosphate (FPP) and isopentyl pyrophosphate (IPP) to form GGPP, This reaction is catalysed by GGPP synthase. This first step is immediately followed by a tail to tail dimerisation of GGPP, catalysed by the enzyme phytoene synthase, to form phytoene by the catalytic action of phytoene dehydrogenase-4H. The genes encoding components of the lycopene commercial production of lycopene which is used as a food colourant. Plants transformed with the phytoene dehydrogenase-4H coding sequence are protected from the herbicide norflurazon. (Updated on 25-MAR-2003) to protected from the herbicide norflurazon. (Updated on 25-MAR-2003)
                                                                                                                                                                                                                                                                                                                                                                    E. herbicola; geranyigeranyl pyrophosphate synthase; pARC376; GGPP synthase; biosynthesis; carotemoid; lycopene; farnesyl pyrophosphate; phytoene; FPP; isopentyl pyrophosphate; IPP; tail to tail dimerisation; phytoene synthase; phytoene dehydrogenase-4H; food colourant; herbicide; norflurazon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding Erwinia herbicola phytoene dehydrogenase-4H - used for prodn. of lycopene, and to produce transgenic plants resistant to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%; Score 763.5; DB 2; Length 307; 56.0%; Pred. No. 9.8e-72; ive 40; Mismatches 84; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proffitt J, Mukharji I, Yarger J;
                                                                                                                                                                                                                                                                                                      Geranylgeranyl pyrophosphate synthase.
AAW00170 standard; protein; 307 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2, Fig 2; 87pp; English.
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90US-0052551.
90US-00562674.
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91US-00785568
                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pantoea agglomerans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-308824/31
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Geranylgeranyl pyrophosphate synthase.
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90US-0052551.
90US-00562674.
91US-00662921.
93US-00095726.
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                                                                                                                  50.0%;
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                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-414592/38.
                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT91541
                                                                                      Sequence 307 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (STAD ) AMOCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mukharji I,
Brinkhaus FL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
15-JAN-1998
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28-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1993;
                                                                                                                                                159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brwinia sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM32469;
                                                                                                                  Query Match
Best Local S
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                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transformed plants containing DNA encoding Erwinia herbicola enzymes - esp. geranyl:geranyl pyrophosphate synthase and phytoene synthase, allows large scale production of phytoene.
                                                                                                                                                               256
                                              136
                                                              LDLACAVELTHTASLWLDDMPCMDNAELRRGQPTTHKKFGESVALLASVGLLSKAFGLIA 135
                                                                                                    196
                                                                                                                                  195
                                                                                                                                                                                           255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequences given in AAW00341-42 represent the wild type and an N-terminally truncated form of geranylgeranyl pyrophosphate (GGPB) synthase. GGPB synthase is a enzyme which, along with phytoene synthase (see also AAW00343), caralyse the formation of carotemoids, particularly phytoene. The N-terminally truncated form of GGPP synthase has the first thirteen amino acids replaced by four heterologous amino acids derived from the plasmid pARC306A. This enzyme is about twice as active as the wild type enzyme. A C-terminal truncated protein was found to have even higher activity and was cloned into plasmid pARC489D. The GGPP synthase
                  75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wild type; N-terminally truncated; geranylgeranyl pyrophosphate; GGPP; GGPP synthase; phytoene; pARC106A; pARC489D; transit peptide; tobacco; chloroplast; skin disorder.
                                                                                                                                                                                EAEGLTPIAKTRAVSELSTAIGMQGLVQGQFKDLSEGDKPRSADAILLTNQFKFSTLFCA
                                                                                                                                ATGDLPGERRAQAVNELSTAVGLÓGLVLGÓFRDLNDAALDRTPDAILSTNHLKTGILFSA
                                                                                                                                                               STOMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTDTGKDINQDAGKSTLVNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proffitt J, Mukharji I, Yarger J;
                                                                                                                                                                                                                                       GSGAVEERLROHLRLASEHLSAACONGHSTTOLFIOAMFDKKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                               Wild type geranylgeranyl pyrophosphate synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 2, 61pp, English.
                                                                                                                                                                                                                                                                                                                           AAW00341 standard; protein; 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90US-00487613.
90US-00525551.
90US-00562674.
91US-00662921.
91US-00785569.
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                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brinkhaus FL,
                                                                                                                                                                                                                                                                                                                                                                                      (revised)
                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-383742/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pantoea agglomerans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (STAD ) AMOCO CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT41741.
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28-FEB-1991;
30-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAR-1990;
18-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                      16-0CT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                  10-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ausich RL;
                                                                                                                                                                                                                                                                                                                                                          AAW00341;
                                                                                                      137
                                                                                                                                                                                                                         257
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                                                                                                                                                                                                                                                                                                SULT 14
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lycopene cyclase; recombinant enzyme; transgenic organism; beta-carotene;
yeast; plant; vitamin A; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding Brwinia herbicola lycopene cyclase - for producing recombinant enzyme, and transgenic organisms with increased beta-carotene
                                                                                                                                                                                                                                                                                                                                                                                                                                   136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STQMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTDTGKDINQDAGKSTLVNLL 256
                                                                                                                                                                                                                                                                                                                           91
coding sequences may be attached to the transit peptide sequence given AAM00344, for transport into tobacco chloroplasts. This allows the tobacco plants to produce high levels of phytoene for use in the treatment of skin disorders. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDLACAVEMVHAASLILDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFGVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 EAEGLTPIAKTRAVSELSTAIGMOGLVQGOPKDLSEGDKPRSADAILLTNOFKTSTLFCA
                                                                                                                                                                                                                                                                                                                              17 EQLLADIDSRLDQLLPVQGERDCVGAAMREGTLAPGKRIRPMLLLLTARDLGCAISHGGL
                                                                                                                                                                                                                                                                                                                                                                            16 EVMRQSIDDHLAGLLPETDSQDIVSLAMREGVMAPGKRIRPLIMLLAARDLRYQGSMPTL
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                           ï
                                                                                                                                                                                                                 Length 307;
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                                                                                                                                                                                                                       DB 2;
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                                                                                                                                                                                                                          Score 763.5; DB 2
Pred. No. 9.8e-72;
                                                                                                                                                                                                                                                                           40; Mismatches
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Example 2; Fig 2; 102pp; English

A novel DNA molecule has been isolated which encodes an Brwinia herbicola lycopene cyclase enzyme that converts lycopene to beta-carotene. The DNA molecule comprises at 1825 bp and is present in the plasmids pARC1510, pARC1510. The present in the plasmids amino acid sequence corresponding to the nucleotide base sequences of certain preferred DNA segments of the structural gene for geranyigeranyl pyrophosphate (GGPP) synthase. The new DNA molecule can be used to produce the recombinant enzyme and transgenic organisms, e.g. yeasts or plants, with increased beta-carotene levels. Here carotene is used as a colourant in margarine and butter and as an intermediate for vitamin A, and may prevent cancer. (Updated on 25-MAR-2003 to correct PF field.) **8888888888888888**

Sequence 307 AA;

1; Gaps Query Match 50.0%; Score 763.5; DB 2; Length 307; Best Local Similarity 56.0%; Pred. No. 9.8e-72; Matches 159; Conservative 40; Mismatches 84; Indels 1;

17 EQLIADIDSRLDQLLPVQGERDCVGAANREGTLAPGKRIRPMLLLLTARDLGCAISHGGL 76

77 LDLACAVEMVHAASLIEDDMPCMDDAQMRRGRPTIHTQYGEHVAILAAVALLSKAFGVIA 136

197 STOMASIAANASCEARENLHRFSLDLGQAFQLLDDLTDGMTDTGKDINQDAGKSTLVNLL 256

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257 GSGAVEERLROHLRLASEHLSAACONGHSTTGLFIQAWFDKKLA 300

search completed: February 29, 2004, 14:43:51
Job time : 39.9246 secs

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Q7wt72 marine bact
Q9Th4 paracoccus
P94790 flavobacter
Q9YNB mucor circi
Q940t3 rhodocyclus
Q91p99 rhodocyclus
Q7858 phaffia rho
Q13506 phaffia rho
Q13506 phaffia rho
Q13506 methanobact
Q271X9 streptomyce
Q9TiX9 streptomyce
Q9TiX9 methanobact
Q9TiX9 marine bact
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Q9WFS6 marine bact
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093hp2 streptomyce
09jbb2 shodocyclus
09jpb2 shodocyclus
09cfc6 rhodobacter
09cfc1 listeria in
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Q88sw3 lactobacill
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM 1371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments.";
Nucleic Acids Res. 30:3927-3935 (2002).
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Bacteria; Firmicutes; Baciliales; Bacillaceae; Oceanobacillus.
NCBI_TaxID=182710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.5%; Score 1337; DB 16; Length 494; 53.4%; Pred. No. 5.7e-97; ive 90; Mismatches 134; Indels 4;
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GO; GO:0016491; F:oxidoreductase activity; IEA.
Oxidoreductase; Complete proteome.
SEQUENCE 494 AA; 56213 MW; 4F325BA8B4810B56 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last Bequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Phytoene dehydrogenase (EC 1.3.-).
0B2459.
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Q7WT72
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497 AA; 57217 MW; 70814ED59449BBFF CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Bacteria, Firmicutes, Bacillales, Staphylococcus.
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GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR002137; Amino oxidase.
InterPro; IPR08151; Phytn_dehydro.
Pfan; PP01593; Amino oxidase; 1.
ProDom; PD139017; Phytn_dehydro; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.5%;
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Matches 252; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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SEQUENCE 497 AA;
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187 LVEILNYFIKYVGSSPYDAPALMNLLPYIQYHYGLMYVKGGMYGMAQAMEXLAVELGVEI 246
                                                                                                                                                      242 HTNSEVTKLKKDSTGNVIAATLADDSBIKGDIFISNMEVIPTYEKILMEKSSYIKKLTKK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                424 WIPLDIQAKYYSNQGSIYGVVADRFKNLGFKAPQRSSELSNLYFVGGSVNPGGGMPMVIL 483
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                                                                                                                                                                                                                                                                                                                                                                                                  305 FEPSCSGLVLHLGVDRLYPQLAHHNFFYSDHPREHFDAVFKSHRLSDDPTIYLVAPCKTD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 YEPSSGGLVLHIGVRONSYPQLSHINFFPSHNIKEQRNQVFHKAQLPDDPTIYLVNTNKTD 361
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MEDIATE=211952; PubMed=1141816;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani Ui Y., Takahabin N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
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BMB1. AP003365; BASS8726.1; -
BMB1. AP003137; BAB43655.1; -
GO: GO:0006118; P:electron transport; IEA.
InterPro: IPR001837; Amino oxidase.
InterPro: IPR00181; Phytn dehydro.
Pfam; PF01593; Amino oxidase; 1.
Probom; PD139017; Prytn dehydro; 1.
Probom; PD139017; Prytn dehydro; 1.
Prypothetical protein; Complete proteome.
SEQUENCE 497 AA; 57174 MW; E20EBSDDP5141C9D CRC64;
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Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypotherical protein SAV2564.
SAV2564 OR SA2351.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 SGOOVSEKT 489
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                                                                                                                                                                                              187 LVEILNYPIKYVGSSPYDAPALMNILPYIQYHYGLWYVKGGMYGMAQAMEKLAVELGVEI 246
                                                                                                                                             127 QRFLDYSKNLCTETEAGYFAKGLDGFWDLLKFYGPLRSLLSFDVFRSMDQGVRRFISDPK 186
                                                                                                                                                                                                                                                                                                                                                                        183 IRQMIGYFIKYVGSSSYDAPAVLSMLFHMQQEQGLWYVEGGIHHLANALEKIAREEGVTI 242
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IFEALFTGAGKNMADYVQIOKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGPGTYAQF 126
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Baba T., Takeuchi F., Kuroda M., Yuzawa H., Acki K.-I., Oguchi A.,
Baba T., Taweuchi F., Kuroda M., Yuzawa H., Cui L.,
Yamamoto K., Hiramatsu K.,
"Genome and virulence determinants of high virulence community-
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365

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183 IRQMIGYPIKYVGSSSYDAPAVISMLFHMQQEQGLWYVEGGIHHLANALEKLAREEGVTI 242
                                                                                                                                                                                                                 363 TQAPVGYENIKVLPHIPYIQ-DQPPTTEDYAKFRDKILDKLEKMGLTDLRKHIIYEDVWT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 TMPHIFEALFTGAGKNMADYVQIQKVEPHWRNFFE-----DGSVIDLCEDAETQRRE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 LRDFTGGESTGGGYESFIERSKOLHGVSDRFFFWRSIGGLADTWEVGGAFSAAVLKDVLS 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 HTGARVDNIKTYORRVTGVRLDTGEFVKADYIISNMEVIPTYKYLIHLDTQRLNKLEREF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 RIDABVSEIGKODGRACAVKLANGDVIPADIVVSNNEVIPAMSKELRSPASEEKKKOR-F
                                                                                                                  BPSCSGLVLHLGVDRLYPOLAHHNFFYSDHPREHFDAVFKSHRLSDDPTIYLVAPCKTDP
                                                                                                                                           36 AQAPAGCEIIKILPHIPHLDPDKLLTAEDYSALRERVLVKLERMGLTDLRQHIVTEEYWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SNDNORVIVIGAGLGGLSAAISLATAGFSVQLIBKNDKVGGKLNIMTKDGFTFDLGPSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDKL--GPGTYAQFQRFLDYSKNLCTETEAGYFAKGLDGFWDLLKFYGP-----LRSLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 FDVPRSMDQGVRRFISDPKLVEILNYFIKYVGSSPYDAPALMNELPYIQYHYGLWYVKGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R., "Complete genome sequence of the marine planctomycete Pirellula sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
Planctomycetaceae; Pirellula.
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Local Similarity 36.6%; Pred. No. 1.7e-61;
les 189; Conservative 107; Mismatches 193; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
EMBL; BX294154; CAD77312.1; -.
Oxidoreductase; Complete proteome.
SRQUERNCE 534 AA; 57855 MW; C486215FA450B965 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-).
RB11943.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhodopirellula baltica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Matches
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                                                                                                                                                                                                                                                                                                                     QRFLDYSKNLCTETEAGYFAKGLDGFWDLLKFYGPLRSLLSFDVFRSMDQGVRRFISDPK 186
                                                                                 187 LVEILNYFIKYVGSSPYDAPALMKLLPYIQYHYGLWYVKGGMYGMAQAMEKLAVELGVEI 246
                                                                                                                                                                                                                   247 RLDAEVSEIQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMBKLLRSPASELKKMQR-F 305
                                                                                                                                                                                                                                          243 HTGARVDNIKTYQRRVTGVRLDTGEFVKADYIISNMEVIPTYKYLIHLDTQRLNKLEREF 302
                                                                                                                                                                                                                                                                                              EPSCSGLVIHLGVDRIYPQLAHHNFFYSDHPREHFDAVFKSHRLSDDPTIYLVAPCKTDP 365
                                                                                                                                                                                                                                                                                                                                                                           366 AQAPAGCEIIKILPHIPHLDPDKLLTAEDYSALRERVLVKLERMGLTDLRQHIVTEEYWT 425
                                                                                                                                                                                                                                                                                                                                                                                                363 TQAPVGYENIKVLPHIPYIQ-DQPFTTEDYAKFRDKILDKLEKMGLTDLRKHIIYEDVWT 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 QRVIVIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKLAIMTKDGFTFDLGPSILTMPH 66
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SEQUENCE FROM N.A.

Wieland K.E., Goetz F.;

"Regulation of the Staphyloxanthin biosynthesis in Staphylococcus aureus Naman."

Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.

EMBL, X97985; CAA66626.1;

EMBL, X97985; CAA66626.1;

InterPro.; PROBABISI; Phytn. dehydro.

ProDom; PD139017; Phytn. dehydro; 1.

SEQUENCE 439 AA; 50829 WW, AB03097B55EB3862 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q53589;
01-NOV-1996 (TERMELrel. 01, Created)
01-NOV-1996 (TERMELrel. 01, Last sequence update)
01-NOV-1996 (TERMELrel. 24, Last annotation updat
01-TIN-2003 (TERMELrel. 24, Last annotation updat
Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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Matches 206; Conservative
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360 MYVYRPTKYDDSVAPPGKDIIYVLVPVPNLS-SGIDWKKETHRYRBLVIKKLERQGVTDL 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 YGLWYVKGGMYGMAQAMEKLAVELGVBIRLDAEVSBIQKQDGRACAVKLANGDVLPADIV 278
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----KKMORFEPSCSGLVIHLGVDRLYPQLAHHNFFYSDHPREHFDAVFKSHRLSDDPT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 ELYREVPELTGRNPDDYIPMERIDEMYNVPFGNTPEDRYQISSDLIQLIDEIEA-ISDKO
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                                                                                                                                                                                                                                                                                                                                                      415 RQHIVTEEYWTPLDIQAKYYSNQGSIYGVVADRFKNLGFKAPQRSSELSNLYFVGGSVNP
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                                                                                                                                                                        355 IYLVAPCKTDPAQAPAGCELIKILPHIPHLDPDKLLTAEDYSALRERVLVKLERMGLTDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
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28.1%; Score 731; DB 16; Length 511;
Best Local Similarity 32.9%; Pred. No. 4.4e-49;
Matches 174; Conservative 122; Mismatches 161; Indels 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMELrel. 23, Created)
01-MAR-2003 (TrEMELrel. 23, Last sequence update)
01-OCT-2003 (TrEMELrel. 25, Last annotation update)
Phytoene dehydrogenase (phytone desaturase) (EC 1.3.-).
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Oxidoreductase; Complete proteome.
SEQUENCE 511 AA; 58463 MW; 8E70FD9F71D406AB CRC64;
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EMBL; APO04601; BAC14417.1; -

GO; GO:0016491; F:oxidoreductase activity; IBA.

GO; GO:00166118; F:oxidoreductase activity; IBA.

InterPro; IPRO00759; Adrndx_reductase.

InterPro; IPRO002937; Amino_oxidase.

Pfam; PF01593; Amino_oxidase; 1.
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MEDLINE=99061957; PubMed=9843979;

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Xiong J., Inoue R., Bauer C.E.;

Tracking molecular evolution of photosynthesis by characterization of a major photosynthesis gene cluster from Heliobacillus mobilis.";

Proc. Nati. Acad. Sci. U.S.A. 95:14851-14856 (1998).

R major photosynthesis gene cluster from Heliobacillus mobilis.";

PRE, AC0800021, AAC84034.1; -..

R MSL, AP0800021, AAC84034.1; -..

R GO, GO:0006118; P:electron transport; IEA.

RO, GO:0006118; P:electron transport; IEA.

R InterPro; IPR0002937; Amino_oxidase.

R InterPro; IPR000159; Adradx reductase.

R InterPro; IPR000159; Adradx dehydro.

R InterPro; IPR001100; Pyr redox.

R PRINTS; PR00411; PNDRDFASE.

R RINTS; PR00411; PNDRDFASE.

R PRINTS; PR00411; PNDRDFASE.

R PRINTS; PR00411; PNDRDFASE.

R PRODOM; PD139017; Phytn dehydro; 1.

R PCDOM; PD139017; Phytn dehydro; 1.
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01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Hyphomicrobiaceae; Xanthobacter.
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33.1%; Pred. No. 4.1e-47;
ive 87; Mismatches 237; Indels
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SEMILATED THE STORY NOT HEAD.

Kamiunten H., Hirata R.;

"Isolation and characterization of carotenoid biosynthesis genes from partoea agglomerans pv. miletiae Wist 801.";

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB076662; BAB79603.1; "REMED, TEA.

GO; GO:000618; P:Oxidoreductase activity; IEA.

GO; GO:0009058; P:Diosynthesis; IEA.

A GO; GO:0009058; P:Diosynthesis; IEA.

K GO; GO:0006118; P:Diosynthesis; IEA.

InterPro; IPR008151; Amino_oxidase.

R InterPro; IPR008151; Phytn_dehydro.

R PRODOM; PD13917; Phytn_dehydro; I.

R PRODOM; PD1391017; Phytn_dehydro; I.

R ROSITE; PS00982; PHYTOENE DH; I.
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             VSNMEVIPAMEKLLRSPASELK----KMORFEPSCSGLVLHLGVDRLYPQLAH-HNFFYS 333
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                                          DHPREHFDAVFKSHRLSDDPTIYLVAPCKTDPAQAPAGCEIIKILPHIPHLDPDKLLTA-
                                                                                                                                                                                                          ----EDYSALRERVLVKLERMG-LTDLRQHIVTERVMTPLDIQAKYYSNQGSIYGVVAD
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
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Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2003 (TrEMBLrel. 24,
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71 LFTGAGKNMADYVQIQKVEPHWRNFFEDGSVIDLCEDABTQRRELDKLGPGTYAQFQRFL 130
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                                       TPLDIQAKYYSNQGSIYGVVADRFKNLGFKAPQRSSELSNLYFVGGSVNPGGGMPMVTLS 484
360 PSLAPEGCGSYYVLAPVPHLGTANLDWAVEGPRLRDRIFDYLECHYMPGLRSQLVTHRMF 419
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                                                                    420 TPFDFRDELNAWQGSAFSVEPILTQSAWFRPHNRDKHIDNLYLVGAGTHPGAGIPGVIGS
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MEDIINE-94236237; PubMed-8180698;
MEDIINE-94236237; PubMed-8180698;
Charg Y.S., Liu E.M., Lee L.Y., Lin T.P., Hung C.H., Chen C.L.,
Chang Y.S., Liu S.T.,
"Analysis of the gene cluster encoding carotenoid biosynthesis in
Brainia herbicola Ehol3.";
Microbiology 140:331-339(1994).
EMBL; M90698; AAA21263.1;
                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
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ive 90; Mismatches 226; Indels
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GO, GO:0009058; P:biosynthesis; IEA.
GO, GO:000518; P:biosynthesis; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR0012937; Amino oxidase.
InterPro; IPR00151; Phytn dehydro.
Pfam; PF01593; Amino oxidase; 1.
Probom; PD139017; Phytn dehydro; 1.
Probom; PD139017; Phytn dehydro; 1.
PROSTIE; P800982; PHYTOENE DH; 1.
SEQUENCE 492 AA; 55010 MW; 2D65E1A2A32D0635 GRC64;
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Last annotation update)
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1.8e-45;
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(TrEMBLrel. 24,
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Best Local Similarity 33.33
Matches 164; Conservative
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01-JUN-2003 (TrEMBLrel
Phytoene dehydrogenase
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                              DPAQAPAGCEIIKILPHIPHLDPDKLLTAEDYSALRBRVLVKLBRMGLTDLRQHIVTSEY 423
                                                                                                           424 WIPLDIQAKYYSNQGSIYGVVADRFKNLGFKAPQRSSELSNLYFVGGSVNPGGGMPMVIL 483
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Enterobacteriaceae; Pantoea.
WCBI_TaxID=66269;
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deSouza M.L., Kollmann S.R., Schroeder W.A.,
"Carotenoid Biosynthesis (WO 02/079395 A2).";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY166713, AAN85599.1;
GO, GO:0016491; F:oxidoreductase activity; IEA.
GO, GO:001659; P:biosynthesis; IEA.
GO, GO:000518; P:biosynthesis; IEA.
GO, GO:000518; P:biosynthesis; IEA.
InterPro; IPR008159; Amino oxidase.
InterPro; IPR008159; Bac phytoene_db.
PERM; PRO1593, Amino oxidase; 1.
PROSITE; PS00982; PHYTOENE DH; 1.
SEQUENCE 492 AA; 54836 WW; F3DCD224547A5FBA CRC64;
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Last annotation update)
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26.4%; Score 687; DB 2;
Best Local Similarity 33.3%; Pred. No. 1.2e-45;
Matches 164; Conservative 87; Mismatches 229;
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                                                                                                                                                                                               484 SGOLVRDKIVADL 496
                                                                                                                                                                                                                                       487 SAKATAGLILADL 499
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Pantoea stewartii.
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RPLD--YSKOLCTETEAGYF----AKGLDGFWDLLKFYGPLRSLLSFDVFRSM---DQG 177
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Last sequence update}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus (strain MW2).
Bacteria, Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                           463 SNLYFVGGSVNPGGGMPMVTLSGQLVRDKIVADLQ 497
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31.5%; Pred. No. 2e-44;
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EMBL, AP004830; BAB96347.1, -.

GO, GO:0006118; P:electron transport; IEA.

InterPro; IPR0020759; Adrind reductase.

InterPro; IPR002037; Amino oxidase.

InterPro; IPR002037; Amino oxidase.

Pfam; PF01593; Amino oxidase.
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ProDom; PD139017; Phytn_dehydro; 1.
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01-0CT-2002 (TrEMBLrel. 22,
01-0CT-2003 (TrEMBLrel. 25,
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SEQUENCE FROM N.A.
SPECIES=S.aureus (strain NUSO), and S.aureus (strain NUS);
MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui I., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N. K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba T.,
Hatcori M., Ogasawara N., Hayashi H., Hiramatsu K.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                 8 RVIVIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSILTMPHI
                                                         305 FEPSCSGLVLHLGVDRLYPQLAHHNFFYSDHPREHFDAVFKSHRLSDDPTIYLVAPCKTD
                                                                                                                               PACAPAGCELIKILPHIPHLDPDKLLTAEDYSALRERVLVKLERMGLTDLRQHIVTEEYW
                                                                                                                                                                                                    TPLDIQAKYYSNQGSIYGVVADRFKNLGFKAPQRSSELSNLYFVGGSVNPGGGMPMVTLS
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25.9%; Score 672; DB 10; DELBURY 31.5%; Pred. No. 2e-44;
Best Local Similarity 31.5%; Pred. No. 2e-44;
Matches 162; Conservative 120; Mismatches 191; Indels
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus (strain Mu50 / ATCC 700699),
Staphylococcus aureus (strain N315).
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GO, GO:0006118, P:electron transport;
InterPro; IPR002959, Adrida reductase.
InterPro; IPR002937, Amino oxidase.
InterPro; IPR002051, MAD BS.
InterPro; IPR008151; Phyth dehydro.
Pfam; PF01593; Amino oxidase; 1.
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ProDom; PD139017; Phytn_dehydro; 1.
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                                                                                                                                                                                                                                                                              185 GOLVRDKIVADL 496
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480 AKATAGLMLEDL 491
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CRTN OR SAV2561 OR
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SEQUENCE 502 AA
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290 APIKKYP?HKIADLDYSCSAPLMYIGIDIDVTDQVRLHNVIFSDDFRGNIEBIFBG-RLS 348
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                                                                                                       LAVELGVEIRLDAEVSE--IQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMEKLLRSP 295
                                                                                                                                                                                                                                                                                                                   ASELK----KMORFEPSCSGLVLHLGVD-RLYPQLAHHNFFYSDHPREHFDAVFKSHRLS 350
                                                                                                                                                                                                                                                                                                                                                                                                                                            351 DDPTIYLVAPCKTDPAQAPAGCEIIKILPHIPHLD-----PDKLLTABDYSALRERVL 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 YDPSIYVYVPAVADKSLAPEGKTGİYVLMPTPBLKTGSGIDWSDEALTQQ----IKEIIY 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      405 RKLATIEVFEDIKSHIVSETIFTPNDFEQTYHAKFGSAFGLMPTLAQSNYKREQNVSRDY 464
                                                               VRRFISDPKLVBIINYFIKYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGMYGMAQAMEK 237
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2 KIAVIGAGVTGLAAAARIASQGHEVTIFEKNNNVGGRMNQLKKDGFTFDMGPTIVMMPDV

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                    122 SFLTDVYKK---YEIARRYFIERTYRKPSD------FYN-MTSLVQGAKLKTIMHADQL 170
                                                           VRRFISDPKLVBILNYFIKYVGSSPYDAPALANLLPYIQYHYGLWYVKGGMYGMAQAMEK 237
                                                                             LAVELGVEIRLDAEVSE--IOKODGRACAVKLANGDVLPADIVVSNMEVIPAMEKLIRSP 295
                                                                                                                                         290 APIKKYPPHKIADLDYSCSAFLMYIGIDIDVTDQVRLHNVIFSDDFRGNIEBIFEG-RLS 348
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                                                                                                                                                                                                                                                                                                                        128 RPLD--YSKNICTETEAGYF----AKGLDGFWDLLKFYGPLRSLLSFDVFRSM---DQG
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Bravo J.M., Poralla K., Goetz F.;
Genetic and biochemical analyses of the biosynthesis of the yellow
carotenoid 4,4'-diapomeurosporene of Staphylococcus aureus.";
J. Bacteriol. 176:7719-7726(1994).
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Last annotation update)
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25.7%; Score 667; DB 2; L.
Best Local Similarity 31.3%; Pred. No. 4.9e-44;
Matches 161; Conservative 120; Mismatches 192;
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Bacteria, Firmicutes, Bacillales, Staphylococcus
NCBI_TaxID=1280;
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EMBL; X73889; CAA52098.1; -. A73889;
GO; GO:0006118; Pelectron transport;
InterPro; IPRO00759; Adrndx reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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InterPro; IPR000151; Phytn_dehydro.
Pfam: PP01593; Amino oxidase; 1.
PRNTMS; PR00419; ADKEDTASE;
ProDom; PD139017; Phytn_dehydro; 1.
SEQUENCE 506 AA; 57231 MW; 3CA3
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MEDLINE=95095943; PubMed=8002598;
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25,
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01-JAN-1998 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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Indels

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REPUBLICE FROM N.A.

REPUBLICE FROM N.A.

REPUBLICE 520504483; PubMed=11016950;

RA NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

RA NG W.V., Kennedy S.P., Baliga N.S., Thorsson V., Sbrogna J.,

RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

RA Lasthauser B., Keller K., Gruz R., Danson M.J., Hough D.M.,

RA Adam K., Freitas T., Hou, K., Pohlschroder M., Spudich J.L., Jung K.-H.,

RA Adam M., Freitas T., Hou, S., Danisla C.J., Dennis P.P., Omer A.D.,

RA Enhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

RT. Genome sequence of Halobacterium species NRC-1.";

RT. Genome sequence of Halobacterium species NRC-1.";

RT. Froc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

REMEL, ALSO, 1848420.

BR. HA4520. H849230.

C. EMEL, ALOOSO'S; AAG19932.1;

DR. GO, 60:0015036; Fdisulfide oxidoreductase activity; IEA.

BR. InterPro; IPRO01237; PAD_DYL redox.

DR. InterPro; IPRO01237; PAD_DYL redox.

BR. InterPro; IPRO01237; Anino_oxidase.

BR. InterPro; IPRO01297; Anino_oxidase.

BR. PRINTS; PRO0419; ADJREPASE.
                                                                                                                122 SFLTDVYKK---YBIARRYFLBRTYRKPSD-----FYN-MTSLVQGAKIKTLNHADQL 170
                                                                                                                                                                                 LAVELGVEIRLDAEVSE - - IQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMEKLLRSP 295
                                                                                                                                                                                                                                                              ASELK----KWQRFEPSCSGLVLHLGVD-RLYPQLAHHNFFYSDHPREHFDAVFKSHRLS 350
                                                                                                                                                                                                                                                                                                                                            290 APIKKYPPHKIADLDYSCSAFLMYIGIDIDVTDQVRLHNVIFSDDFRGNIEEIFEG-RLS 348
                                                                                                                                                                                                                                                                                                                                                                                                 351 DDPIYLVAPCKTDPAQAPAGCBIIKILPHIPHLD-----PDKLLTABDYSALRERVL 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 VKLERMGL-TDLRQHIVTEEYWTPLDIQAKYYSNQGSIYGVVADRFKNLGFKAPQRSSEL 462
                                                                            128 RFLD--YSKNLCTETEAGYF----AKGLDGFWDLLKFYGPLRSLLSFDVFRSM---DQG 177
                                                                                                                                                            178 VRRFISDPKLVEILNYFIKYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGMYGMAQAMEK 237
                                                                                                                                                                                                                                                                                                                                                                                                                          FEALFTGAGKNMADYVQIQKVEPHWRNFFEDGSVIDLCEDABTQRRELDKLGPGTYAQFQ 127
                             62 YKDVFTACGRAYEDYIELRQLAYIYDVYFDHDDRITVPTDLAELQQMLESIEPGSTHGFM 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Halobacterium sp. (strain NRC-1 / ArCC 700922 / JCM 11081).
Archaea; Buryarchaecta; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           512 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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CRIII OR VNG1684G.
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01-OCT-2003
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412 SY---RDIVLDDIAENTGVDLRDRIVVEERRSVSEFADRYNSHQGTALGLAHTLRQTALF 468
                                                                                                                                                                                                                                                                                                                                                                         111 ORRELDKLGPGTYAQFQRFLDYSKNLCTETBAGYFAKGLDGF------WDLLKFYG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 VKQVFDAYEPGAGDVLDDYLAQAKE-----NYEVGMEHFVKTDRPRVRDWMDPKLAE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 HPREHEDAVEKSHRLSDDPTIYLVAPCKTDPAGAPAG-CEIIKILPHIDPPDKLLTAE 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         353 DWDTHFAQIFDDFAWPDDFAYLCVPSKTDDTVAPDGHSNLFALVPVAPGLD-DTPAVR 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 DYSALRERVLVKLERMGLTDLRQHIVTEEYWTPLDIQAKYYSNGGSIYGVVADRFKNIGF 453
                                                                                                                                                                                                                                                                                                                                       ---DGSVIDLCEDAET 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 VSNMEVIPAMEKIL----RSPASELKKMQRFEPSCSGLVI.HLGVDRLYPQLAHHNFFYSD 334
                                                                                                                                                                                                                                                                                     68
                                                                                                                                                                                                                                                              9 VAVIGAGFGGLSTACYLADAGADVTVVEKTDQIGGRASTLERDGFRFDMGPS#YLMPDVF
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                                                                                                                                                                                   55; Gaps
                                                                                                                        Query Match

25.5%; Score 662.5; DB 17; Length 512;
Best Local Similarity 32.4%; Pred. No. 1.1e-43;
Matches 169; Conservative 81; Mismatches 217; Indels 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   454 KAPQRSSELSNLYPVGGSVNPGGGMPNVTLSGQLVRDKIVAD 495
PRINTS; PR00368; FADPNR.
ProDom; PD139017; Phytn dehydro; 1.
FAD; Flavoprotein; Oxidoreductase; Complete proteome.
SEQUENCE 512 AA; 56274 MW; 95C75E5A059F9126 CRC64;
                                                                                                                                                                                                                                                                                                                                             EALFTGAGKNMADYVQIQKVEPHWRNFFE---
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sarch completed: February 29, 2004, 14:50:45
bb time : 42.8667 secs

haemophilus pseudomonas drosophila homo sapien drosophila sulfolobus

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bacillus capsicum agkistrodon methanococc buchnera ap

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified antis statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SNDNQRVIVIGAGLGGLSAALSLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSIL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R PIR; S32169; S32169.
R InterPro; 1PR0002937; Amino oxidase.
R InterPro; 1PR0008150; Bac_phytoene_dh.
R InterPro; 1PR0008150; Bac_phytoene_dh.
R InterPro; 1PR0008150; NaD_BS.
R InterPro; 1PR0008151; PHyton dehydro.
R Pfam; PF01593; Amino oxidase; 1.
R PR1MTS; PR0419; AMXENTASE.
R ProDom; PD139017; PHyton dehydro; 1.
R PROSITE; PS00982; PHYTORNE DH; 1.
R PROSITE; PS00982; PHYTORNE DH; 1.
R PROSITE; PS00982; PHYTORNE DH; 1.
Carccenoid blosyntheseis; Oxidoreductase; PAD; Flavoprotein; NAD.
T NP BIND
11 44 PAA, 57783 MW; CBCDD74ABSF9RCB CRC64;
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                           P44732 1
P16640 E
P16640 E
P18487 C
O96566 C
O97355 E
P813883 E
O24164 E
P57303 E
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Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
                                                                                                                                                                                                                                                                                                                                                                              01-CCT-1996 (Rel. 34, Created)
01-CCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase)
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NCBI_TaxID=34;
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1 MOSNDNQRVIVIGAGLGGLS......MPMVTLSGQLVRDKIVADLQ 497
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                       GenCore version
Copyright (c) 1993 - 2004
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                                                                      64 LMPEVFEETFRAVGRRIEDYLTLLRCDPNYRVHFRDRSDVTFTSELCAMGRELERVEPGS 123
                                                                                                                 YAQFQRPLDYSKNLCTETEAGYFAKGLDGFWDLLKFYGPLRSLLS-----FDV--FRS 173
 TIYLVAPCKTDPAQAPAGCEIIKILPHIPHLDPDKLLTAEDYSALRERVLVKLERMGLTD
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proc. Natl. Acad. Sci. U.S.A. 87:9975-9979(1990)
-!- FUNCTION: This enzyme converts phycone into lycopene via the intermediaries of phytofluene; zeta-carotene and neurosporene by the introduction of four double bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
NCBI_TaxiD=549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91088634; PubMed=2263648; Armstrong G.A., Alberti M., Hearst J.E.; Conserved enzymes mediate the early reactions of carotenoid
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SIMILARITY: Belongs to the phytoene dehydrogenase family.
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01-AUG-1991 (Rel. 19, Last sequence update)
28-EEB-2003 (Rel. 41, Last annotation update)
phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase)
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EMBL; M38423; AAA24820.1; -.

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MEDLINE=91072214; PubMed=2254247;
Misawa N., Nakagawa M., Kobayashi K., Yamano S., Izawa Y.,
Misawa K., Harashima K.;
"Elucidation of the Erwinia uredovora carotenoid biosynthetic pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pantoca ananas (Erwinia uredovora).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
                                                                                                                                                                                                                                                                                  NAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                              Carotenoid biosynthesis; Oxidoreductase, FAD, Flavoprotein,
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(Phytoene desaturase)
                                                                                                                                                                                                                                                                                                                                                                                                                                      29.6%; Score 770; DB 1; Length 49 larity 34.7%; Pred. No. 3.5e-51; Conservative 93; Mismatches 213; Indels
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492 AA; 54503 MW; 8EDC5DB1562083F2 CRC64;
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01-MAY-1991 (Rel. 18, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update
Phytoene dehydrogenase (EC 1.14.99.-) (Phyto
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PIR, A39273; A33120.
InterPro; IPR002937; Amino_oxidase.
InterPro; IPR008150; Bac_phytoene_dh.
InterPro; IPR008151; Phytn_dehydro.
Ffan; PF01593; Amino_oxidase; 1.
ProDom; PD139017; Phytn_dehydro; 1.
PROSITE; PS00982; PHYTOENE_DH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 LFTGAGKNMADYVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGPGTYAQFQRFL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 DYSRAVFKE---GYLKLGTVPF---LSFRDMLRAAPQLAKLQAWRSVYSKVASYIRDEHL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 KRMSNSLFVLYFGLNHHHDQLAHHTVCFGPRYRBLIDBIFNHDGLASDFSLYLHAPCVTD 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 LFALAGKQIKETVELEPVTPFYRLCWESGKVFNYDNDQTRLBAQIQQFNPRDVBGYRQFL 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 VEILNYFIKYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGMYGMAQAMEKLAVELGVEIR 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDAEVSEIQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMEKLL-RSPAS--ELKKMQR 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 INARVSHMETTGNKIBAVHLEDGRRFILTQAVASNADVVHTYRDLLSQHPAAVKQSNKLQT 299
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                                                                      Bacteriol. 172:6704-6712(1990). This enzyme converts phytoene into lycopene via the intermediaries of phytofluene, zeta-carotene and neurosporene the introduction of four double bonds.
       functional analysis of gene products expressed in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Product, Fullyati, ..., Program DH; 1.

PROSITE, PSCOGDE, PHYTOENE DH; 1.

Carctenoid biosynthesis, Oxidoreductase; FAD; Flavoprotein; NAD.

NP BIND 5, 38 FAD (ADP PART) (POTENTIAL).

A 29 AA: 55007 MW; PA4CD4E34A9C6413 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                      -!- COFACTOR: FAD (Probable).
-!- PATHWAY: Carotenoid biosynthesis.
-!- SIMILARITY: Belongs to the phytoene dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.8%; Score 671; DB 1; Length 492; 32.7%; Pred. No. 1.3e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.7%; Pred. No. 1.3e-z., ive 89; Mismatches 230; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; D37802; D37802.
InterPro; IPR002937, Amino oxidase.
InterPro; IPR00150; Bac phytoene dh.
InterPro; IPR008151; Phytn dehydro.
Pfam; PF01593, Amino oxidase; 1.
ProDom; PD139017; Phytn dehydro; 1.
PROSITE; PS00982; PHYTOENE_PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D90087; BAA14127.1; -.
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                                                                                     Bacteriol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 ILNYFIKYVGSSPYDAPALMNILLPYIQYHYGLWYVKGGKYGMAQAMEKLAVELGVEIRLD 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 PSCSGLVLHLGVDRLYPQLAHHNPPYSDHPREHFDAVFKSHRLSDDPTIYLVAPCKTDPA 366
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Misawa N., Satomi Y., Kondo K., Yokoyama A., Kajiwara S., Saito T.,
Ohtani T., Miki W.;
Chitani T., Miki W.;
Structure and functional analysis of a marine bacterial carotenoid
biosynthesis gene cluster and astaxanthin biosynthetic pathway
proposed at the gene level.";
J. Bacteriol. 177:6575-6584(1995)
J. Bacteriol. 177:6575-6584(1995)
J. PUNCTION: This enzyme converts phytoene into lycopene via the
intermediaries of phytofluene, zeta-carotene and neurosporene by
the introduction of four double bonds (By similarity).
J. COFACTOR: PAD (Probable).
J. PATHWAY: Carotenoid biosynthesis. Involved in astaxanthin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to the phytoene dehydrogenase family
01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase)
                                                                                                                                                                                 Agrobacterium aurantiacum.
Racteria, Proteobacteria, Alphaproteobacteria, Rhizobiales;
Rhizobiaceae, Khizobium/Agrobacterium group; Agrobacterium.
NCBL_TaxID=44155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92; Mismatches 241; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAD (ADP PART) (POTENTIAL).
5F251AF11D679358 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.8%; Score 645; DB 1; 30.8%; Pred. No. 1.2e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002937; Amino oxidase.
InterPro; IPR008150; Bac phytoene dh.
InterPro; IPR008151; Phytn dehydro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01593; Amino oxidase; 1.
ProDom; PD139017; Phytn dehydro; 1.
PROSITE; PS00982; PHYTOENE DH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               501 AA; 54806 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D58420; BAA09594.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biosynthetic pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 30.8
hes 151; Conservative
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                        OAPAGCEIIKILPHIPHLDPDKLLTAEDYSALRERVLVKLERMGLTDLROHIVTERYWTP 426
                                                                                                                    369 MAPPGMSTHYVLABVPHLGRADIDWAVEGPRYADRILASLEBRLIPNLRANLTTTRIFTP 428
                                                                                                                                                                                                                                                                            429 SDFASELNAHHGSAFSVEPILTQSAWFRPHNRDKTIRNFYLVGAGTHPGAGIPGVVGSAK 488
                                                                                                                                                                                                                        427 LDIQAKYYSNQGSIYGVVADRFKNLGFKAPQRSSELSNLYFVGGSVNPGGGMPMVTLSGQ 486
309 WSMSLFVIHFGLREAPKDVAHHTILFGPRYKELVNEIFKGPKIAEDPSLYLHSPCTTDPE 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: This enzyme converts phytoene into zeta-carotene via the intermediary of phytofluene by the symmetrical introduction of two double bonds at the C-ll and C-ll' positions of phytoene.
-!- COFACTOR: FAD (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
Phycomyces.
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PROSITE; PS00982; PHYTOENE DH; 1.
Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD;
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01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99...) (Phytoene desaturase)
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Matches 157; Conservative 100; Mismatches 223; Indels
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BOEBF682B12FB591 CRC64;
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InterPro; IPR002937; Amino oxidase.
InterPro; IPR008150; Bac_Dhycoene_dh.
InterPro; IPR008151; Phytn dehydro.
InterPro; IPR008151; Phytn dehydro.
InterPro; IPR008151; Amino_oxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phycomyces blakesleeanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                         487 LVRDKIVADL 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                 489 ATACVMLSDL 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=NRRL 1555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI TaxID=4837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ruiz-Hidalgo M.J.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                             122 FLRFLDFMKESHTHYBGGVEMAIKQNPETIWKLIRLQYVP- ALFRLHIFDFVYSRAAKY 179
                                                                                                                    182 ISDPKLVEILNYPIKYVGSSPYDAPALMNLLPYIQYHYGLR (VKGGMYGMAQAMEKLAVE 241
                                                                                                                                                                                               242 -LGVEIRLDAEVSEIQKQD--GRACAVKLANGDVLPADIVV; NMEVIPAMEKLLRSPASE 298
                                                                                                                                                                                                                                    240 KPGARPIYEAPVAKINTDDKGKKVTGVTLQSGEVIEADAVV;NADLVYAYHNLLPPCRWT 299
                                                                                                                                                                                                                                                                               299 LKRONORFEPSCSGLVLHLGVDRLYPQLAHENFFYSDHPREHFDAVFKSHRLSDDFTIYLV 358
                                                                                                                                                                                                                                                                                                     300 INTLAEKKIISSSISFYWSLKRVVPELDVHNIPLABAFKES:DEIFTDHKMPSELSFYVN 359
                                                                                                                                                                                                                                                                                                                                                                                  360 LPSRIDPTAAPPGKDSMIVLVPIGHM-KSKTNEAEDYTMIVKRARROWILBVLERRIGITN 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 FORFLDYSKNLCTETBAGY---PAKGLDGFWDLLKF-YGPLRSLLSFDVFRSMDQGVRRF 181
                                                                                                                                                                                                                                                                                                                                                           359 APCKTDPAQAPAGCEIIKILPHIPHLDPDKLLTABDYSAL----RERVLVKLE-RMGLTD 413
65 LPEEAFRALDEKIEDHVELLRCHNNYKVHFDDGDKIQLSSDLSRWKPEMERIEGPD---G 121
                                                                                                                                                           180 FKTKKMRMAFTFQSMYMGMSPYDSPAVYNLLQYTEFAEGIW: PKGGFNTVIQKLENIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                        414 LRQHIVTEEYWTPLDIQAKYYSNQGSIYGVVADRFKALGFKAPQRSS--ELSNLYFVGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=MR403;
WEDLINE-9122367; PubMed=8467787;
FORTES M., Rulz-Vazquez R.M., Murillo F.J.;
Fortes M., Rulz-Vazquez R.M., Murillo F.J.;
Frortes M., Rulz-Vazquez R.M., Murillo F.J.;
Excorth phase dependence of the activation of a bacterial gene for carotenoid synthesis by blue light.";
EMBO J. 12:1265-1275(1993).
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01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14,99.-) (Phytoene desaturase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, Deltaproteobacteria, Myxococcales,
Cystobacterineae, Myxococcaceae, Myxococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              529 AA.
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Interpro; IPR002937; Amino_Oxidase.
Interpro; IPR008150; Bac_phytoene_dh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      472 VNPGGGMPMVTLSGQLVRDKI 492
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                                                                                                                                                                                                                                                                               124 AQFQRFLD----YSKNLCTETEAGYFAKGLDGFWDLLKFYGP--LRSLLSFDVFR 172
                                                                                                                                                                                                                                                                                                                                              129 SALROWMEDGREKYGIAYOKFICTSA------DINIGYYAPWRIAPTLRFKPWQ 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LERMCLTDLRQHIVTEEYWTPLDIQAXYYSNQGSIYGVVADRFKNLGFKAPQ-RSSELSN 464
                                                                                                                                                                                                                                 68
                                                                                                                                                                                                    ORVIVIGAGLGGLSAALSLATAGFSVQLIEKNDKVGGKLNIMT---KDGFTFDLGPSILT
                                                                                                                                                                                                                        173 SMDQGVRRFISDPKLVEILNYFIKYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGMYGMA
                                                                                                                                                                                                                                                                                                                                                                                                      TLYROLDGPFHDDRVTYALAYPSKYLGLHPTTCSSVFSVIPFLELAFGVWHVEGGFRELS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 RSPASELKK-----MORFEPSCSGLVLHLGVDRLYPQLAHHNFFYSDHPRB-HFDAVFKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HVDLEDPPFYVCNPGVTDPSGAPAGHSTLYVLVPTPNTGRPVDWVKTE--QALRERIPAM
                                                                                                                                                                          Gaps
                                                                                  reductase; FAD; Flavoprotein; NAD. AD (ADP PART) (POTENTIAL). 53536A8DFD0D24BC CRC64;
                                                                                                                                                                          38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cercospora nicotianae.
Bukaryota; Pungi, Ascomycota; Pezizomycotina;
Dobinideomycetes et Chaetothyriomycetes incertae sedis;
Mycosphaerellaceae; mitosporic Mycosphaerellaceae; Cercospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the Cercospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 desaturase)
                                                                                                                                                DB 1; Length 529
                                                                                                                                                             Local Similarity 30.3%; Pred. No. 4.6e-41; es 155; Conservative 110; Mismatches 208; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FBB-1996 (Rel. 33, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (BC 1.14.99.-) (Phytoene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Isolation, sequence, and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nicotianae phytoene dehydrogenase gene.";
Appl. Environ. Microbiol. 60:2766-2771(1994)
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                                                                                                      FAD (ADP PART)
      InterPro; IPROBERS; PNYEN, dehydro.
Pfam; PF0153; Amino oxidas; 1.
PRINTS; PR00419; ADXEDTASE.
ProDom; PD13017; Phytn dehydro; 1.
PROSITE; PS00982; PHYTOENE_DH; 1.
Carotenoid biosynthesis; Oxidoreductase; NP_BIND
                                                                                                                                              24.6%; Score 638; 30.3%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ATCC 18366;
MEDLINE=94368091; PubMed=8085820;
Ehrenshaft M., Daub M.B.
                                                                                                                    529 AA; 58420 MW;
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                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 FRWETAVKKILLSEDGGVAKGVELEDGRRLEADVVVNNSDLVYAYBKLLPIKTFYAESLK 307
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intermediary of phytofluene by the symmetrical introduction of double bonds at the C-11 and C-11' positions of phytoene. COFACTOR: FAD (Probable).
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PIR, T48646; T48646.
InterPro; IPRO08150; Bor phytoene dh.
InterPro; IPRO08151; Phytn dehydro.
ProDom; P1139017; Phytn dehydro; 2.
PROSITE; PS00982; PHYTOENE DH; 1.
Carotenoid biosynthesis; Oxidoreductase; PAD; Flavoprotein; NAD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.3%; Score 631.5; DB 1; Length 621; 29.0%; Pred. No. 1.8e-40;
                                                                                                        -!- COFACTOR: FAD (Probable).
-!- PATHWAY: Carotenoid biosynthesis.
-!- SIMILARITY: Belongs to the phytoene dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105; Mismatches 214; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ADP PART) (POTENTIAL)
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621 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 VKGGMYGMAQAMEKLAVELGVEIRLDAEVSEIQKQDG-----RACAVKLANGDVLPADI 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 LIMALHPFESIWHRAGAYFKTDRMQRVFTFATMYMGMSPFDAPATYSLLQYSELAEGIWY 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=74-OR23-1A / FGSC 987;

STRAIN=74-OR23-1A / FGSC 987;

STRAIN=904-195; Pubmed=2144609;

Schmidhauser T.J., Lauter F.R., Russo V.E.A., Yanofsky C.;

"Cloning, sequence, and photoregulation of al-1, a carotenoid

biosynthetic gene of Neurospora crassa.";

Mol. Cell. Biol. 10:5044-5070(1990).

Herbynthetic gene of phytofluene by the symmetrical introduction of two double bonds at the C-11 and C-11' positions of phytoene.
                                                                                                   01.MAY-1991 (Rel. 18, Created)
01.MAY-1991 (Rel. 18, Last sequence update)
15.MAR-2004 (Rel. 43, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase) (Albino-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR008151; Phytn_dehydro.
Pfam; PR01593; Amino oxidase; 1.
ProDom; PD139017; Phytn dehydro; 1.
PR05ITE; PS00882; PHYTOENE DH; 1.
Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD;
                                                                                                                                                                                                                                                                                                                                           Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- COFACTOR: FAD (Probable).
-!- PATHWAY: Carotenoid biosynthesis.
-!- INDUCTION: By photoinduction.
-!- SIMILARITY: Belongs to the phytoene dehydrogenase family.
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PIR, A35319, A35919,
InterPro, IPR002937, Amino oxidase.
InterPro, IPR008150, Bac phytoene_dh.
InterPro, IPR008150, NAD_BS.
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595 AA; 66367 MW;
                                        STANDARD;
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AL-1.
Neurospora crassa.
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                                                              278 VVSNMEVIPAMEKLIRSPASELK----KMORFEPSCSGLVLHLGVDRLYPQLAHHNFFYS 333
                                                                                                                                                   334 DHPREHFDAVFKSHRLSDDPTIYLVAPCKTDPAQAPAGCE-IIKILP--HI-----PHLD 385
                                                                                                                                                                                          348 REYKESFDAIFERQALPDDFSFYIHVPSRVDPSAAPPDRDAVIALVPVGHLLQNGQPELD 407
                                                                                                                                                                                                                                         386 POKLLTARDYSALRERVIJVKLE-RMGLTDLRQHIVTEEYW-TPLDIQAKYYSNQGSIYGV 443
                                                                                                                                                                                                                                                                408 WPTLV----SKARAGVLATIQARTGLS--LSPLITEEIVNTPYTWETKFNLSKGAILGL 460
288 VVVNADLVYTYNNLLPKEIGGIKKYANKLANRKASCSSISFYWSLSGMAKELETHNIFLA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIJURE-89313663; PubMed=2747617; Armstrong G.A., Alberti M., Leach F., Hearst J.E.; Armstrong G.A., Alberti M., Leach F., Hearst J.E.; Mucleotide sequence, organization, and nature of the protein products of the carotenoid biosynthesis gene cluster of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bartley G.B., Schmidhauer T.J., Yanofsky C., Scolnik P.A.;

"Carotenoid desaturases from Rhodobacter capsulatus and Neurospora
"Carotenoid desaturasis from Rhodobacter capsulatus and Neurospora
domains homologous to flavoprotein disulfide oxidoreductases.";
J. Biol. Chem. 265:16020-16024 (1990).

-!-FUNCTION: This enzyme converts phytoene into zeta-carotene via intercediazy of phytofluene by the symmetrical introduction of double bonds at the C-11 and C-11' positions of phytoene.
                                                                                                                                                                                                                                                                                                                                                  461 AHDFFNVLAFRPRIXAQGMDNAYFVGASTHPGTGVPIVLAGAKITAEQILEE 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
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MEDLINE-89327279; PubMed=2546948;
Bartley G.E., Scolnik P.A.;
Carotemoid biosynthesis in photosynthetic bacteria. Genetic characterization of the Rhodobacter capsulatus CrtI protein.";
J. Biol. Chem. 264:13109-13113 (1989).
                                                                                                                                                                                                                                                                                                                      444 VADRFKNLGFKAPQRSSELSNLYFVGGSVNPGGGMPMVTLSGQLVRDKLVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- COFACTOR: FAD (Probable).
-!- PATHWAY: Carotenoid and chlorophyll biosynthesis.
-!- SIMILARITY: Belongs to the phytoene dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1990 (Rel. 15, Created)
1-AUG-1990 (Rel. 15, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14, 199.) (Phytoene desaturase).
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Biol. Chem. 264:18260-18260 (1989).
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                         EMBL: X52291, CAA73540.1; -...
EMBL: Z1165; CAA77540.1; -...
PIR: A32617, A32617.
InterPro; IPR0012937, Amino oxidase.
InterPro; IPR0012937, Amino oxidase.
InterPro; IPR0018151, Phytn dehydro.
InterPro; IPR0018151, Phytn dehydro.
Pfan; PF015937, Amino oxidase; 1.
PRINTS; PR00419, ADXRDTASE.
PROSTIE; R800419, ADXRDTASE; 1.
PROSTIE; R800419, ADXRDTASE DH; 1.
PROSTIE; R800419, Phytn dehydro; 1.
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P54980; Q9RPD0;
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase).
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Best Local Similarity 28.3%; Pred. No. 3.3e-34;
Matches 146; Conservative 111; Mismatches 215; Indels 44; Gaps
                                                SEQUENCE FROM N.A.
STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
IMAGELINE-94292403; PubMed-8021167;
IMAGELINE-94292403; PubMed-8021167;
ILANGTH Steps in carotenoid biosynthesis: sequences and
"Early steps in carotenoid biosynthesis: sequences and
"Early steps in carotenoid biosynthesis: sequences and
"Franscriptional analysis of the crt1 and crt8 genes of Rhodobacter
sphaeroides and overexpression and reactivation of crt1 in
"J. Bacterichia coli and R. sphaeroides.";
J. Bacteriol. 176:3859-3869(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01593; Amino_oxidase, 1.
Probom; PD139017; Phyrn dehydro; 1.
PROSITE; PS010982; PHYTOENE BH; 1.
Phocrosynthesis; Chlorophyll biosynthesis; Carotenoid biosynthesis; Oxidoreductase; PAD; Flavoprotein; NAD.
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
MEDLINE=95238278; PubMed=7721699;
Lang H.P., Cogdell R.J., Takaicis, S., Hunter C.N.;
"Complete DNA sequence, specific ThS insertion map, and gene assignment of the carotenoid biosynthesis pathway of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PATHWAY: Carotenoid biosynthesis.
-!- SIMILARITY: Belongs to the phytoene dehydrogenase family.
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T -> S (IN REF. 3).
L -> F (IN REF. 3).
Q -> P (IN REF. 3).
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PIR; T50745; T50745.
InterPro; IPR002937; Amino oxidase.
InterPro; IPR008150; Bac phycoene_dh.
InterPro; IPR008150; Bac phycoene_dh.
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                                                                                                                                                                                                                                                                                                                                              laeroides.";
Bacteriol. 177:2064~2073(1995).
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Rhodobacteraceae; Rhodobacter.
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395 395 C
518 AA; 57244 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COFACTOR: FAD (Probable)
                   NCBI_TaxID=1063;
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STRAIN-ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;

KRELINE-9528278; PubMed=7721699;

A REDELINE-9528278; PubMed=7721699;

A Complete DNA sequence, specific Tn5 insertion map, and gene assignment of the carotenoid biosynthesis pathway of Rhodobacter sphaeroides.";

J. Bacteriol. 177:2064-2073(1995);

J. Bacteriol. 177:2064-2073(1995);

J. Bacteriol. 177:2080-2073(1995);

J. Bacteriol. 177:2080-208788 TO SPHEROIDENE TO DEMETHYLSPHEROIDENE OR METHORIPOSPORENE TO SPHEROIDENE.

J. COPACTOR: PAD (Probable).

J. COPACTOR: PAD (Probable).

J. SATHWAY: Carotenoid and chlorophyll biosynthesis.

J. SAMILARITY: Belongs to the phytoene dehydrogenase family.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
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STRAINSTICC (17023 / 2.4.1 / NCIB 8253 / DSM 158;
STRAINSTICC (17023 / 2.4.1 / NCIB 8253 / DSM 158;
MEDLINE=92307398; PubMed=1612412;
Gari E., Toledo J.C., Gibert I., Barbe J.;
"Nucleotide sequence of the methoxyneurosporene dehydrogenase from Rhodobacter sphearoides: comparison with other bacterial earoremoid dehydrogenases.";
FEMS Microbiol. Lett. 72:103-108 (1992).
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FED-2003 (Rel. 41, Last annotation update)
Methoxyneurosporene dehydrogenase (EC 1.14.99.-).
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7 KVVVVGAGMGGLASAIRLARAGCEVTLLEARRAPGGRWRTLPSVAGPVDAGPTVLTLIRBV 66
234 ALARLADDOGVRLRYGAPVAGILRQGGRPTGVQLADGRTLPADHIVFNGDPAALLAGCLG
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ID _CRTI STRGR STANDARD; PRT, 507 AA.

CP54981; P72447;
DT 01-0CT-1996 (Rel. 34, Created)
DT 01-0CT-1996 (Rel. 34, Last sequence update)
DT 18-PEB-2003 (Rel. 41, Last annotation update)
DB Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase).
GRI OR CRIE.
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                                                                                                                                                                                                                                              Schumann G., Nurnberger H., Sandmann G., Kruegel H.J.;
"Activation and analysis of cryptic crt genes for carotenoid
biosynthesis from Streptomyces griseus.";
Mol. Gen. Genet. 252.658-66(1996).
-!- FUNCTION: This enzyme converts phytoene into zeta-carotene via the intermediary of phytofluene by the symmetrical introduction of two double bonds at the C-11 and C-11' positions of phytoene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATHWAY: Carotenoid biosynthesis. SIMILARITY: Belongs to the phytoene dehydrogenase family
Streptomyces griseus.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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InterPro; IPRO00799; Adrindx reductase.
InterPro; IPRO01799; Adrind caidase.
InterPro; IPRO08150; Bac_phytoene_dh.
InterPro; IPRO080505; MAD_BS.
InterPro; IPRO080505; MAD_BS.
InterPro; IPRO08151; Phytn dehydro.
Pfam; PF01593; Amino_oxidase; 1.
PRUTQS; PRO0419; ADXEDTASE.
ProDom; PD139017; Phytn dehydro; 1.
PROSITE; PS00982; PHYTOENE_DH; 1.
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SEQUENCE FROM N.A.
SEQUENCEJA933;
MEDIINE=97074881; PubMed=8917308;
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hes 146; Conservative
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409 MGLTDLRQHIVTEEYWTPLDIQAKYYSNQGSIYGV---VADRFKNLGFKAPQRSSBL--- 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 BALFTGAGKNMADYVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGPGTYA----
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-!- COPACTOR: PAD (Probable).
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Streptomycineae, Streptomycetaceae, Streptomyces.
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1-OCT-1996 (Rel. 34, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99..) (Phytoene desaturase)
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                                                                                                                                                                                                                                                                                                                                                            508 AA.
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InterPro; IPR000759; Adrndx reductase.
InterPro; IPR002937; Amino Oxidase.
InterPro; IPR002937; Amino Oxidase.
InterPro; IPR008150; Bac phytone_dh.
InterPro; IPR008151; Phytn_dehydro.
Pfam; PF01593; Amino oxidase; I.
PRINTS; PR00419; ADXRDTASE.
PROSTTE; P800982; PHYTOENE DH; I.
Carotenoid biosynthesis; Oxidoreductase; FAI
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SYNY3
InterPro;
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                                                                                                                                                                                                                                                                                                                                     EMPGLGSAIEVEGLVTPVD----WTAOGHAAGTPPSVAHTFPOTG---PFRPGNLVRGT 459
                                     RLDARIGHEVSDERLRRVFSFQALYAGVPPARALAAYAVIAYMDTVAGVYFPRGGMHALP 233
                                                                                                                                                  -RSPASELKKMORFEPSCSGLVLHLGVDRLYPQLAHINFFYSDHPREHFDAVFKSHRLSD 351
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 SMDQGVRRFISDPKLVEILNYFIKYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGMYGMA 232
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RAMADAAADAGASFRYGQSVITKLERSGDRVIAV-VIDQBRIACDAVVLIPD-LPVSYRLL
                                                                                                                                                                      292 GRSPHRPLP----LRHSPSAVILHAGTDRTWPNLAHHTISFGAAWKSTPHELTRTGELMS
                                                                                                                                                                                                                                                                                                     410 GLTDLRQHIVTBEYWTPLDIQAKYYSNQGSIYGV---VADRFKNLGFKAPQRSSEL---
                                                                         OAMEKLAVELGVETRLDAEVSETOKODGRACAVKLANGDVLPADIVVSNMEVI PAMEKLL
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MEDLINE=89313663; PubMed=2747617;
MEDLINE=89313663; Alberti M., Leach F., Hearst J.E.;
"Nucleotide sequence, organization, and nature of the protein products of the carotenoid biosynthesis gene cluster of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90368827; PubMed=2144293; Barliey G. S., Scolnik P.A.; Barliey G. S., Schmidhauser T.J., Vanofsky C., Scolnik P.A.; Barliey G. S., Schmidhauser T.J., Vanofsky C., Scolnik P.A.; Carotenoid desaturases from Rhodobacter capsulatus and Neurospora crassa are structurally and functionally conserved and contain crassa are structurally and functionally conserved and contain Genanis homologous to flavoprotein disulfide oxidoreductases."; J. Biol. Chem. 265:16020-16024(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- COFACTOR: FAD (Probable).
-!- PATHWAY: Carotenoid and chlorophyll biosynthesis.
-!- SIMILARITY: Belongs to the phytoene dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FB-2003 (Rel. 4), Last amotation update)
Methoxyneurosporene dehydrogenase (EC 1.14.99.-).
                                                                                                                                                                                                                                                                                                                                                                          SNEYFVGGSVNPGGGMPMVTLSGQLVRDKI 492
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PIR; S04406; S04406. InterPro; IPR002937; Amino_oxidase.

EMBL; X52291; CAA36537.1; -. EMBL; Z11165; CAA77544.1; -.

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14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 RFDHLTTGLWEAFHRSVIAAPKPDLWRIAAATVTRPQLWPALRPGL-----TWRDLLAH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 FISDPKLVBILNYFIKYVGSSPYDAPALMNILPYIQYHYGLWYVKGGMYGMAQAMEKLAV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 HFKDPRLAQLFGRYATYVGGRPGATPAVLSLIWQAEVQ-GVWAIREGWHGVAAALARVAE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 ELGVBIRLDAEVSEIQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMEKLLRSPA-SEL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 KKMORPEPSCSGLYLHLGVDRLYPQLAHHNFFYSDHPREHFDAVFKSHRLSDDPTIYLVA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BALFTGAGRNWADYVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKU-GPGTYAQFQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFLDYSKNLCTETEAGYFAKGLDGFWDLL-----KFYGPLRSLLSFDVFRSMDQGVRR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 -CAQDREMQAP-----VPEIERFEIIMNGPAGHQPFPQEEAQCRARTFPMLAAM 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLT---DLRQHIVTEBYWTPLDIQAKYYSNQGSIY-----GVVADRFKNLGFKAPQRSSE 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405 GLTPSPDPETRALT----TPALLSRRFPGSLGAIYGGSPEGTLAT-----FRRPLARTG 454
                                                                                                                                                                                                                                                                                                                     99
                                                                                                                                                                                                                                                                                                     240 AKGVRPHYGAKAKRIVRKEGRVTAVBIETGVSIPCGACIFNGDPGALRDGLAGDARASM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 PCKTD-PAQAPAGCELIKILPHIPHLDPDKLLT-----AEDYSALRBRVLVKLERM
                                                                                                                                                                                                                                                                              9 VIVIGACIGGISAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSILTMPHIF
                                                                                                                                                                                                                                     Gaps
InterPro; IPR008151; Phytn dehydro.
Pfam; PF01593; Amino oxidase; 1.
Probom; P139017; Phytn, dehydro; 1.
PROSITE; PS00982; PHYTOENE DH; 1.
Photosynthesis; Chlorophyll biosynthesis; Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92256820; PubMed=1581575;
Martinez-Ferez I.M., Viogue A.;
Mucleotide sequence of the phytoene desaturase gene from
Synechocystis sp. PCC 6803 and characterization of a new mutation
which confers resistance to the herbicide norflurazon.";
Plant Mol. Biol. 18:981-983(1992).
                                                                                                                                                                                                                                     59;
                                                                                                                                                                                           DB 1; Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-1992 (Rel. 24, Created)
01-PEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase)
PDS OR CRID OR SLR1254.
                                                                                                                                                                                       Query Match
Best Local Similarity 27.4%; Pred. No. 7.5e-30;
Matches 141; Conservative 88; Mismatches 226; Indels
                                                                                                                       AD (ADP PART) (POTENTIAL)
D1180A023FPEB5A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Cyanobacteria; Chroococcales; Synechocystis
NCBL_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                472 AA
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                                                                                                                                FAD
                                                                                                                                                    494 AA; 52312 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synechocystis sp. (strain PCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
REVISIONS TO C-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-1992
01-FEB-1996
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MEDLINE=97661201; PubMed=8965231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu B., Nakamura Y.,
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu B., Nakamura Y.,
Myajima N., Hisrosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Mateuno A., Muraki A., Nakazaki N., Naruo K.,
Vamada M., Yasuda M., Tabata S.,
Yamada M., Yasuda M., Tabata S.;
Yamada M., Yasuda M., Tabata S.;
Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
DNA Res. 3:109-136(1996).
I- FUNCTION: This enzyme converts phytoene into zeta-carotene via the
intermediary of phytofluene by the symmetrical introduction of two
double bonds at the C-11 and C-11' positions of phytoene.
I- COPACTOR: NAD, NADP, or PAD (probable).
I- BRZYME REGULARION: Inhibited by the herbicide norflurazon in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the BMID cutstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license electrometry of the statement of the statement of the statement of the statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --SKNLCTETEAGYFAKGL------DGF-WD--L 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 LKFYGPLRSLLSFDVFRSMDQGVRRFISDPK-----LVBILMYFIKYVGSSPY----DA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PALMNILLPYIQYHYGLWYVKGGMYGMAQAMEKLAVELGVEIRLDAEVSEI-QKQDGRACA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 VKL-----ANGDVLPADIVVSNMEVIPAMEKLIRSP---ASELKKONQRFEPSCSGLVLHL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 RVIVIGACIGACISAAISLATAGPSVQLIEKNDKVGGKLNI-MTKDGFTFDLGPSILTMPH 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 AKQNIPPR--IEKEVFIAMSKAL-NFI-DPDEISATILLTALNRFLQEKNGSKMAFLDGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RVVIAGAGLAGLACAKYLADAGFTPVVLERRDVLGGKIAAWKDEDGDWYETGLHI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65; Mismatches 186; Indels 183; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S74886; S74886.
InterPro; IPR00759; Adradx reductase.
InterPro; IPR001613; Amineoxid £1.
InterPro; IPR02337; Amino oxidase.
PRIMTS: PR00419; ADXROTASE.
PRIMTS: PR00757; AMINEOXDASE.
Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      non-competitive way.
PATHWAY: Carotenoid biosynthesis.
SUBCELLULAR LOCATION: Membrane-associated (Probable).
SIMILARITY: Belongs to the phytoene dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 472;
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NP BIND

1 23 FAD (ADP PART) (POTENTIAL).

VARTANT 195 195 R -> C (CONFERS RESISTANCE TO
Vioque A.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81D089A6DAA28758 CRC64;
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Best Local 9
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317 GVDRLYPQLAHHNF-----FYSDHP---REHFDAVFKSHRLSDDPTIYLVAPCKTDPA 366
                                                   Q-----APAGCELIKILP-HIPHLDPDKLLTAEDYSALRERVLVKLERMGLTDL 414
                                                                                                                                  415 RQHIVTBEYWTPLDIQAKYYSNQGSIYGVVADRFKNLGFKAPQRSSELSNLYFVGGSVNP 474
                                                                                                                                                 357 ODWIGKSDERIVAATWARİKOLFPOHFNGDNPARL----
                                                                                                                                                    475 G--GGMPMVTLSGQLVRDKIVAD
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Search completed: February 29, 2004, 14:45:02 Job time : 11.3764 secs us-09-941-947a-24.rpr

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GenCore version 5.1	- 2004	
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	Copyright	

1 protein - protein search, using sw model

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February 29, 2004, 14:34:14; Search time 13.8338 Seconds (without alignments) 3455.835 Million cell updates/sec Ë

.tle: :rfect score:

US-09-941-947A-24 2598 1 MNSNDNQRVIVIGAGLGGLS.......MPMVTLSGQLVRDKIVADLQ 497 squence:

oring table:

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 arched:

stal number of hits satisfying chosen parameters:

st-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries .nimum DB seq length: 0 iximum DB seq length: 2000000000

PIR 78:*
2: Diri:*
2: Dir2:*
3: Dir3:*

ıtabase

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	14	hypothetical prote	phytoene dehydroge		squalene synthase		phytoene dehydroge	zeta-carotene desa			phytoene dehydroge	phytoene dehydroge			phytoene desaturas		phytoene dehydroge	phytoene dehydroge	probable phytoene				phytoene dehydroge	methoxyneurosporen	phytoene dehydroge	methoxymeurosporen	methoxyneurosporen	methoxyneurosporen
SUMMARIES		E90061	T31463	832169	A33120	S52586	B90061	D37802	HB4320	AG2509	543324	843139	535306	T48646	A35919	T50910	T46822	B55548	E69108	A32617	T36968	B84327	AH1199	S49620	C75466	523633	T50745	S49624	T50893	T50749
	DB	5	N			7																								N
	Length	497	517	517	492	492	502	492	512					621	595	511	582	448	514	524	523	536	490	518	548	495	518	486	525	
d	Query Match	2.0	30.0	29.8	29.6	26.4	25.9	25.8	25.5	25.2	25.1	24.7	24.6	24.3	1	24.0	23.8	$^{\circ}$	S	22.4	22.3	21.9	21.3	21.1	20.9	20.9	20.9	20.5	20.1	ان و و
	Score	1287	779	773	770	685	672	671	662.5	654	653	641.5	638	631.5	624.5	623	618.5	595	590.5	581.5	580	568.5	554	548	544	543.5	543	532.5	521	517.5
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phytoene dehydroge	methoxymeurosporen	phytoene desaturas	hydroxyneurosporen	probable carotenoi	phytoene dehydroge	hypothetical prote	hypothetical prote	methoxyneurosporen	hypothetical prote	hypothetical prote	hypothetical prote	phytoene dehydroge	hypothetical prote	probable phytoene	hypothetical prote
AF1557	S04406	T51119	832171	T34971	A99470	H83880	AB2064	D75297	A86203	875951	S746B9	G90413	AC2446	B75561	A96612
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488	494	528	485	206	454	498	506	490	587	501	507	518	503	511	574
19.9	18.9	17.9	17.7	16.4	15.2	14.9	13.4	12.4	12.0	11.9	11.6	11.3	10.7	7.6	9.6
516	490.5	465	460	425.5	396	386	347	322.5	313	308	301.5	293.5	277	252	250.5
30	31	32	33	34	32	36	37	38	en en	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 B90061 bypochetical protein SA2351 [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Species: Staphylococcus aureus C;Species: Staphylococcus aureus C;Species: Staphylococcus aureus C;Species: Staphylococcus aureus C;Species: Socoti R;Accession: E90061 R;Accession: E90061 R;Accession: E90061 R;Accession: E90061 R;Accession: E90061 A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Status: preliminary A;Molecule type: DNA
A;Residues: 1-497 <kur> A;Cross-references: GB:BAD00018; PID:q13702514; PIDN:BAB43655.1; GSPDB:GN00149</kur>
A:Experimental source: strain N315
Cidenetics:
A;Gene: SA2351

366 AQAPAGCEIIKILPHIPPHDPDKILTARDYSALRERVIVKLERMGLTDLRQHIVTEEYMT 425

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A.Accession: S67952
A.Molecule type: DNA
A.Residues: 9-37;462-488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKYTPQKINSMEVTCGAFMLYLGVARRYDNIHIJANIYFTFDYKYSMDELFTRQQLPQDPA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SK:IEFERIYTPETFQNRFNTYQGAAFGLAPSLFQSGYFRPHIKSKEVPNLYFSGASVHP 478
                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: EMBL:AF080002; NID:g3820536; PID:g3820561; PIDN:AAC84034.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 FEALFTGAGKUMADYVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGPGT---- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --YAQFQRFLDYSKNLCTETEAGYFAKGLDGFWDLLKFYGPLRSLLSFDVFRSMDQGVRR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 RYLAQIHRRYQVAREKPIEKS---FTKPSD-FFNIDTLIG----MMQLRTLNNMYDDIAR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FISDPKLVBILNYFIKYVGSSPYDAPALMNLLPYIQYHY-GLWYVKGGMYGMAQAMEKLA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 VELGVEIRLDAEVSEIQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMEKLLRSPASEL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----KKONORFEPSCSGLVLHLGVDRLYPQLAHHNFYSDHPREHFDAVFKSHRLSDDPT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    355 IYLVAPCKTDPAQAPAGCEIIKILPHIPHLDPDKLLTAEDYSALRERVLVKLERMGLTDL 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RQHIVTEEYWTPLDIQAKYYSNQGSIYGVVADRFKNLGFKAPQRSSELSNLYFVGGSVNP 474
485
                 69
                                                                                                                                                                                         // Species: Heliobacillus mobilis policies city neilougulius mobilis pate: 02-Sep-2000 #text_change 15-Sep-2000 #Accession: T3.46.
// Accession: T3.46.
// Accession: T3.46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 XVIVVGSGAGGMSAAVRLANQGWDVTVLEKEATPGGRISAIQAEGYSIDVGPTIMMADDV
PLDIQAKYYSNQGSIYGVVADRFKNLGFKAPQRSSELSNLYFVGGSVNPGGGMPMVTLSG
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                                                                                                                                                                                 robable diapophytoene dehydrogenase crtN - Heliobacillus mobilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
30.0%; Score 779; DB 2; Length 51'
Best Local Similarity 34.7%; Pred. No. 1.3e-52;
Matches 174; Conservative 107; Mismatches 196; Indels
                                                                                                                                                                                                                                                                                                                                   ;Status: preliminary; translated from GB/EMBE/DDBJ;Molecule type: DNA;Residues: 1-517 <xIO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: phytoene dehydrogenase
                                                                                                  COVADKINA 490
                                                                  QLVRDKIVA 494
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lypothetical protein 2 - Myxococcus xanthus

RESULT . 332169

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C;Species: Myxococcus xanthus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 29-Sep-1999
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 29-Sep-1999
C;Accession: 53126; 567952
R;Botella, J.; Murillo, F.; Ruiz-vazquez, R.
Submitted to the EMBL Data Library, March 1993
A;Description: Nucleotide and deduced protein sequences of a carotenoid gene cluster in A;Reference number: 532168
A;Accession: 532169
A;Accession: 532169
A;Accession: 532169
A;Accessive cest Remain DX1050
B;Botella, J.A.; Murillo, F.J.; Ruiz-Vazquez, R.
B;Botella, J.A.; Murillo, F.J.; Ruiz-Vazquez, R.
B;Botella, J.A.; Murillo, F.J.; Ruiz-Vazquez, R.
A;Reference number: 33, 238-248, 1995
A;Tile: A cluster of structural and regulatory genes for light-induced carotenogenesis
A;Reference number: S67950; MUID:96061955; PMID:7588751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 AMEKLAVELGVEIRLDABVSEIQKQDGRACAVKLANGDVLPADIVVSNWEVIPAMEKLLR 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 YAQFQRFLDYSKNLCTETEAGYFAKGLDGFWDLLKFYGPLRSLLS-----FDV--FRS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293
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N;Alternate names: phytoene desaturase
C;Species: Erwinia herbicola
C;Species: Erwinia herbicola
C;Accession: A39273; A33120
R;Armstrong, G.A.; Alberti, M.; Hearst, J.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 9975-9979; 1990
A;Title: Conserved enzymes mediate the early reactions of carotenoid biosynt
A;Reference number: A39273; MUID:91088634; PMID:2263648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         353 SPYVNAPTRTDASLAPEGKDALYVLVPVPHQHPDLDWKVEG-PKVRAKFFARMAELGFPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 MDQGVRRFISDPKLVBILNYFIKYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGMYGMAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              354 TIYLVAPCKTDPAQAPAGCEIIKILPHIPHLDPDKLLTAEDYSALRERVLVKLERMGLTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 STQGRRIVVVGAGYGGLAAAARLAHQGFDVQVFBKTQGPGGRCNRLQVDGFTWDLGPTIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SNDNQRVIVIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
29.8%; Score 773; DB 2; Length 51
Best Local Similarity 34.7%; Pred. No. 3.8e-52;
Matches 174; Conservative 99; Mismatches 205; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         472 VNPGGGMPMVTLSGQLVRDKIV 493
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Gaps

12;

247

299

364 359

304

Genetics:

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131 DYSKOLCTETEAGYFAKGLDGFWDLLKFYGPLRS---LLSFDVFRSMDQGVRRFISDPKL 187
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A;Experimental source: strain N315
                                                                 11 VIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSILTMPHIFRA
                                                                                         6 VIGAGFGGLALAIRLQAAGIPVLELEQRDKPGGRAYVYEDQGFTFDAGPTVITDPSAIEE
                                                                                                                                                        LFTGAGKNWADYVQIQKVEPHWRNFFEDGSVIDLCEDABTQRRELDKLGPGTYAQFQRFL
                                                                                                                                                                                       188 VEILNYFIKYVGSSPYDAPALMNILPYIQYHYGLWYVKGGMYGMAQAMEKLAVELGVEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                  LDAEVSEIQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMEKLL-RSPAS--ELKKMQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 INARVSHMETTGDTIBAVHLEDGRRFFTRAVASNADVVHTYRDILSQHPAAVKQSKKLQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 FEPSCSGLVLHLGVDRLYPQLAHHNFFYSDHPREHFDAVFKSHRLSDDPTIYLVAPCKTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 KRMSNSLFVLYFGLMHHHDQLAHHTVCFGPRYKELIHEIFNHDGLADDFSLYLHAPCVTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 SSLAPEGCGSYYVLAPVPHLGTANLDWTVEGPRLRDRI FBYLEQHYMPGLRSQLVTQRMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPLDIQAKYYSNQGSIYGVVADRFKNLGFKAPQRSSELSNLYFVGGSVNPGGGMPMVTLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 RVIVIGAGLGGLSAAISLATAGFSVQLIBKNDKVGGKLNIMTKDGFTFDLGPSILTMPHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
25.9%; Score 672; DB 2; Length 502
Best Local Similarity 31.5%; Pred. No. 2.6e-44;
Matches 162; Conservative 120; Mismatches 191; Indels
Best Local Similarity 33.3%; Pred. No. 2.5e-45;
Matches 164; Conservative 90; Mismatches 226; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superfamily: phytoene dehydrogenase
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A;Molecule type: DNA
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                                                                                  Cross-references: GB:M38423; NID:g148401; PIDN:AAA24920.1; PID:g148402; Cross-the authors translated the codon CAG for residue 181 as Phe, TCC for residue 187:Note: strain Ehol0; ATCC 39368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDN:AAA21263.1; PID:g148397
Lo the EMBL Data Library, April 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 ALERKSM-----SNSLFVLYFGLNQPHSQLAHHTICFGPRYRELIDBIFTGSALADDFSL 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORFLDYSKNLCTETEAGYFAKG---LDGFWDLLKFYGPLRSLLSFDVFRSMDQGVRRFIS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPKLVEILNYFIXYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGMYGMAQAMEKLAVELG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 VEIRLDAEVSEIQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMEKLL-----RSP 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQLVTQRIFTPADFHDTLDAHLGSAFSIBPLLTQSAWFRPHNRDSDIANLYLVGAGTHPG 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
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                                                                                                                                                                                                                                                                                                                                                                                      2 KKTVVIGAGFGGLALAIRLQAAGIPTVLLEQRDKPGGRAYVWHDQGFTFDAGPTVITDPT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary; nucleic acid sequence not shown; translation not shown Nolecule type: DAA; Residues: 1-492 <LIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tytoene dehydrogenase (BC 1.3.-.-) - Erwinia herbicola
;Species: Erwinia herbicola
;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 29-Sep-1999
                                                                                                                                                                                                                                                                                                                                                              7 QRVIVIGAGEGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSILTMPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     356 YLVAPCKTDPAQAPAGCEIIKILPHIPHLDPDKLLTABDYSALRERVLVKLERMGLTDLR
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                          Length 492;
                                                                                                                                                                                                                                                                  Query Match
29.6%; Score 770; DB 2; Length 492
Best Local Similarity 34.7%; Pred. No. 6.1e-52;
Matches 174; Conservative 93; Mismatches 213; Indels
                                                                                                                                                                           ;Gene: crt1
;Superfamily: phytoene dehydrogenase
;Keywords: carotenoid biosynthesis; oxidoreductase
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NOCe: the nuclectide sequence was submitted
Superfamily: phytoene dehydrogenase
*Reywords: oxidoreductase
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                Status: preliminary
Molecule type: DNA
Residues: 1-492 <ARM>
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DB 2; Length 492;

26.4%; Score 685;

Query Match

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Gaps

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Length 502;

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Ring, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, f. Reineady, S.P.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
Aptuthors: Hou, S.; Daniells, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L. A; Reference number: A84160; MUID:20504483; PMID:11016950
A; Accession: H94320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-512 <STO>
A.Residues: 1-515 <STO>
A.Cross-references: GB:AE004437; NID:g10581152; PIDN:AAG19932.1; GSPDB:GN00138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 EBFFASFDSHPSDYYGLIRLDPHYRIFFKDNBGRRPGRDAPGLAVDTDGDTIDVTPDREQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------DGSVIDLCEDAET 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----WDLLKFYG 160
                                                                         PAQAPAGCEIIKILPHIPHIDPDKULTAEDYSALRERVI,VKLERMGLTDLRQHIVTEEYW 424
300 RRMSNSLFVLYFGIANHHDQLAHHTVCFQPRYRELIDEIFNHDGLAEDFSLYLHAPCVTD
                                                                                                                                                                                                      C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 VKQVFDAYEPGAGDVLDDYLAQAKE-----NYEVGMEHFVKTDRPRVRDWMDPKLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 VAVIGAGPGGLSTACYLADAGADVTVVEKTDQIGGRASTLERDGFRFDMGPSWYLMPDVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 LWYVKGGMYGMAQAMEKLAVELGVEIRLDABVSEIQKQDGRACAVKLAN--GDVLPADIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSNMEVI PAMEKLL ----RSPASELKKMORFEPSCSGLVLHLGVDRLYPQLAHHNFFYSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DWDTHFAQIFDDPAWPDDFAYYLCVPSKTDDTVAPDGHSNLFALVPVAPGLD-DTPAVRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 PIRSILSEDVFRSMDQGVRRFISDPKIVEILNYFIKYVGSSPYDAPALMNLLPYIQYHYG
                                                                                                     SSLAPEGCGSYYVLAPVPHLGTANLDMTVEGPKLRDRIFAYLEQHYMPGLRSQLVTHRMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 VIVIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSILTMPHIF
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                                                                                                                                                                       TPLDIQAKYYSNQGSIYGVVADRFKNLGFKAPQRSSELSNLYFVGGSVNPGGGMPMVTLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.5%; Score 662.5; DB 2; 32.4%; Pred. No. 1.5e-43; ive 81; Mismatches 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 EALFIGAGKNMADYVQIQKVEPHWRNFFE-----
                                                                                                                                                                                                                                                                             GQLVRDKIVADL 496
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AKATAGLMLEDL 491
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wes 169; Conserv
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Best Local S:
Matches 169
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A,Gene: crt11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E Misawa, N.; Nakagawa, M.; Kobayashi, K.; Yamano, S.; Izawa, Y.; Nakamura, K.; Harashim Bacteriol. 172, 6704-6712, 1990
I. Bacteriol. 172, 6704-6712, 1990
I. Tifler Elucidation of the Erwinia uredovora carotenoid biosynthetic pathway by function, Reference number: A37802; MUID:91072214; PMID:2254247
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                                                                   LAVELGVEIRLDAEVSE--IQKQDGRACAVKLANGDVIPADIVVSNMEVIPAMEKLIRSP 295
                                                                                                                                                                                                                                                             ASELK----KMORFEPSCSGLVLHLGVD-RLYPQLAHHNFFYSDHPREHFDAVFKSHRLS 350
                                                                                                                                                                                                                                                                                                                                                                                                                               351 DDPTIYLVAPCKTDPAQAPAGCEIIKTLPHIPHLD-----PDKLLTAEDYSALRERVL 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKLERMGL-TDLRQHIVTEEYWTPLDIQAKYYSNQGSIYGVVADRFKNLGFKAPQRSSEL 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             405 RKIATIEVFEDIKSHIVSETIFTPNDFEQTYHAKFGSAFGLMPTIAQSNYYRPQNVSRDY 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPALAGKOLKEYVELLPVTPFYRLCWESGKVFNYDNDQTRLEAQIQQFNPRDVEGYRQPL 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DYSRAVFKE---GYLKLGTVPF---LSPRDMLRAAPQLAKLQAWRSVYSKVASYIEDEHL 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Species: Erwinia uredovora
Jacte: 31-May-1991 #sequence_revision 31-May-1991 #text_change 20-Jun-2000
;Accession: D37802
                                                                                                                                VRRFISDPKLVEILMYFIKYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGMYGMAQAMBK
                                                                                                                                                                                                                                                                                                                                                           290 APIKKYPPEKIADLDYSCSAFLMYIGIDIDVTDQVRLHNVIFSDDFRGNIEZIFEG-RLS
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N.Molecule type: DNA
N.Residues: 1-492 <MIS>
N.Kresidues: 1-492 <MIS>
N.Cross-references: GB:D90087; NID:g216681; PIDN:BAAi4127.1; PID:g216685
N.Staywords: phytocene dehydrogenase
N.Staywords: oxidoreductase
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Best Local Similarity 32.7%; Pred. No. 3e-44;
Matches 161; Conservative 89; Mismatches 230; Indels
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                                                                                                                                                                                                                                                       Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And Reference number: AB1807; MUID:21595285; PMID:11759840 Accession: AG2509
                                                                                                                                                                                                   Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
lakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
B. Res. B., 205-213, 2001
                                                                                                                     (strain PCC 7120) plasmid pCC7120alpha
                                                                                                              ita-carotene desaturase [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC71
Species: Nostoc sp. PCC 7120
Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
Accession: AG2509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                         Cross-references: GB:BA000020; PIDN:BAB78339.1; PID:g17135793; GSPDB:GN00180
Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTIYLVAPCKTDPAQAPAGCEIIKILPHIPH----LDPDKLLTAEDYSALRERVLVKLER 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIFBALFTGAGKOMADYVQIQKVEPHWRNFFBDGSVIDLCEDAETQRRELDKLGPGTYAQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLAVELGVEIRLDABVSEIQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMEKLLRSPA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEL---KAWARFEPSCSGLVLHLGVDRLYPQLAHNFFYSDHPREHFDAVFKSHRLSD-D 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 RGRYTDNKLGQMQPSCSTFMLXLGINRRYEDLPHHQIYLSDNIRRLERPWVDDSALDETD 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 NORVIVIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSILTMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKKVAIVGAGPGGLATAIRLAGLGYQVRIFEAABRVGGRMRGFBVDSYAFDTGPTILQLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVRRFISDPKLVEILNYFIKYVGSSPYDAPALMNLLPYIQYHYGLWYVXGGMYGMAQAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGLTDLRQHIVTEEYWTPLDIQAXYYSNQGSIYGVVADRFKNLG-FKAPQRSSELSNLYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 25.2%; Score 654; DB 2; Length 49; Local Similarity 32.2%; Pred. No. 6.5e-43; es 158; Conservative 112; Mismatches 187; Indels
                 KAPQRSSELSNLYFVGGSVNPGGGMPMVTLSGQLVRDKIVAD 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: phytoene dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGGSVNPGGGM 478
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IGGAVHPGSGL 476
                                                                                                                                                                                                                                                                                                                     Status: preliminary
Molecule type: DNA
Residues: 1-499 <KUR>
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Matches
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sta-carotene desaturase - Anabaena sp. (strain PCC 7120) :Species: Anabaena sp.

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desaturase: funct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIIYLVAPCKTDPAQAPAGCEIIKILPHIPH----LDPDKLLTAEDYSALRERVLVKLER 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FORFLDYSKULCTETEAGYF----AKGIDGFW---DILKFYGPIRSILSFDVFRSMDQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGLTDLRQHIVTREYWTPLDIQAKYYSNQGSIYGVVADRFKNLG-PKAPQRSSELSNLYP 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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NyAlternate names: phytoene desaturase
Cispecies: Phycomyces blakesleeanus
Cispecies: Phycomyces blakesleeanus
Cispacesion: 843139
R;RularHidalgo, MJ.
R;RularHidalgo, MJ.
A;Reference number: 843139
A, Variety: PCC 7120
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C; Accession: $43324; $6231, $62324
A; A; Accession: $43324; MUD: 94154256; PMID: 8111038
A; Accession: $43324
A; Molecule type: DNA
A; Residues: 1-499 < LIN>
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Bur. J. Biochem. 236, 115-120, 1996
A;Title: Blochemical characterization of purified zeta-carotene desaturase
A;Reference number: S62214; MUID:96184887; PMID:8617254
A;Accession: S62214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HIFEALFTGAGKNMADYVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGPGTYAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 KLAVELGVEIRLDAEVSEIQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMBKLLRSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 NORVIVIGAGLGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSILTMP
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:D26095; NID:g439477; PIDN:BAA05091.1; PID:g439478
A;Experimental source: PCC7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.1%; Score 653; DB 2; Length 499; Best Local Similarity 32.4%; Pred. No. 7.8e-43; Matches 159; Conservative 109; Mismatches 189; Indels
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Gaps

38;

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C;Accession: T48646
R;Ehrenshaft, M.; Daub, M.E.
Appl. Environ. Microbiol. 60, 2766-2771, 1994
A;Title: Isolation, sequence and characterization of the Cercospora nicotianae phytoene A;Teterence number: Z24498; MJID:94368091; PMID:8085820
                                                                                                                                                                                                                                                                                                                                    SMDQGVRRFISDPKLVEILNYFIKYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGMYGMA 232
                                                                                                                                                                                                                                                                                                                                                                QAMEKLAVELGVEIRLDAEVSEIQKQDGRACAVKLANGDVLPADIVVSNMEVIPAMEKLL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 RSPASELKK-----MORPEPSCSGLVLHLGVDRLYPQLAHHNFFYSDHPRE-HPDAVFKS 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HRLSDDPTIYLVAPCKTDPAQAPAGCEIIKILPHIPHLD-PDKLLTAEDYSALRERVLVK 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356 HVDLBDPPFYVCNPGVTDPSGAPAGHSTLYVLVPTPNTGRPVDWVKTE--QALRERIPAM 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 AQPQRFLD-----YSKNLCTETEAGYFAKGLDGFWDLLKFYGP--LRSLLSFDVFR 172
                                                                                                                                                                                                                                                                   LERMGLTDLRQHIVTERYWTPLDIQAKYYSNQGSIYGVVADRFKNLGFKAPQ-RSSELSN 464
                                                                                                                                     64 MPHIFEALFTGAGKNMADYVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGPGTY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A gene: PDH1

C;Function: <PDH2>
A;Description: <PDH2>
A;Description: <PDH2>
A;Description: <PDH2>
A;Description: dehydrogenation of phytoene
A;Description: dehydrogenation of phytoene
A;Description: dehydrogenation of phytoene
C;Superfamily: phytoene dehydrogenase
C;Superfamily: phytoene dehydrogenase
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Species: Cercompora nicotianae
C.Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 IVIGAGLGGLSAAISLATAGFSVQLIBKNDKVGGKLNIMTKDGFTFDLGPSILTMPHIFE
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                                           7 ORVIVIGACICCUSAAISLATAGFSVQLIBKNDKVGGKLNIMT---KDGFTFDLGPSILT
                                                                          A;Cross-references: EMBL:U03903; NID:g433144; PIDN:AAB86988.1; PID:g433145
A;Experimental source: ATCC 18366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phytoene dehydrogenase (EC 1.-.-.) [validated] - Cercospora nicotianae
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155; Conservative 110; Mismatches 208; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: T48646
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-621 <EHR>
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es 162; Conserv
                                                                                                                                                                                                                                                                                                                                                                                          176
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3. MDO J. 12, 1265-1275, 1993
4. Title: Growth phase dependence of the activation of a bacterial gene for carotenoid
4. Acterance number: S35306; MJID:93223667; PMID:8467787
4. Accession: S35306
4. MJD:94. Company of the activation of a bacterial gene for carotenoid
4. Maccession: B35306
4. Maccelle type: DNA
4. Residues: 1-529 < FONA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 LKKMORFEPSCSGLVLHLGVDRLYPQLAHHNFFYSDHPREHFDAVFKSHRLSDDPTIYLV 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 TNTLAEKKLTSSSISFYWSLKRVVPELDVHNIFLAEAFKESFDEIFTDHWAFELSFYVN 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 APCKIDPAQAPAGCEIIKILPHIPHLDPDKLLTAEDYSAL----RERVLVKLE-RMGLTD 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414 LROHIVTEEYWTPLDIOAKYYSNOGSIYGVVADRFKNLGFKAPORSS--BLSNLYFVGGS 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419 FIDLVEHEEVNDPSIWOKKFNLWRGSILGLSHDVLQVLWFRPSTQDSTGRYKNLFFVGAS 478
                                                                                                                                                                                                                                                                                                                                                                                                                                             67 IPEALFTGAGKNMADYVQIQKVEPHWRNPFEDGSVIDLCEDAETQRRELDKL-GPGTYAQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORFLDYSKNLCTETEAGY --- PAKGLDGFWDLLKF-YGPLRSILSFDVFRSMDQGVRRF 181
                                                                                                                                                                                                                                                                                                                                                                             phytoene dehydrogenase (EC 1.3.-.-) - Myxococcus xanthus
N.Alternate names: phytoene desaturase
Nyxococcus xanthus
S.Jbate: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 29-Sep-1999
                                                                                                                                                                                                                                                                                                                                                7 ORVIVIGACIGGLSAAISLATAGFSVOLIEKNDKVGGKLNIMTKDGFTFDLGPSILTMPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 ISDPKLVEILNYFIKYVGSSPYDAPALMNILPYIQYHYGLWYVKGGMYGMAQAMEKLAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 -LGVEIRLDAEVSEIQXQD--GRACAVKLANGDVLPADIVVSNMEVIPAMEKLLRSPASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: EMBL:M94727; NID:g150079; PIDN:AAA25390.1; PID:g150080
                                      .;Status: preliminary
.;Modecule type: DNI
.;Redidues: 1-583 <RUI.>
.;Cross-references: EMBL:X78434; NID:g468556; PIDN:CAA55197.1; PID:g468557
                                                                                                                                                                                                                                          Query Match 24.7%; Score 641.5; DB 2; Length 583; Best Local Similarity 31.3%; Pred. No. 7.6e-42; Matches 157; Conservative 100; Mismatches 223; Indels 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             638; DB 2;
No. 1.2e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 479 THPGTGVPIVLAGSKLTSDQV 499
                                                                                                                                                                       Superfamily: phytoene dehydrogenase; Keywords: oxidoreductase
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Best Local Similarity
            Accession: S43139
                                                                                                                                                       Introns: 197/2
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Length 621;

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phytoene dehydrogenase [imported] - Rubrivivax gelatinosus C;Species: Rubrivivax gelatinosus C;Species: Rubrivivax gelatinosus C;Species: Rubrivivax gelatinosus C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000 C;Accession: T50910 F8;Pogashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K. submitted to the EMBL Data Library, November 1999 Appecraption: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photosynt A;Reference number: 225270 A;Accession: T50910
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                                                                                                                                                                                                                                                                                                                                                              460
                                                                                                                                                                           VVVNADDLVYTYNNLJDPKEIGGIKKYANKLNNRKASCSSISFYWSLSGMAKELETHNIFLA 347
                                                                                                                                                                                                                                   DHPREHFDAVFKSHRLSDDPTIYLVAPCKTDPAQAPAGCE-IIKILP--HI----PHLD 385
                                                                                                                                                                                                                                                            386 PDKLLTAEDYSALRERVLVKLE-RMGLTDLRQHIVTERYW-TPLDIQAKYYSNQGSIYGV 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M-READQC--YELGFRILGDKAFDIVGDLIK-AAPL--IVKLRGWRSLHQMVSSHLKHPK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246
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                        227
                                                                224 VKGGMYGMAQAMEKLAVELGVEIRLDAEVSEIQKQDG-----RACAVKLANGDVLPADI 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALFTGAGKNMADYVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKLGFGTYAQFQRF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDYSKNICTETEAGYPA---KGLDGFWDLLKFYGPLRSLLSFDVFRSMDQGVRRFISDPK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLDAEVSZIOKODGRACAVKLANGDVLPADIVVSNMEVIPAMEKLL----RSPASELKKM 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERGHYSMGLFVWYFGTDRRYEDVPHHMWVLGPRYRELLDDIPRKKKKLASDPSIYLHRPTA 374
                                                                                                      PRGGFHKVLDALVKIGERMGVXYRLNTGVSQVLTDGGKNGKKPKATGVQLENGEVLNADL
                                                                                                                                                   VVSNMEVIPAMEKLLRSPASELK----KMORFEPSCSGLVLHLGVDRLYPQLAHHNFFYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 IVIGACLGGLSAAISLATAGFSVQLIEKNDKVGGKLNIMTKDGFTFDLGPSILTMPHIFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVEILNYFIKYVGSSPYDAPALMNLLPYIQYHYGLWYVKGGMYGMAQAMEXCLAVELGVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               444 VADRPKNIGFKAPQRSSELSNLYFVGGSVNPGGGMPMVTLSGQLVRDKIVAD 495
                                                                                                                                                                                                                                                                                                                                                                                                                            20;
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24.0%; Score 623; DB 2; L
Best Local Similarity 31.1%; Pred. No. 1.7e-40;
Matches 154; Conservative 106; Mismatches 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A)Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-511 - NNG-
A,Cross-references: EMBL:AB034704; PIDN:BAA94063.1
A,Experimental source: strain IL144
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                                                                                                                                                                                             288
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Species: Neurospora crassa

'Bate: O9-Nov-1990 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000

'Accession: A35919

Schmidhauser, T.J.; Lauter, P.R.; Russo, V.E.A.; Yanofsky, C.

1. Cell. Biol. 10, 5064-5070, 1990

Accession: A35919; MuID:90377195; PMID:2144609

Accession: A35919; MuID:90377195; PMID:2144609

'Accession: preliminary

'Status: preliminary

Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: GB:MS7465; GB:M33867; NID:g168746; PIDN:AA333555.1; PID:g168747; Note: the authors translated the codon CTC for residue 157 as Glu, and GAG for residue sources the authors processes as sources as Glu, and GAG for residue skeywords: transmembrane process.
                                                                                                                                                                           245
                                                                                                                                                                                                      KTDPAQAPAGCBIIKILPHIPHL-----A 392
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        ALFTGAGKNM-ADYVQIQKVEPHWRNFFEDGSVIDLCEDAETQRRELDKL-GPGTYAQFQ 127
                                 RIFAELGTSLEQEGVXLLKCEPNYMIHFSDGEKFTLSSDLSVMKTEVEKWEGKEGYTRYL 130
                                                                                         185
                                                                                                                                 131 EFLKESHGHYELSVREVLLRNFBGLTAMLR---ÞEFLRHLLQLHPFESIWTRAGKYFWTE 187
                                                                                                                                                                                                                                                            246 IRLDAEVSEI--QKQDGRACAVKLANGDVLPADIVVSNMEVIPAMEKLL--RSPASELKK 301
                                                                                                                                                                                                                                                                                                    3.07
                                                                                                                                                                                                                                                                                                                                            302 MORFEPSCSGLVLHLGVDRLYPQLAHHNFFYSDHPREHFDAVFKSHRLSDDPTIYLVAPC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       366 RVDSTAAPEGKDSVVVLVPVGHLLEEDRHASQAHQLSASRNGHISSASPPDQPGLTPTEK 425
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                                                                                                                                                                                                                                                                                  GR--PGSCSSISFYWALDRQVPELRAHNIFLADEYRESFDSIFKGGLIPDBEPSFYNWPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFLDYSKNLCTETEAGYPAKGLDGFWDLLKFYGP--LRSLLSFDVFRSMDQGVRRFISDP
                                                                                                                                                                           KLUBILNYFI KYVGSSPYDAPALMNLLPYJQYBYGLWYVKGGMYGMAQAMEKLAVELGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BDYSAL ----RERVLVKLERMGLTDLRQHIVTEEYWTPLDIQAKYYSNQGSIYGVVADRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SELSNLYFVGGSVNPGGG
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24.0%; Score 624.5; DB 2; Length 5
Best Local Similarity 29.7%; Pred. No. 1.6e-40;
Matches 158; Conservative 110; Mismatches 201; Indels
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⁴⁸¹ VTLSGQLVRDKIVAD 495 | :| : : : | 492 VIMSAKAL-ESVLPD 505

earch completed: February 29, 2004, 14:52:41 lob time : 15.8338 secs